



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 18, 2026 – 07:09 AM UTC

PDB ID : 8IQ1 / pdb_00008iq1
Title : Crystal structure of hydrogen sulfide-bound superoxide dismutase in reduced state
Authors : Zhou, J.H.; Huang, W.X.; Cheng, R.X.; Zhang, P.J.; Zhu, Y.C.
Deposited on : 2023-03-15
Resolution : 1.80 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

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A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

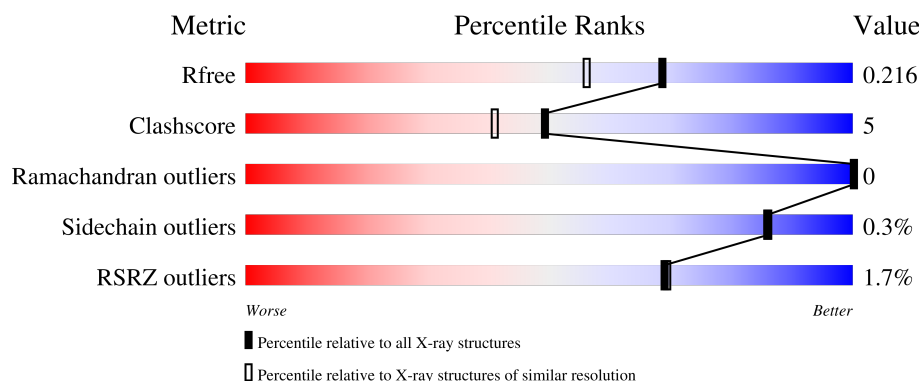
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.80 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	7662 (1.80-1.80)
Clashscore	190562	8479 (1.80-1.80)
Ramachandran outliers	187476	8391 (1.80-1.80)
Sidechain outliers	187428	8390 (1.80-1.80)
RSRZ outliers	180081	7663 (1.80-1.80)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	151	 3% 93% 6%
1	B	151	 0% 90% 9%
1	C	151	 2% 95% 5%
1	D	151	 0% 91% 9%
1	E	151	 0% 92% 8%

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Mol	Chain	Length	Quality of chain
1	F	151	% 92% 8%
1	G	151	5% 91% 7%
1	H	151	% 90% 9%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	EDO	F	206	-	-	X	-
4	EDO	H	205	-	-	X	-
4	EDO	H	206	-	-	X	-
7	CL	E	204	-	-	X	-

2 Entry composition [i](#)

There are 9 unique types of molecules in this entry. The entry contains 9897 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Superoxide dismutase [Cu-Zn].

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	151	Total	C	N	O	S	0	0	0
			1076	661	194	217	4			
1	B	151	Total	C	N	O	S	0	1	0
			1078	661	196	216	5			
1	C	151	Total	C	N	O	S	0	1	0
			1081	663	195	218	5			
1	D	151	Total	C	N	O	S	0	1	0
			1082	664	197	216	5			
1	E	151	Total	C	N	O	S	0	1	0
			1084	665	196	218	5			
1	F	151	Total	C	N	O	S	0	1	0
			1086	666	197	218	5			
1	G	148	Total	C	N	O	S	0	0	0
			1055	649	188	214	4			
1	H	151	Total	C	N	O	S	0	1	0
			1080	662	194	219	5			

- Molecule 2 is COPPER (II) ION (CCD ID: CU) (formula: Cu).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Cu	0	0
			1	1		
2	B	1	Total	Cu	0	0
			1	1		
2	C	1	Total	Cu	0	0
			1	1		
2	D	1	Total	Cu	0	0
			1	1		
2	E	1	Total	Cu	0	0
			1	1		
2	F	1	Total	Cu	0	0
			1	1		

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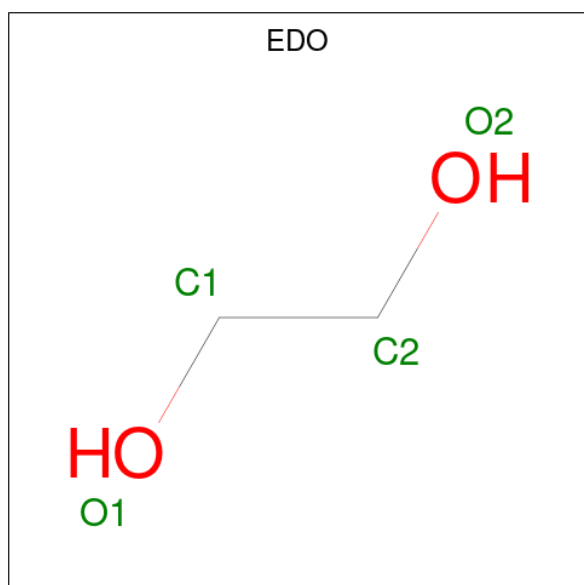
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	G	1	Total 2	Cu 2	0	1
2	H	1	Total 2	Cu 2	0	1

- Molecule 3 is ZINC ION (CCD ID: ZN) (formula: Zn).

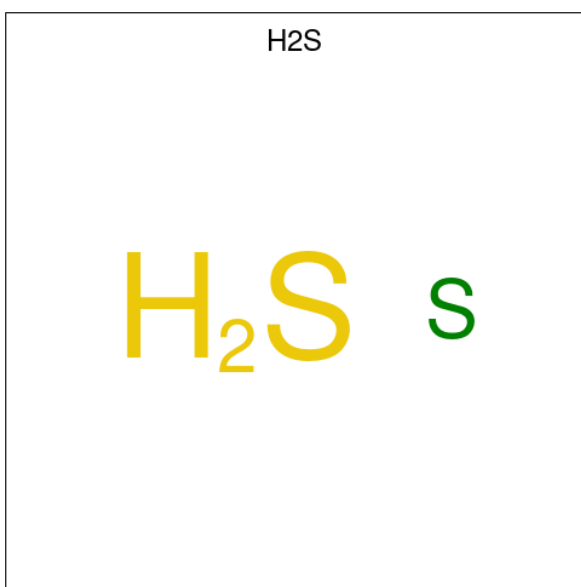
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total 1	Zn 1	0	0
3	B	1	Total 1	Zn 1	0	0
3	C	1	Total 1	Zn 1	0	0
3	D	1	Total 1	Zn 1	0	0
3	E	1	Total 1	Zn 1	0	0
3	F	1	Total 1	Zn 1	0	0
3	G	1	Total 1	Zn 1	0	0
3	H	1	Total 1	Zn 1	0	0

- Molecule 4 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



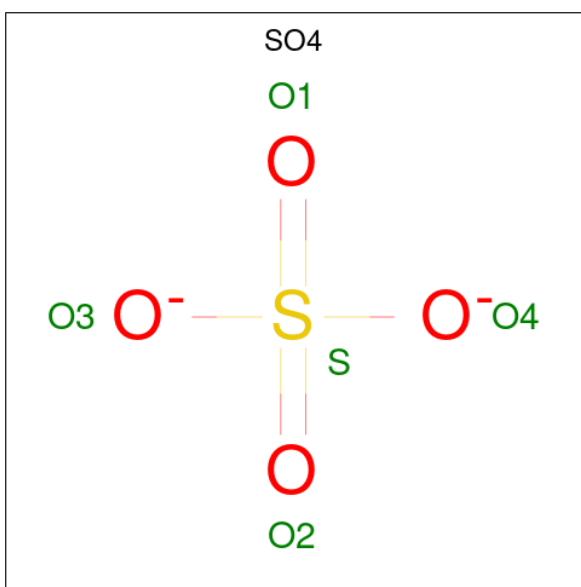
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O 4 2 2	0	0
4	B	1	Total C O 4 2 2	0	0
4	B	1	Total C O 4 2 2	0	0
4	B	1	Total C O 4 2 2	0	0
4	B	1	Total C O 4 2 2	0	0
4	C	1	Total C O 4 2 2	0	0
4	C	1	Total C O 4 2 2	0	0
4	C	1	Total C O 4 2 2	0	0
4	D	1	Total C O 4 2 2	0	0
4	F	1	Total C O 4 2 2	0	0
4	F	1	Total C O 4 2 2	0	0
4	F	1	Total C O 4 2 2	0	0
4	F	1	Total C O 4 2 2	0	0
4	G	1	Total C O 4 2 2	0	0
4	H	1	Total C O 4 2 2	0	0
4	H	1	Total C O 4 2 2	0	0
4	H	1	Total C O 4 2 2	0	0
4	H	1	Total C O 4 2 2	0	0

- Molecule 5 is HYDROSULFURIC ACID (CCD ID: H2S) (formula: H₂S) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	1	Total	S	0	0
			1	1		
5	E	1	Total	S	0	0
			1	1		
5	G	1	Total	S	0	0
			1	1		

- Molecule 6 is SULFATE ION (CCD ID: SO₄) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	B	1	Total	O	S	0	0
			5	4	1		

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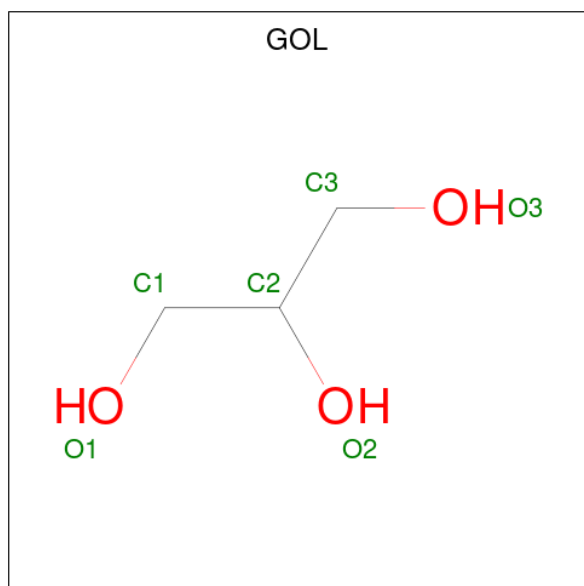
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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	D	1	Total	O	S	0	0
			5	4	1		

- Molecule 7 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	B	1	Total	Cl	0	0
			1	1		
7	C	1	Total	Cl	0	0
			1	1		
7	D	1	Total	Cl	0	0
			1	1		
7	E	2	Total	Cl	0	0
			2	2		
7	H	2	Total	Cl	0	0
			2	2		

- Molecule 8 is GLYCEROL (CCD ID: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	E	1	Total	C	O	0	0
			6	3	3		

- Molecule 9 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	147	Total 147	O 147	0	0
9	B	162	Total 162	O 162	0	0
9	C	131	Total 131	O 131	0	0
9	D	167	Total 167	O 167	0	0
9	E	172	Total 172	O 172	0	0
9	F	119	Total 119	O 119	0	0
9	G	125	Total 125	O 125	0	0
9	H	136	Total 136	O 136	0	0

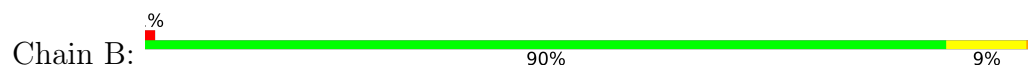
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: Superoxide dismutase [Cu-Zn]



- Molecule 1: Superoxide dismutase [Cu-Zn]



- Molecule 1: Superoxide dismutase [Cu-Zn]



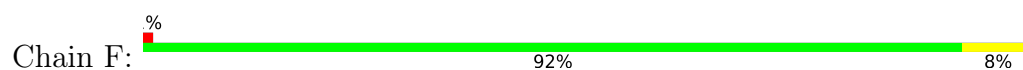
- Molecule 1: Superoxide dismutase [Cu-Zn]



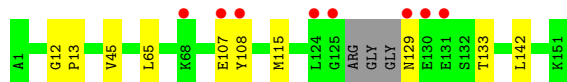
- Molecule 1: Superoxide dismutase [Cu-Zn]



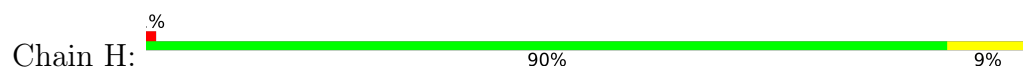
- Molecule 1: Superoxide dismutase [Cu-Zn]



- Molecule 1: Superoxide dismutase [Cu-Zn]



- Molecule 1: Superoxide dismutase [Cu-Zn]



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	46.13Å 69.96Å 91.34Å 98.69° 94.83° 103.31°	Depositor
Resolution (Å)	38.28 – 1.80 38.28 – 1.80	Depositor EDS
% Data completeness (in resolution range)	90.9 (38.28-1.80) 91.0 (38.28-1.80)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.42 (at 1.79Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, R_{free}	0.184 , 0.217 0.183 , 0.216	Depositor DCC
R_{free} test set	4592 reflections (4.54%)	wwPDB-VP
Wilson B-factor (Å ²)	18.0	Xtriage
Anisotropy	0.091	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 44.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	9897	wwPDB-VP
Average B, all atoms (Å ²)	23.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.37% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, CU, EDO, H2S, SO4, CL, GOL

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.45	1/1094 (0.1%)	0.58	0/1483
1	B	0.36	0/1096	0.58	1/1486 (0.1%)
1	C	0.33	0/1099	0.58	0/1490
1	D	0.51	2/1100 (0.2%)	0.64	1/1490 (0.1%)
1	E	0.42	0/1102	0.65	0/1493
1	F	0.35	0/1104	0.57	0/1495
1	G	0.39	0/1072	0.63	0/1454
1	H	0.40	0/1098	0.66	0/1489
All	All	0.41	3/8765 (0.0%)	0.61	2/11880 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	F	0	1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	41	HIS	C-O	-6.18	1.17	1.23
1	A	90	ASN	N-CA	-5.09	1.39	1.46
1	D	39	GLY	C-O	-5.07	1.18	1.23

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	39	GLY	N-CA-C	6.42	120.94	111.76
1	B	38	GLU	CA-CB-CG	-5.69	102.72	114.10

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	F	144[B]	CYS	Mainchain

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1076	0	1029	6	0
1	B	1078	0	1032	11	0
1	C	1081	0	1031	9	0
1	D	1082	0	1043	6	0
1	E	1084	0	1040	15	0
1	F	1086	0	1047	11	0
1	G	1055	0	1005	10	0
1	H	1080	0	1027	18	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
2	E	1	0	0	0	0
2	F	1	0	0	0	0
2	G	2	0	0	0	0
2	H	2	0	0	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
3	E	1	0	0	0	0
3	F	1	0	0	0	0
3	G	1	0	0	0	0
3	H	1	0	0	0	0
4	A	4	0	6	0	0
4	B	16	0	24	2	0
4	C	12	0	18	3	0
4	D	4	0	6	0	0
4	F	16	0	24	8	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	G	4	0	6	3	0
4	H	16	0	24	13	0
5	B	1	0	0	0	0
5	E	1	0	0	0	0
5	G	1	0	0	0	0
6	B	5	0	0	0	0
6	D	5	0	0	0	0
7	B	1	0	0	1	0
7	C	1	0	0	0	0
7	D	1	0	0	0	0
7	E	2	0	0	2	0
7	H	2	0	0	0	0
8	E	6	0	8	2	0
9	A	147	0	0	0	0
9	B	162	0	0	0	0
9	C	131	0	0	2	0
9	D	167	0	0	0	0
9	E	172	0	0	1	0
9	F	119	0	0	1	0
9	G	125	0	0	0	0
9	H	136	0	0	2	0
All	All	9897	0	8370	86	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 5.

The worst 5 of 86 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:38:GLU:HG2	1:B:39:GLY:N	1.86	0.89
1:F:141:ARG:NH2	4:F:206:EDO:H12	1.94	0.82
1:G:13:PRO:HD2	4:G:204:EDO:H12	1.65	0.77
1:G:142:LEU:O	4:G:204:EDO:H22	1.85	0.77
1:C:130:GLU:H	1:C:130:GLU:CD	1.95	0.73

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	149/151 (99%)	147 (99%)	2 (1%)	0	100	100
1	B	150/151 (99%)	147 (98%)	3 (2%)	0	100	100
1	C	150/151 (99%)	147 (98%)	3 (2%)	0	100	100
1	D	150/151 (99%)	147 (98%)	3 (2%)	0	100	100
1	E	150/151 (99%)	148 (99%)	2 (1%)	0	100	100
1	F	150/151 (99%)	147 (98%)	3 (2%)	0	100	100
1	G	144/151 (95%)	140 (97%)	4 (3%)	0	100	100
1	H	150/151 (99%)	147 (98%)	3 (2%)	0	100	100
All	All	1193/1208 (99%)	1170 (98%)	23 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	112/117 (96%)	110 (98%)	2 (2%)	51	43
1	B	113/117 (97%)	113 (100%)	0	100	100
1	C	113/117 (97%)	113 (100%)	0	100	100
1	D	114/117 (97%)	114 (100%)	0	100	100
1	E	114/117 (97%)	114 (100%)	0	100	100
1	F	115/117 (98%)	115 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	G	111/117 (95%)	111 (100%)	0	100	100
1	H	113/117 (97%)	112 (99%)	1 (1%)	70	67
All	All	905/936 (97%)	902 (100%)	3 (0%)	86	86

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	15	GLN
1	A	90	ASN
1	H	130	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 15 such sidechains are listed below:

Mol	Chain	Res	Type
1	F	15	GLN
1	H	129	ASN
1	F	51	ASN
1	H	137	ASN
1	H	19	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 49 ligands modelled in this entry, 25 are monoatomic and 3 are modelled with single atom - leaving 21 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
4	EDO	F	204	-	3,3,3	0.34	0	2,2,2	0.62	0
4	EDO	H	205	-	3,3,3	0.33	0	2,2,2	0.45	0
8	GOL	E	206	-	5,5,5	0.79	0	5,5,5	1.35	1 (20%)
4	EDO	C	204	-	3,3,3	0.43	0	2,2,2	0.58	0
4	EDO	F	206	-	3,3,3	0.06	0	2,2,2	0.12	0
6	SO4	D	204	-	4,4,4	0.31	0	6,6,6	0.33	0
4	EDO	B	206	-	3,3,3	0.41	0	2,2,2	0.61	0
4	EDO	B	204	-	3,3,3	0.41	0	2,2,2	0.56	0
4	EDO	C	205	-	3,3,3	0.50	0	2,2,2	0.27	0
4	EDO	F	205	-	3,3,3	0.41	0	2,2,2	0.80	0
4	EDO	H	206	-	3,3,3	0.14	0	2,2,2	0.09	0
4	EDO	C	203	-	3,3,3	0.38	0	2,2,2	0.57	0
4	EDO	B	207	-	3,3,3	0.06	0	2,2,2	0.11	0
4	EDO	B	205	-	3,3,3	0.45	0	2,2,2	0.48	0
4	EDO	F	203	-	3,3,3	0.46	0	2,2,2	0.41	0
6	SO4	B	208	-	4,4,4	0.24	0	6,6,6	0.31	0
4	EDO	D	203	-	3,3,3	0.48	0	2,2,2	0.23	0
4	EDO	A	203	-	3,3,3	0.32	0	2,2,2	0.68	0
4	EDO	H	203	-	3,3,3	0.44	0	2,2,2	0.16	0
4	EDO	G	204	-	3,3,3	0.44	0	2,2,2	0.49	0
4	EDO	H	204	-	3,3,3	0.31	0	2,2,2	0.51	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	EDO	F	204	-	-	0/1/1/1	-
4	EDO	H	205	-	-	1/1/1/1	-
8	GOL	E	206	-	-	2/4/4/4	-
4	EDO	C	204	-	-	1/1/1/1	-
4	EDO	F	206	-	-	1/1/1/1	-
4	EDO	B	206	-	-	1/1/1/1	-
4	EDO	B	204	-	-	0/1/1/1	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	EDO	C	205	-	-	0/1/1/1	-
4	EDO	F	205	-	-	1/1/1/1	-
4	EDO	H	206	-	-	1/1/1/1	-
4	EDO	C	203	-	-	1/1/1/1	-
4	EDO	B	207	-	-	1/1/1/1	-
4	EDO	B	205	-	-	0/1/1/1	-
4	EDO	F	203	-	-	0/1/1/1	-
4	EDO	D	203	-	-	1/1/1/1	-
4	EDO	A	203	-	-	0/1/1/1	-
4	EDO	H	203	-	-	0/1/1/1	-
4	EDO	G	204	-	-	1/1/1/1	-
4	EDO	H	204	-	-	0/1/1/1	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	E	206	GOL	C3-C2-C1	-2.11	104.05	111.80

There are no chirality outliers.

5 of 12 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
8	E	206	GOL	O2-C2-C3-O3
8	E	206	GOL	C1-C2-C3-O3
4	B	207	EDO	O1-C1-C2-O2
4	C	204	EDO	O1-C1-C2-O2
4	D	203	EDO	O1-C1-C2-O2

There are no ring outliers.

11 monomers are involved in 31 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	H	205	EDO	5	0
8	E	206	GOL	2	0
4	C	204	EDO	3	0
4	F	206	EDO	5	0
4	B	204	EDO	1	0
4	H	206	EDO	5	0
4	B	207	EDO	1	0
4	F	203	EDO	3	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	H	203	EDO	1	0
4	G	204	EDO	3	0
4	H	204	EDO	2	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	151/151 (100%)	0.09	4 (2%) 57 57	11, 22, 37, 45	0
1	B	151/151 (100%)	-0.14	1 (0%) 84 85	9, 19, 37, 47	1 (0%)
1	C	151/151 (100%)	0.06	3 (1%) 65 65	11, 24, 38, 52	1 (0%)
1	D	151/151 (100%)	-0.32	0 100 100	8, 17, 30, 37	1 (0%)
1	E	151/151 (100%)	-0.30	0 100 100	11, 18, 31, 43	1 (0%)
1	F	151/151 (100%)	0.02	2 (1%) 75 75	10, 24, 38, 43	1 (0%)
1	G	148/151 (98%)	0.29	8 (5%) 31 30	13, 22, 38, 48	0
1	H	151/151 (100%)	0.14	2 (1%) 75 75	11, 22, 36, 49	1 (0%)
All	All	1205/1208 (99%)	-0.02	20 (1%) 69 69	8, 21, 37, 52	6 (0%)

The worst 5 of 20 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	108	TYR	4.1
1	G	129	ASN	4.1
1	G	108	TYR	3.9
1	G	125	GLY	3.7
1	C	130	GLU	3.2

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	EDO	C	203	4/4	0.68	0.18	36,37,39,42	0
4	EDO	A	203	4/4	0.69	0.22	32,32,35,37	0
4	EDO	B	205	4/4	0.73	0.24	33,34,35,36	0
4	EDO	F	204	4/4	0.76	0.14	27,29,30,32	0
7	CL	B	209	1/1	0.77	0.26	49,49,49,49	0
4	EDO	F	205	4/4	0.80	0.16	36,36,36,36	0
4	EDO	H	206	4/4	0.81	0.15	20,20,20,20	0
4	EDO	B	206	4/4	0.81	0.12	36,36,38,40	0
4	EDO	C	204	4/4	0.83	0.16	35,35,36,37	0
4	EDO	H	205	4/4	0.83	0.23	27,28,29,34	0
4	EDO	C	205	4/4	0.83	0.12	30,30,33,34	0
3	ZN	H	202	1/1	0.83	0.11	18,18,18,18	0
7	CL	C	206	1/1	0.83	0.19	55,55,55,55	0
4	EDO	F	206	4/4	0.84	0.27	28,29,30,31	0
7	CL	E	205	1/1	0.85	0.28	45,45,45,45	0
4	EDO	H	204	4/4	0.86	0.15	34,34,35,36	0
4	EDO	G	204	4/4	0.86	0.20	28,30,33,35	0
8	GOL	E	206	6/6	0.86	0.15	26,28,30,31	0
4	EDO	F	203	4/4	0.87	0.11	27,27,30,32	0
4	EDO	D	203	4/4	0.88	0.11	32,32,33,33	0
4	EDO	H	203	4/4	0.89	0.18	31,34,34,34	0
7	CL	E	204	1/1	0.89	0.19	45,45,45,45	0
7	CL	H	207	1/1	0.90	0.10	46,46,46,46	0
4	EDO	B	204	4/4	0.90	0.15	29,30,31,33	0
4	EDO	B	207	4/4	0.91	0.13	26,29,31,34	0
5	H2S	B	203	1/1	0.92	0.11	40,40,40,40	0
5	H2S	E	203	1/1	0.92	0.13	40,40,40,40	0
5	H2S	G	203	1/1	0.93	0.09	42,42,42,42	0
6	SO4	D	204	5/5	0.93	0.12	22,33,36,36	0
7	CL	H	208	1/1	0.94	0.09	42,42,42,42	0
6	SO4	B	208	5/5	0.95	0.10	27,28,33,34	0
7	CL	D	205	1/1	0.96	0.07	34,34,34,34	0
2	CU	C	201	1/1	0.99	0.03	23,23,23,23	0
2	CU	F	201	1/1	0.99	0.02	22,22,22,22	0
2	CU	H	201[A]	1/1	0.99	0.03	18,18,18,18	1
2	CU	H	201[B]	1/1	0.99	0.03	18,18,18,18	1
3	ZN	A	202	1/1	0.99	0.02	15,15,15,15	0

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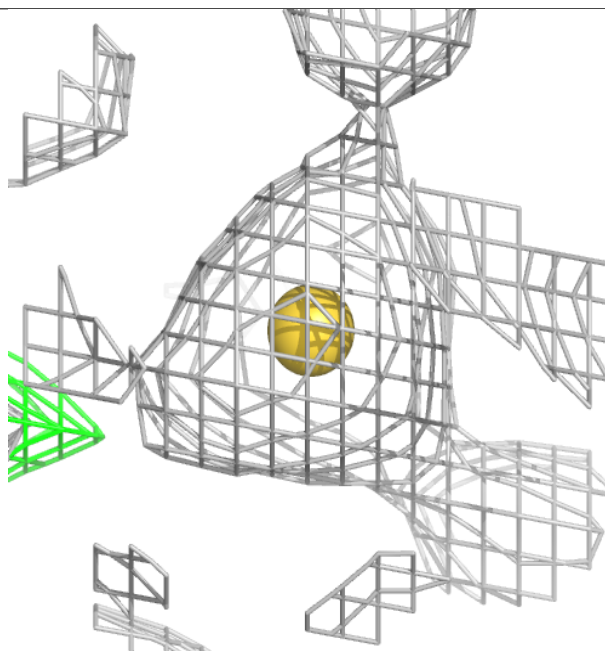
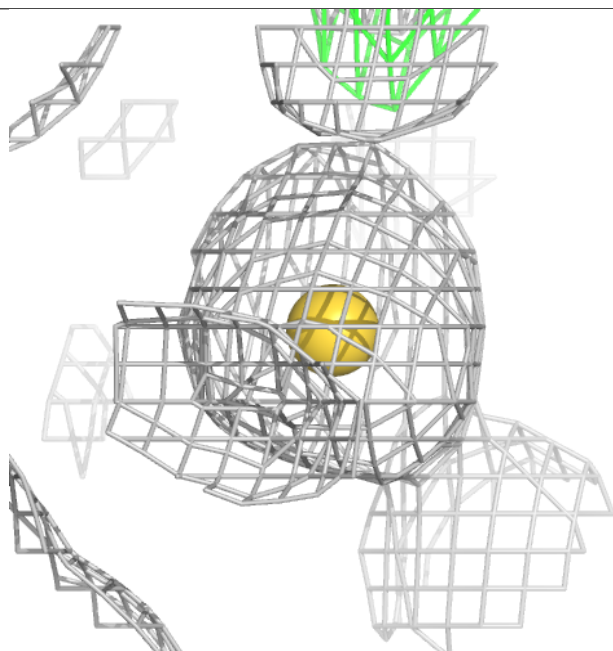
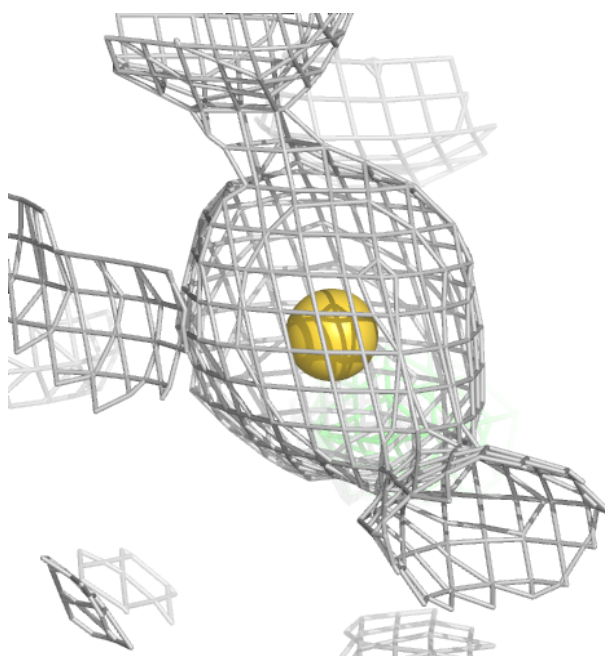
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	ZN	B	202	1/1	0.99	0.02	18,18,18,18	0
3	ZN	D	202	1/1	0.99	0.02	16,16,16,16	0
3	ZN	F	202	1/1	0.99	0.02	20,20,20,20	0
2	CU	A	201	1/1	0.99	0.02	18,18,18,18	0
2	CU	B	201	1/1	0.99	0.02	20,20,20,20	0
3	ZN	E	202	1/1	1.00	0.01	16,16,16,16	0
2	CU	D	201	1/1	1.00	0.01	17,17,17,17	0
3	ZN	G	202	1/1	1.00	0.01	19,19,19,19	0
2	CU	G	201[A]	1/1	1.00	0.01	19,19,19,19	1
2	CU	G	201[B]	1/1	1.00	0.01	16,16,16,16	1
3	ZN	C	202	1/1	1.00	0.02	19,19,19,19	0
2	CU	E	201	1/1	1.00	0.01	18,18,18,18	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

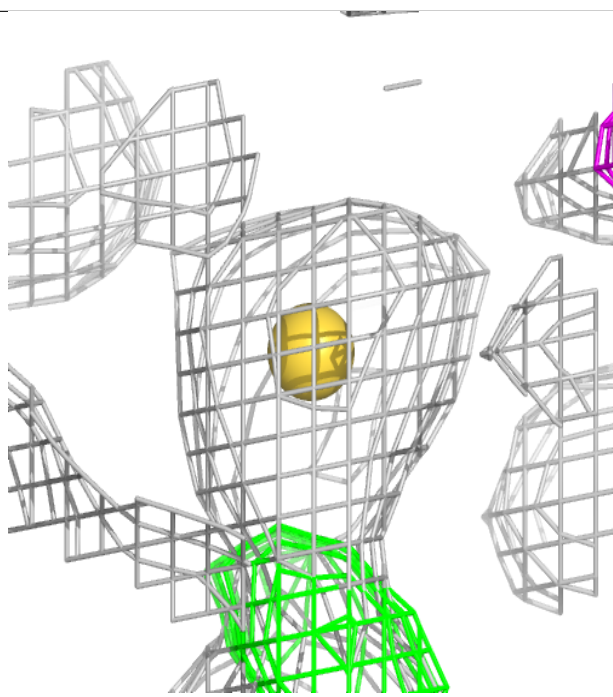
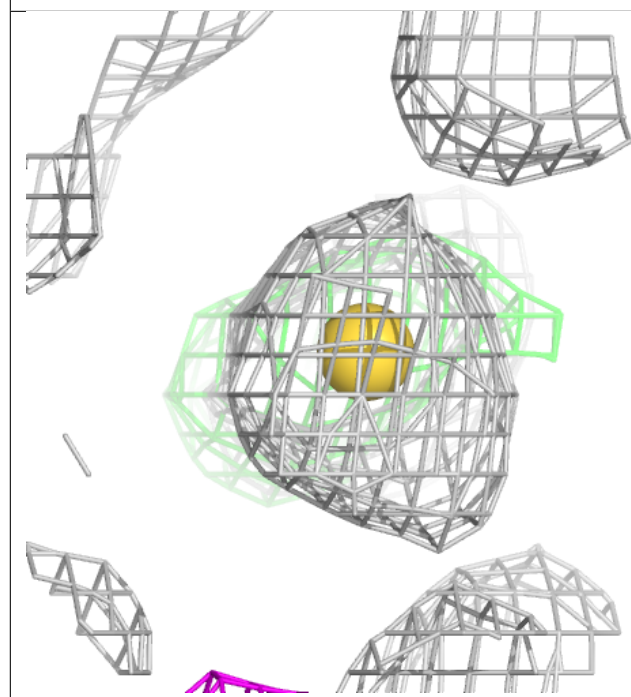
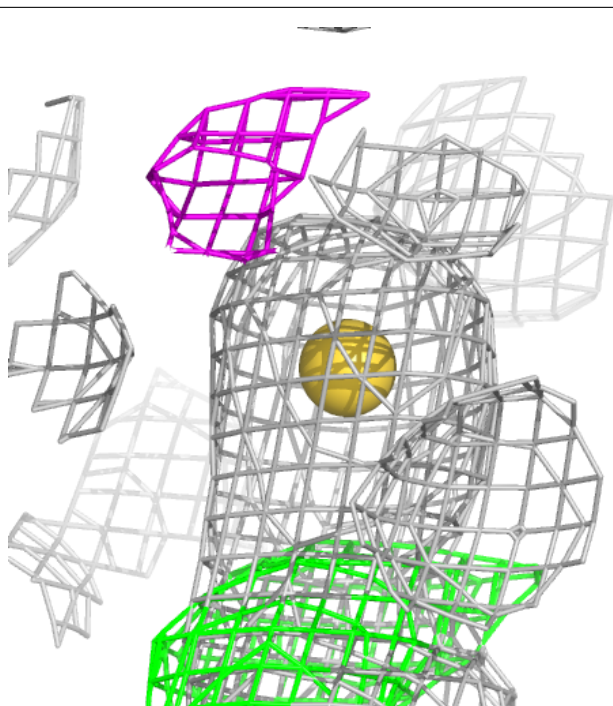
Electron density around H2S B 203:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



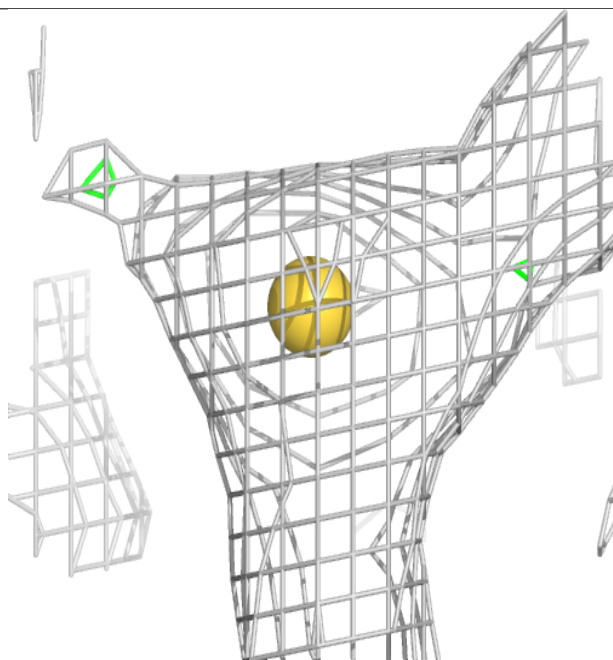
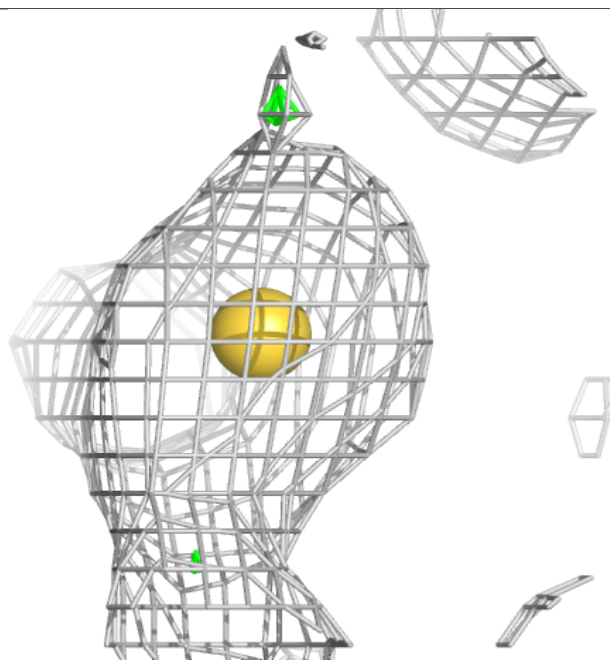
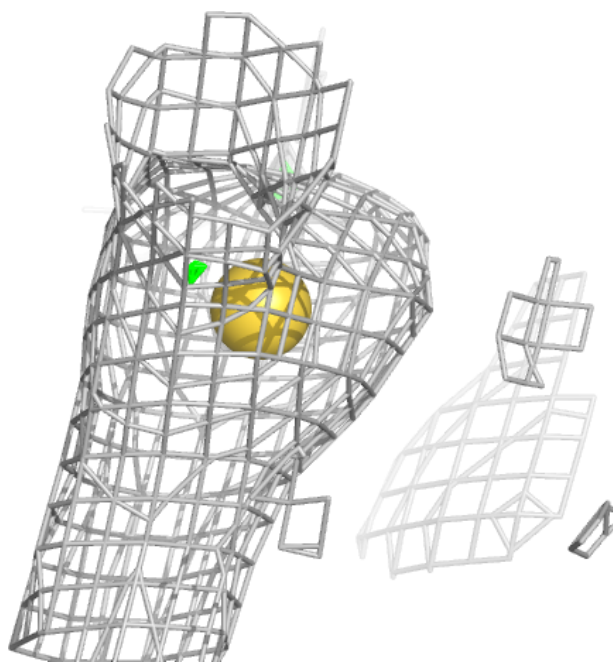
Electron density around H2S E 203:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around H2S G 203:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers [i](#)

There are no such residues in this entry.