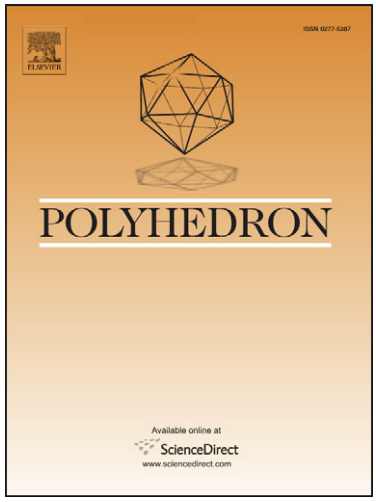
Accepted Manuscript



The difference one ligand atom makes – an altered oxygen transfer reaction mechanism caused by an exchange of selenium for sulfur

Carlos Enrique Abad Andrade, Xiaoli Ma, Wolfram Meyer-Klaucke, Carola Schulzke

PII: S0277-5387(09)00683-4
DOI: 10.1016/j.poly.2009.10.018
Reference: POLY 8102

To appear in: *Polyhedron*

Received Date: 25 April 2009
Accepted Date: 21 October 2009

Please cite this article as: C.E.A. Andrade, X. Ma, W. Meyer-Klaucke, C. Schulzke, The difference one ligand atom makes – an altered oxygen transfer reaction mechanism caused by an exchange of selenium for sulfur, *Polyhedron* (2009), doi: 10.1016/j.poly.2009.10.018

This is a PDF file of an unedited manuscript that has been accepted for publication. As a service to our customers we are providing this early version of the manuscript. The manuscript will undergo copyediting, typesetting, and review of the resulting proof before it is published in its final form. Please note that during the production process errors may be discovered which could affect the content, and all legal disclaimers that apply to the journal pertain.

ACCEPTED MANUSCRIPT

The difference one ligand atom makes – an altered oxygen transfer reaction mechanism caused by an exchange of selenium for sulfur

Carlos Enrique Abad Andrade,[a] Xiaoli Ma,[b] Wolfram Meyer-Klaucke,[c] Carola Schulzke,[d]*

[a] Institut f. Anorganische Chemie, Universitaet Goettingen, Tammannstr. 4, D-37077 Goettingen, Germany

[b] School of Chemical Engineering and Environment, Beijing Institute of Technology, Beijing 100081, China

[c] European Molecular Biology Laboratory (EMBL), Outstation Hamburg at DESY, Notkestr. 85, D-22603 Hamburg, Germany

[d] School of Chemistry, Trinity College Dublin, Dublin 2, Ireland, FAX +49-551-393373, email: schulzkc@tcd.ie

Keywords

metalloenzymes, molybdenum, ligand effects, EXAFS spectroscopy, catalysis

Abstract

The influence of sulfur versus selenium coordination to molybdenum on the oxo transfer reaction mechanisms of functional models for oxidoreductases has been studied. The solution structure of the dimeric molybdenum compound with tridentate bis-anionic ligands containing a thioether function ($^{-}O(CH_2)_3S(CH_2)_3O^{-}$) has been determined using EXAFS spectroscopy to be able to compare a feature of its solution structure to that of its selenoether analogue. A significant difference is found for the solution structures of the two compounds. The thioether group remains coordinated in solution, whereas the selenoether does not. The influence of this difference on the catalytic oxo transfer has been investigated in detail by following the catalytic transition of PPh_3 to $OPPh_3$ with DMSO as oxygen donor with variation of both substrate concentrations.

ACCEPTED MANUSCRIPT

ACCEPTED MANUSCRIPT

Introduction

Molybdenum cofactors are the central parts of enzymes that catalyse oxidation or reduction processes. This usually involves the transfer of two electrons with (the majority) and without an accompanying oxygen atom (O^-) transfer as part of the carbon, nitrogen and sulfur metabolisms.[1,2] In the DMSO reductase family[2] the active site metal molybdenum is bonded directly to the peptide through an amino acid residue being either serinate (alcoholate function)[3], aspartate (carboxylate function)[4], cysteinate (thiolate function)[5] or even the rare selenocysteinate (selenolate function)[6].

The main role of the amino acid coordination is thought to be the stabilization of enzyme substrate complexes. For most enzymes it is not known though, if the different types of amino acids are used randomly or if they are specific and important for each enzyme's reactivity. One particularly interesting case is the direct involvement of a cysteinate residue in bond making and bond breaking in periplasmic nitrate reductases which was revealed by crystallographic studies of two enzymes.[7] In general, however, there seems to be no strict correlation between the kind of atom that is to be oxidized or reduced and the coordinated amino acid. For instance the oxidation of carbon is achieved by active sites with selenocysteinate (formate dehydrogenase from *E. coli*)[6] or cysteinate (formate dehydrogenase from *W. succinogenes*)[1,2,8] coordination. Sulfur is processed by active sites with serinate (DMSO reductase from *R. sphaeroides*)[3a,b] or cysteinate (polysulfide reductase from *W. succinogenes*)[9] coordination. Furthermore the reduction of nitrogen is catalysed by active sites with cysteinate (nitrate reductase from *E. coli*)[10], aspartate (nitrate reductase from *P. pantotrophus*)[4] or serinate coordination (trimetylamine N-oxide reductase from *S. massilia*)[11].

High-valent metal complexes with thioether or selenoether ligands representing hard-soft metal ligand combinations are relatively rare mainly because these compounds are rather unstable.[12] A benefit of this kind of sulfur or selenium ligand is its inertness towards oxidation by metals in high oxidation states. Even though the ether type sulfur or selenium function is different from the thiolate or selenolate functions of the amino acid residues coordinated to the active site metals of the enzymes, they allow the study of differences in properties caused by an exchange of sulfur by the larger, softer selenium with a more metallic character.

ACCEPTED MANUSCRIPT

Recently the influence of sulfur coordination versus selenium coordination on the oxo transfer properties of a specific pair of molybdenum complexes ($[Mo_2O_4(OC_3H_6XC_3H_6O)_2]$ with X = S, Se) has been investigated.[12] The respective S-Mo complex is depicted in figure 1.

In this particular case the selenium complex was the better oxo transfer catalyst compared to the sulfur complex although both performed less efficiently than other known molybdenum based oxo transfer catalysts[13-18]. The slowness of the reactions, however, provided the opportunity to investigate them in detail. Most interesting was the indication that two different reaction mechanisms were active for both otherwise very similar compounds: firstly the characteristics of the development of product with time graphs were different; secondly the sulfur compound reacted with only the oxo accepting substrate while the selenium compound did not; thirdly the Lineweaver-Burke plots showed an about tenfold increase for the maximum velocity of the selenium catalyst while the Michaelis type constants were almost identical; finally ^{77}Se-NMR spectroscopy showed that the Mo-Se bond in solution no longer exists. To determine the solution structure of the sulfur compound was not possible at that time. Furthermore, though the catalytic properties of both compounds were investigated in comparison the specific, presumably distinct, reaction mechanisms were not evaluated. To gain more information about the sulfur compounds' structure in solution it has now been investigated with X-ray absorption spectroscopy (XAS) on the molybdenum K-edge. Because the results revealed the existence of a major difference between the solution structures of both compounds further catalytic investigations have been undertaken in order to determine the reaction mechanisms in greater detail.

Results and discussion

XAS spectroscopy

The experimental x-ray absorption spectrum is divided into two parts: the normalized edge region named X-ray absorption near edge structure (XANES) and the extended x-ray absorption fine structure (EXAFS). Whereas, the XANES serves as a fingerprint for the absorber atom environment and only in a limited number of cases structural information can be extracted, the EXAFS region provides detailed information on type, distance and number of atoms in the environment of the absorber atom. The

ACCEPTED MANUSCRIPT

molybdenum K edge XANES spectrum of $[Mo_2O_4(OC_3H_6SC_3H_6O)_2]$ (Fig. 2) is that of a typical molybdenum(VI) dioxo moiety with respect to shape and pre-edge feature which is caused by a molybdenum 1s → (M=O)π* transition. The height of this feature corresponds to the number of terminal oxo ligands. In the present case it is very similar to that in the spectra of oxidized active sites of enzymes of the sulfite oxidase family and of the CO dehydrogenase with only one molybdopterin ligand and two oxo ligands in a *cis* arrangement.[19-23] The experimental EXAFS (extended X-ray absorption fine structure) spectrum was initially fitted with the X-ray crystallography data[12] taking into account all six atoms directly coordinated to the molybdenum, the second molybdenum and the second sulfur (Fig. 3). The refinement of all distances resulted in slightly smaller values compared to the X-Ray data (see also table 1 in the experimental part). The sulfur atom was fitted to an EXAFS distance of 2.78 ± 0.02 Å (X-ray distance 2.80 Å). The spectrum was also fitted without the sulfur atom. A comparison of the EXAFS spectrum and its FT from experiment and the fits with and without sulfur is shown in Fig. 3. In the absence of the sulfur backscattering contribution the quality of the fit decreased, which is quantified by an increase of the fit index from 0.721 to 0.920. Within the error margins of about 20% for coordination numbers resulting from ab initio EXAFS data analysis variations of this sulfur contribution are compensated by changes in the Debye-Waller factors. Outside this range the refinement becomes worse. Thus a major fraction lacking the sulfur ligand can be excluded. It can therefore be concluded that in the shock frozen solution of $[Mo_2O_4(OC_3H_6SC_3H_6O)_2]$ the molybdenum sulfur bond is still intact. This is a significant difference to the analogous selenium compound $[Mo_2O_4(OC_3H_6SeC_3H_6O)_2]$ at which in solution the selenium is not bound to molybdenum as was shown by ^{77}Se-NMR spectroscopy[12]. Although the X-ray structures of both compounds are even isomorphous their solution structures differ. Both the molybdenum thioether and the molybdenum selenoether bond are very weak due to the unfavourable combination of hard metal and soft ligand. Since selenium is the larger and therefore softer element of both its bond in form of a selenoether to the hard molybdenum(VI) centre is even weaker than that of the thioether function and can be more easily disconnected from the metal upon dissolution. In this case it is implied that the difference in bond strengths is in a region where the molybdenum selenium bond gets disconnected upon solvation but not the molybdenum sulfur bond. A difference in Mo-Se and Mo-S bond strengths for sulfido and selenido ligation to

ACCEPTED MANUSCRIPT

molybdenum in the centre of hydroxylases has been evaluated before, showing that the bond between molybdenum and selenium is indeed significantly weaker with implications for the investigated enzyme's active site composition and its catalytic performance.[24] In case of our model compounds it is reasonable to assume a considerable influence of this difference and the subsequent distinction in their solution structure on their behavior for instance in catalytic processes.

Catalytic reaction mechanisms

The model reaction for oxygen transfer catalysis is the oxidation of PR_3 (R = alkyl or aryl) by DMSO which does not occur without a catalyst at room temperature and can conveniently be followed by ^{31}P-NMR spectroscopy.[25] The solution structures of $[Mo_2O_4(OC_3H_6SC_3H_6O)_2]$ and $[Mo_2O_4(OC_3H_6SeC_3H_6O)_2]$ differ considerably with the molybdenum centers of the sulfur compound in a six-fold coordination sphere and the molybdenum of the selenium complex having one free coordination site. Therefore the two substrates for the oxo transfer catalysis necessarily have to approach the catalytically active Mo/Mo=O moiety consecutively in case of the sulfur compound whereas for the selenium compound a concerted mechanism can be envisioned (fig. 4). To probe this, further catalytic experiments were undertaken in which the concentrations of both substrates were varied. In biochemistry the deviation between a reaction mechanism involving the binding of two substrates to the enzyme (sequential) and a consecutive (ping pong) reaction mechanism, in which one substrate is completely converted before the other is bound, would be determined by varying both substrate concentrations. By measuring the initial velocities dependent on the concentrations and comparing the resulting Lineweaver-Burke plots both mechanisms can be distinguished. Since the two molybdenum complexes showed Michaelis-Menton type kinetic behavior this same kind of study has now been undertaken. Lineweaver-Burke diagrams were drawn in which the reciprocal initial reaction velocity was plotted against the reciprocal PPh_3 concentration (fig. 5). For a large excess of the second substrate DMSO, which was simply used as solvent this has been described previously.[12] When changing the concentration of the second substrate (DMSO) as well, the resulting combined Lineweaver-Burke plots look considerably different dependent on the reaction mechanism. The linear graphs in the combined plots need to be parallel to each other in case of a consecutive mechanism

ACCEPTED MANUSCRIPT

but cross each other somewhere to the left of the y-axis in case of a concerted mechanism. Although the resulting combined Lineweaver-Burke plots for the two catalysts (fig. 5) are neither showing perfectly parallel behavior nor cross each other in exactly one point, it is clear that the sulfur compound tends to comply with the parallel alignment whereas the graphs for the selenium compound are crossing each other in a narrow region. The deviation from ideal behavior is owed to the experimental error based on poor solubility of the catalysts and subsequently very low sample concentrations. However, the characteristics of both plots indicate that the reaction mechanism for the sulfur compound is indeed of a consecutive nature involving the binding of only one substrate at a time. Contrarily the approach of the two substrates PPh_3 and DMSO to the selenium compound's molybdenum seems to be more or less simultaneous. This would explain that the selenium compound is a much better catalyst compared to the sulfur complex with respect to rate, though the rate might in addition be influenced by the different redox potentials of both catalysts. Moreover it explains that in the absence of DMSO the selenium compound is unable to deliver its oxo ligand to PPh_3, which would result in an unfavorable four-fold coordination. Interestingly a proposed mechanism for the selenocysteine containing formate dehydrogenase in nature also involves disconnecting selenium from the active site molybdenum which coincides with our observations.[26]

Conclusion

Although even isomorphous in the solid state the solution structures of $[Mo_2O_4(OC_3H_6SC_3H_6O)_2]$ and $[Mo_2O_4(OC_3H_6SeC_3H_6O)_2]$ differ with a considerable effect on their catalytic oxo transfer properties. In contrast to the molybdenum selenium complex the sulfur molybdenum bond is intact in the solid state as well as in solution. This results in the possibility for the former to follow a concerted catalytic oxo transfer reaction mechanism with the simultaneous binding of both substrates while the sulfur compound can only bind one substrate at a time. As a consequence we observe a consecutive reaction mechanism for the sulfur compound and a concerted reaction mechanism for the selenium compound. This confirms that the use of different ligand atoms can have a considerable influence on the catalytic performance of the respective complexes based on small differences in metal-ligand bond strengths although other deviations may be merely subtle. Together with the

ACCEPTED MANUSCRIPT

knowledge about the influence of sulfide vs. selenide coordination to the active sites of the molybdenum hydroxylases this underlines the possibility of a purposeful use of the specific coordinated amino acid residues at the active sites of the enzymes of the DMSO reductase family.

Experimental

Materials

$[Mo_2O_4(OC_3H_6SC_3H_6O)_2]$ and $[Mo_2O_4(OC_3H_6SeC_3H_6O)_2]$ were prepared as described in the literature.[12] Reagent grade CH_3Cl, CH_2Cl_2, DMF, DMSO, DMF-d_7, DMSO-d_6 and CD_2Cl_2 were dried and distilled prior to use. PPh_3 was used as received. All manipulations were performed under a dry and oxygen free nitrogen atmosphere using Schlenk line techniques.

X-ray spectroscopy

$[\{MoO_2(O(CH_2)_3S(CH_2)_3O)\}_2]$ was dissolved in $CHCl_3$ until saturation (ca. 10^{-4} mol/L). Afterwards, the XAS sample was filled into a 25 µl plastic XAS cuvette, shock frozen and stored at cryogenic temperatures. The K-edge molybdenum X-ray absorption spectrum was recorded at the beam line D2 of the EMBL Outstation Hamburg at DESY (Germany). The DORIS storage ring operated at 4.5 GeV with the positron beam current ranging from 145 mA to 80 mA. An Si(311) double-crystal monochromator scanned X-ray energies around Mo K-edge (19.8-20.8 keV). Harmonic rejection was achieved by a focusing mirror (cut-off energy at 21.5 keV) and a monochromator detuning to 50% of its peak intensity. The sample cells were mounted in a two-stage Displex cryostat and kept at about 20 K. The X-ray absorption spectra were recorded as Mo K_α fluorescence spectra with a Canberra 13-element Germanium solid-state detector. Data reduction, such as background removal, normalization and extraction of the fine structure, was performed with KEMP[27] assuming a threshold energy E_0, Mo = 20002 eV. Sample integrity during exposure to synchrotron radiation was checked by monitoring the position and shape of the absorption edge on sequential scans. No changes were detectable.

EXAFS data analysis was performed with Excurve 9.27[28], using the crystal structure of the pure compound as a starting point. All fits were carried out with k^3-weighted

ACCEPTED MANUSCRIPT

data. The resulting fit parameters are given in table 1; the fit range was 20–1000 eV. The FT and chi plots for each scattering pathway and for both models can be found in the supporting information (figures S1 to S32). Slight deviations of the model from the measured EXAFS below k=6Å^{-1} might be due to the absence of multiple scattering contributions via the central atom in our models. Their importance in metalloproteins has been highlighted[29] recently but is here beyond the scope of the analysis.

Table 1: Two structural models compared to the EXAFS data. Only in the presence of a sulfur ligand a good fit can be obtained. In addition to the above mentioned parameters (coordination number N, effective distance *r,* Debye-Waller factor $2\sigma^2$) the energy threshold of each spectrum (Fermi-Energy shift) has been refined to -7±1 eV for model 1 and -6±2 eV for model 2. [a)] For comparison the X-ray distances in the Mo-S complex[12] are given in parentheses. [b)] In order to lower the number of free parameters in the refinement the Debye-Waller factors for similar donor atoms were jointly refined.

sulfur	Assignment	N	*r* / Å [a)]	$2\sigma^2$ / Å$^2 \cdot 10^3$	Fit index
present	O	2	1.670±0.008 (1.70)	5±1	0.721
	O	1	1.811±0.017 (1.89)	2±1[b]	
	O	1	2.013±0.014 (2.04)	2±1[b]	
	O	1	2.235±0.015 (2.23)	2±1[b]	
	S	1	2.784±0.015 (2.80)	6±3	
	Mo	1	3.490±0.013 (3.50)	5±1	
	S	1	3.785±0.044 (3.88)	7±8	
absent	O	2	1.664±0.010 (1.70)	5±2	0.920
	O	1	1.805±0.026 (1.89)	3±4[b]	
	O	1	2.014±0.016 (2.04)	3±4[b]	
	O	1	2.235±0.016 (2.23)	3±4[b]	
	Mo	1	3.488±0.010 (3.50)	6±1	

Catalysis studies

The catalytic experiments were conducted under N_2 atmosphere at 25°C using Schlenk line technique.

ACCEPTED MANUSCRIPT

$[Mo_2O_4(OC_3H_6SC_3H_6O)_2]$ (0.37 g, 0.02 mmol) or $[Mo_2O_4(OC_3H_6SeC_3H_6O)_2]$ (0.43g, 0.666 mmol) and PPh_3 (20.00, 13.33, 10.00, 6.66, 3.33 mmol) were mixed and 20 ml of solvent was added. In order to obtain different molybdenum:DMSO ratios the solvent was a mixture of CH_2Cl_2 and DMSO giving DMSO solutions in CH_2Cl_2 in concentrations of 14.08 $mol \cdot l^{-1}$ (pure DMSO; 20 ml), 7.04 $mol \cdot l^{-1}$ (10 ml DMSO), 3.52 $mol \cdot l^{-1}$ (5 ml DMSO) and 1.76 $mol \cdot l^{-1}$ (2.5 ml DMSO) respectively. 1.0 ml of DMSO or CH_2Cl_2 was deuterated in order to be able to lock the NMR signals. The conversion from PPh_3 to $OPPh_3$ was monitored by ^{31}P-NMR spectroscopy showing no other signal than those for substrate and product. The NMR-samples were taken from the reaction mixtures at different times and returned to the reaction vessel after having been measured.

The obtained data was used to create Lineweaver-Burke plots with linear fitting of the data points. The R^2 values for the linear fits are summarized in table 2.

Table 2: R^2 values for the linear fits of the data points (reciprocal initial reaction velocity versus reciprocal substrate (PPh3) concentration) for both catalysts and different DMSO concentrations.

DMSO concentration	$[Mo_2O_4(OC_3H_6SC_3H_6O)_2]$	$[Mo_2O_4(OC_3H_6SeC_3H_6O)_2]$
14 M	0.99306	0.9398
7 M	0.99919	0.9693
3.5 M	0.99772	0.9937
1.75 M	0.99753	0.9996

References

[1] J. H. Enemark, J. J. A. Cooney, J.-J. Wang, R. H. Holm, *Chem. Rev.* **2004**, *104*, 1175-1200

[2] R. Hille, *Chem. Rev.* **1996**, *96*(7), 2757-2816

[3] a) H. Schindelin, C. Kisker, J. Hilton, K. V. Rajagopalan, D. C. Rees, *Science* **1996**, *272*, 1615-1621; b) G. N. George, J. Hilton, K. V. Rajagopalan, *J. Am. Chem.*

ACCEPTED MANUSCRIPT

Soc. **1996**, *118*, 1113-1117; c) G. N. George, J. Hilton, C. Temple, R. C. Prince, K. V. Rajagopalan, *J. Am. Chem. Soc.* **1999**, *121*, 1256-1266

[4] M. G. Bertero, R. A. Rothery, M. Palak, C. Hou, D. Lim, F. Blasco, J. H. Weiner, N. C. J. Strynadka, *Nature Struct. Biol.* **2003**, *10*(9), 681-687

[5] J. M. Dias, M. E. Than, A. Humm, R. Huber, G. P. Bourenkov, H. D. Bartunik, S. Bursakov, J. Calvete, J. Caldeira, C. Carveiro, J. J. G. Moura, I. Moura, M. J. Romão, *Structure* **1999**, *7*, 65-79

[6] J. C. Boyington, V. N. Gladyshev, S. V. Khangulov, T. C. Stadtman, P. D. Sun, *Science* **1997**, *275*, 1305-1308

[7] a) S. Najmudin, P. J. Gonzalez, J. Trincao, C. Coelho, A. Mukhopadhay, N. M. F. S. A. Cerqueira, C. C. Romao, I. Moura, J. J. G. Moura, C. D. Brondino, M. J. Romao, *J. Biol. Inorg. Chem.* **2008**, *13*, 737-753; b) M. J. Romão, *Dalton Trans.* **2009**, 4053-4068

[8] M. Bokranz, E. Kojoro, F. Fahrenholz, F. Lauterbach, A. Kröger, *Arch. Microbiol.* **1991**, *156*, 119-128

[9] T. Prisner, S. Lyubenova, Y. Atabay, F. MacMillan, A. Kröger, O. Klimmek, *J. Biol. Inorg. Chem.* **2003**, *8*, 419-426

[10] C. S. Butler, J. M. Charnock, C. D. Garner, A. J. Thomson, S. J. Ferguson, B. C. Berks, D. J. Richardson, *Biochem. J.* **2000**, *352*, 859-864

[11] a) M. Czjzek, J. P. Dos Santos, J. Pommier, G. Giordano, V. Mejean, R. Haser, J. Mol. Biol. 1998, 284, 435-447; b) L. Zhang, K. Johnson Nelson, K. V. Rajagopalan, G. N. George, *Inorg. Chem.* **2008***, 47*, 1074 -1078

[12] X. Ma, C. Schulzke, H.-G. Schmidt, M. Noltemeyer, *Dalton Trans*. **2007**, 1773-1780

[13] K. Most, S. Köpke, F. Dall´Antonia, N. C. Mösch-Zanetti, *Chem. Commun.* **2002**, 1676-1677

ACCEPTED MANUSCRIPT

ACCEPTED MANUSCRIPT

[14] A. Majumdar, K. Pal, S. Sarkar, *J. Am. Chem. Soc.* 2006, 128,4196-4197

[15] J. T. Hoffman, S. Einwaechter, B. S. Chohan, P. Basu, C. J. Carrano, *Inorg. Chem.* **2004**, *43*, 7573-7575

[16] F. J. Arnáiz, R. Aguado, M. R. Pedrosa, A. De Cian, J. Fischer, *Polyhedron* **2000**, *19*, 2141-2147

[17] F. J. Arnáiz, R. Aguado, *Polyhedron* **1994**, *13*, 3257-3259

[18] X. Ma, C. Schulzke, Z. Yang, A. Ringe, J. Magull, *Polyhedron* **2007**, *26*, 5497-5505

[19] S. P. Cramer, R. Wahl, K. V. Rajagopalan, *J. Am. Chem. Soc.* **1981**, *103*, 7721-7727

[20] F. W. Kutzler, R. A. Scott, J. M. Berg, K. O. Hodgson, S. Donaich, S. P. Cramer, C. H. Chang, *J. Am. Chem. Soc.* **1981**, *103*, 6083-6088

[21] G. N. George, J. Hilton, C. Temple, R. C. Prince, K. V. Rajagopalan, *J. Am. Chem. Soc.* **1999**, *121,* 1256-1266

[22] C. J. Doonan, U. Kappler, G. N. George, *Inorg. Chem.* **2006**, *45*, 7488-7492

[23] M. Gnida, R. Ferner, L. Gremer, O. Meyer, W. Meyer-Klaucke, *Biochem.* **2003**, *42*, 222-230

[24] N. Wagener, A. J. Pierik, A. Ibdah, R. Hille, H. Dobbek, *Proc. Nat. Acad. Sci.* **2009**, *106*, 11055-11060

[25] J. M. Berg, R. H. Holm, *J. Am. Chem. Soc.* **1985**, *107*, 925-932

[26] H. C. A. Raijmakers, M. J. Romao, *J. Biol. Inorg. Chem.* **2006**, *11*, 849-854

[27] M. Korbas, D. F. Marsa, W. Meyer-Klaucke, *Rev. Sci. Inst.* **2006**, *77*, article number 063105

ACCEPTED MANUSCRIPT

ACCEPTED MANUSCRIPT

[28] R. W. Strange, L. Alagna, P. Durham, S. S. Hasnain, *J. Am. Chem. Soc.* **1990**, *112*, 4265-4268

[29] K. Hollenstein, M. Comellas-Bigler, L. E. Bevers, M. C. Feiters, W. Meyer-Klaucke, P.-L. Hagedoorn, K. P. Locher, *J. Biol. Inorg. Chem.* **2009**, *14*, 663-672

Acknowledgement

Financial support of the DFG (Deutsche Forschungsgemeinschaft) and the DAAD (Deutscher Akademischer Austausch Dienst) is gratefully acknowledged.

ACCEPTED MANUSCRIPT

ACCEPTED MANUSCRIPT

Figure 1: The schematic structure of $[Mo_2O_4(OC_3H_6SC_3H_6O)_2]$ as previously determined by X-ray crystallography.[12]

Figure 2: The molybdenum K near edge spectrum of $[Mo_2O_4(OC_3H_6SC_3H_6O)_2]$.

Figure 3: Experimental chi (top) and FT (bottom) EXAFS spectra of $[Mo_2O_4(OC_3H_6SC_3H_6O)_2]$ and their fits with and without coordinating sulfur.

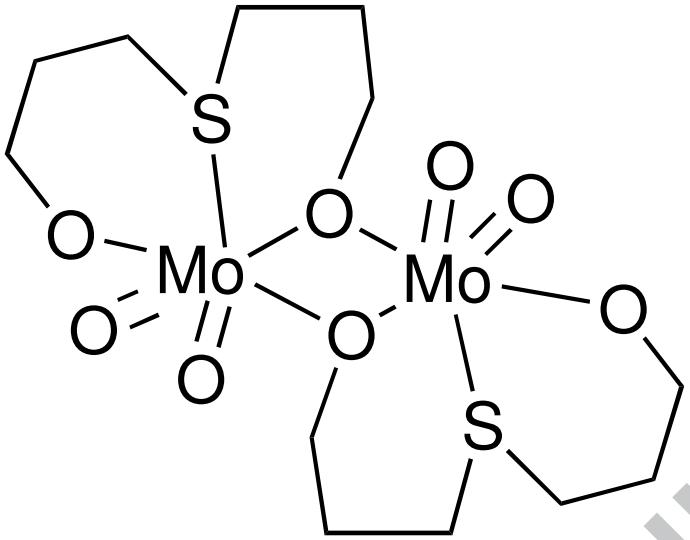
Figure 4: Proposed different reaction mechanisms for the oxo transfer catalysis from DMSO onto PPh_3 for the molybdenum-sulfur catalyst (left) and for the molybdenum-selenium catalyst (right).

Figure 5: Lineweaver-Burke plots for the oxygen transfer catalysis from DMSO onto PPh_3 with the molybdenum-sulfur catalyst (left) and the molybdenum-selenium catalyst (right) with varied PPh_3 and DMSO concentration.

ACCEPTED MANUSCRIPT

ACCEPTED MANUSCRIPT

Fig .1



ACCEPTED MANUSCRIPT

ACCEPTED MANUSCRIPT

Fig .2

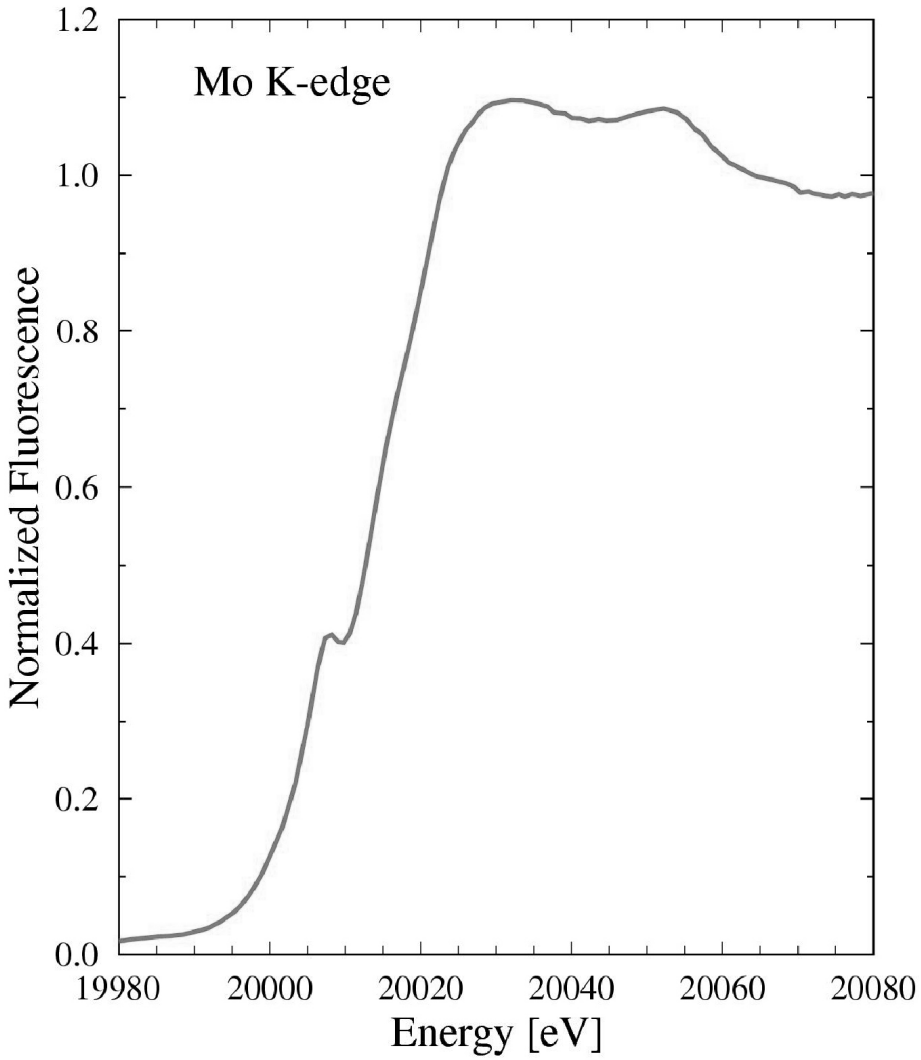
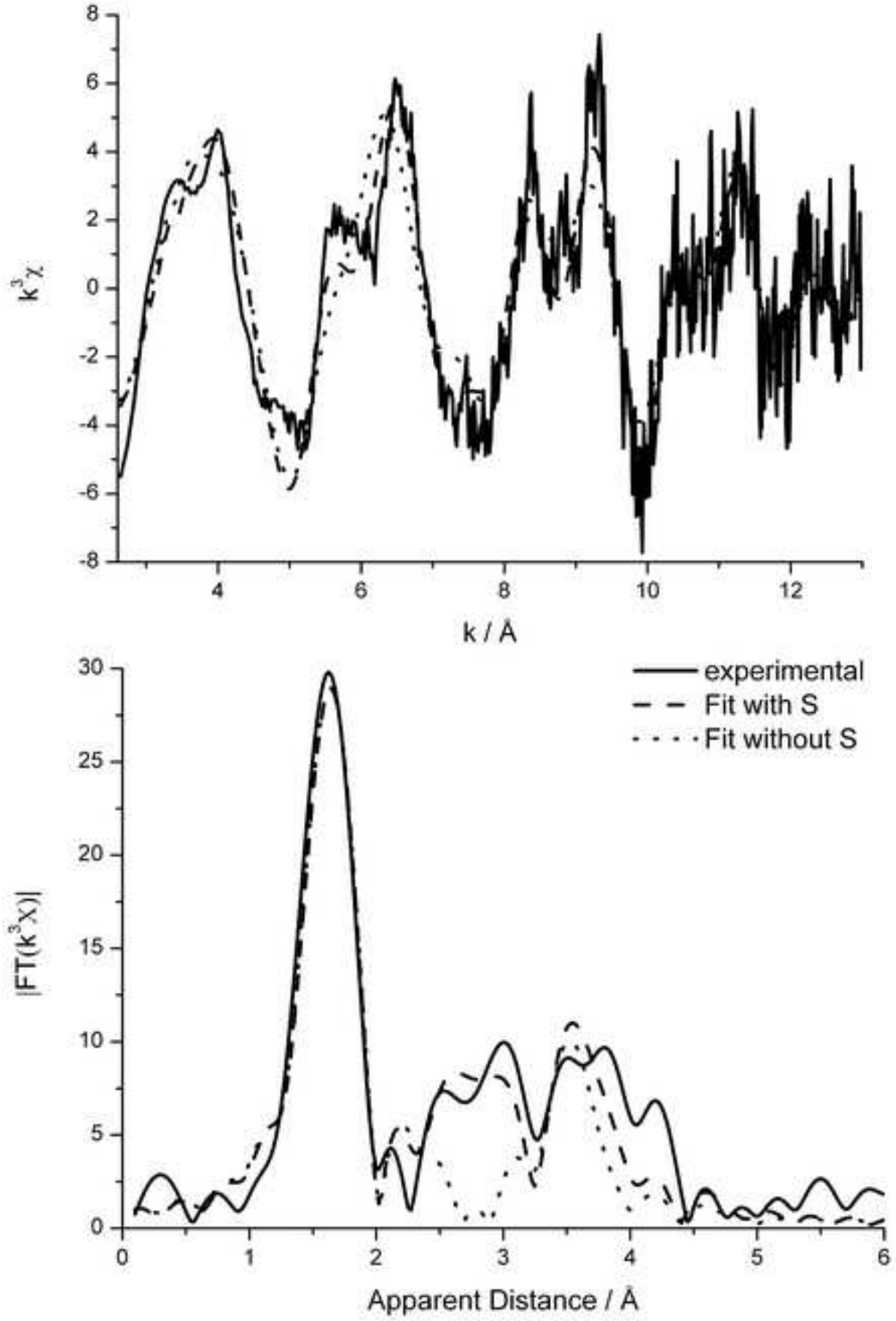


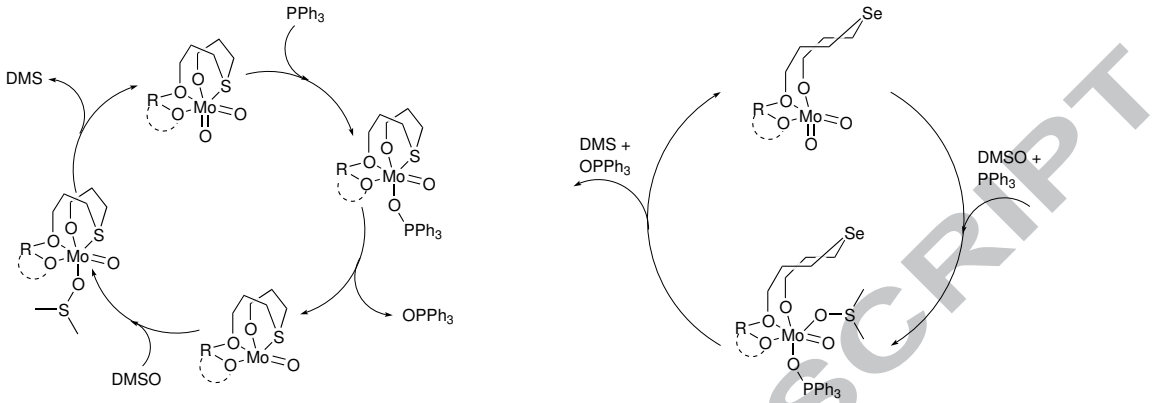
Figure 3

ACCEPTED MANUSCRIPT



ACCEPTED MANUSCRIPT

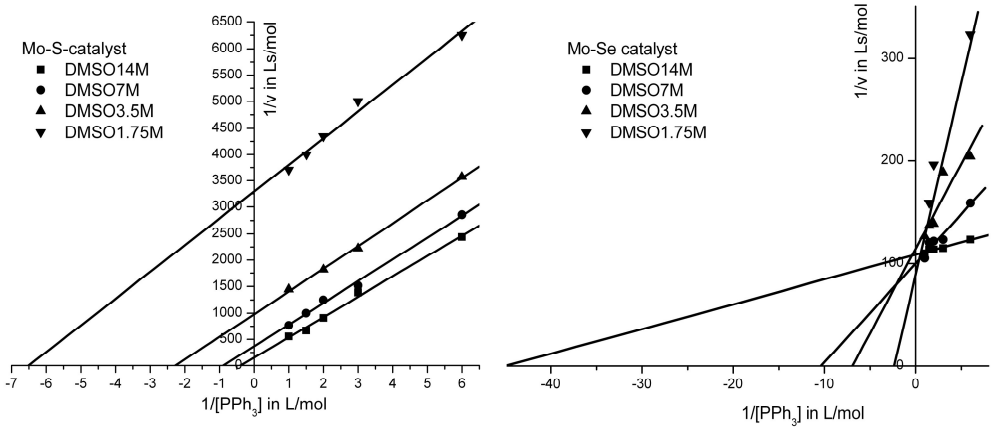
Fig .4



ACCEPTED MANUSCRIPT

ACCEPTED MANUSCRIPT

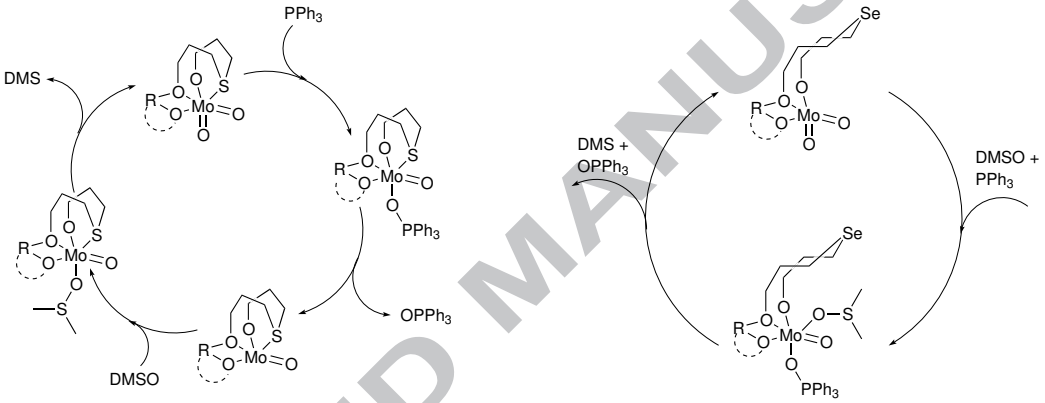
Fig .5



ACCEPTED MANUSCRIPT

Graphical abstract

A thioether versus a selenoether function coordinated to molybdenum is shown to be responsible for the complexes to follow different oxo transfer reaction mechanisms in catalysis, even though the interactions between metal and ligand are only weak and other complex properties are almost identical. A change in size and softness can have a considerable catalytic effect which may be relevant for amino acid coordination to active site metals as well.



ACCEPTED MANUSCRIPT