



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 18, 2026 – 06:02 AM UTC

PDB ID : 4MMO / pdb_00004mmo
Title : The crystal structure of a M20 family metallo-carboxypeptidase Sso-CP2 from *Sulfolobus solfataricus*
Authors : Dupuy, J.; Dutoit, R.; Durisotti, V.; Demarez, M.; Borel, F.; Van Elder, D.; Legrain, C.; Bauvois, C.
Deposited on : 2013-09-09
Resolution : 2.34 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

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

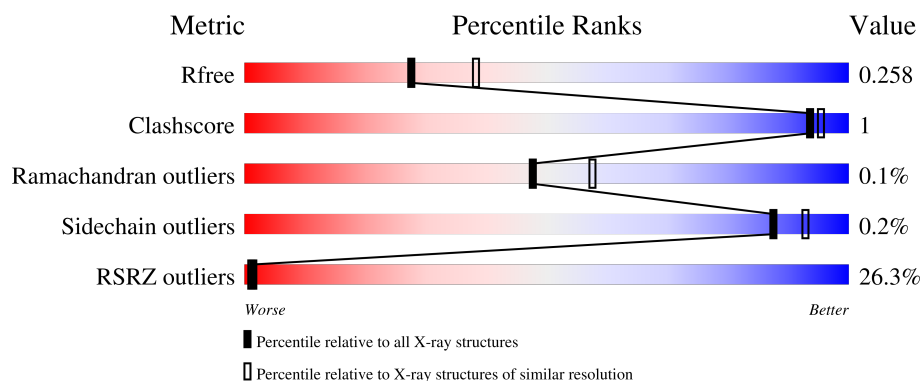
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.34 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	3031 (2.36-2.32)
Clashscore	190562	3127 (2.36-2.32)
Ramachandran outliers	187476	3095 (2.36-2.32)
Sidechain outliers	187428	3095 (2.36-2.32)
RSRZ outliers	180081	3033 (2.36-2.32)

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	437	7% 96% .
1	B	437	42% 85% . 13%

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 12814 atoms, of which 6210 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.

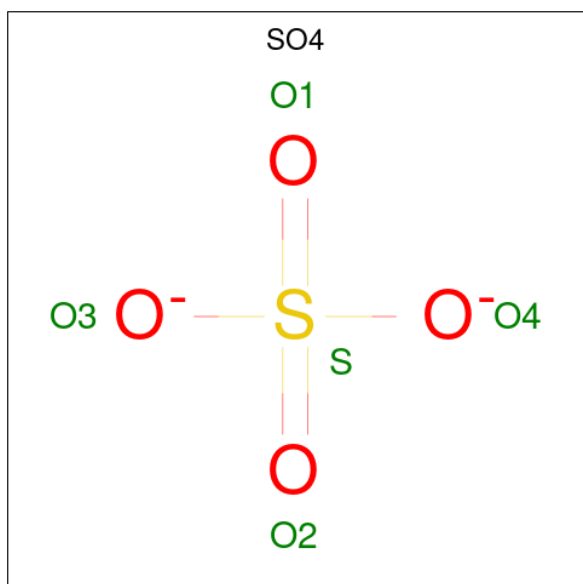
- Molecule 1 is a protein called Sso-CP2 metallo-carboxypeptidase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	437	Total	C	H	N	O	S	0	0	0
			6845	2194	3431	561	650	9			
1	B	382	Total	C	H	N	O	S	0	0	0
			5611	1838	2771	465	530	7			

- Molecule 2 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Zn	0	0
			1	1		

- Molecule 3 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



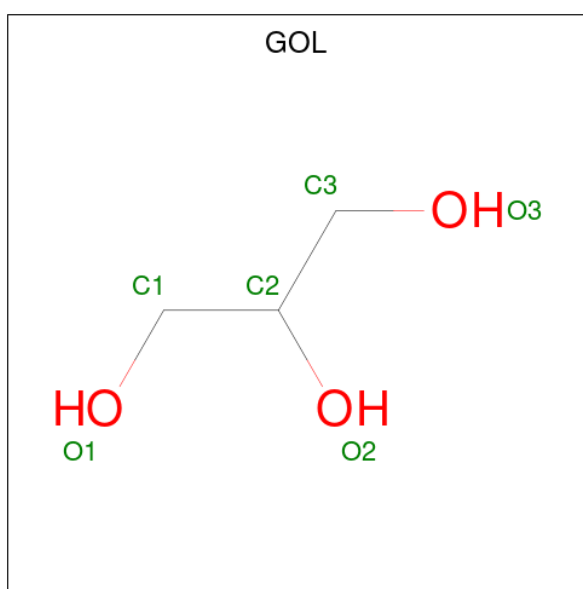
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	S	0	0
			5	4	1		

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

- Molecule 4 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	B	1	Total	C	H	O	0	0
			14	3	8	3		

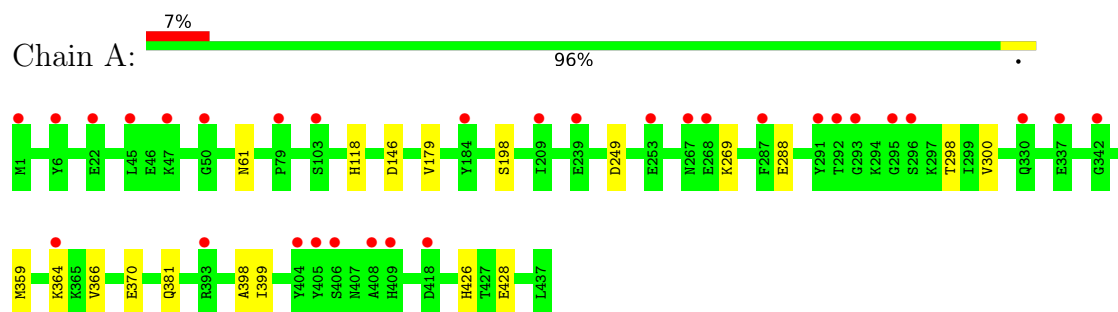
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	188	Total	O	0	0
			188	188		
5	B	130	Total	O	0	0
			130	130		

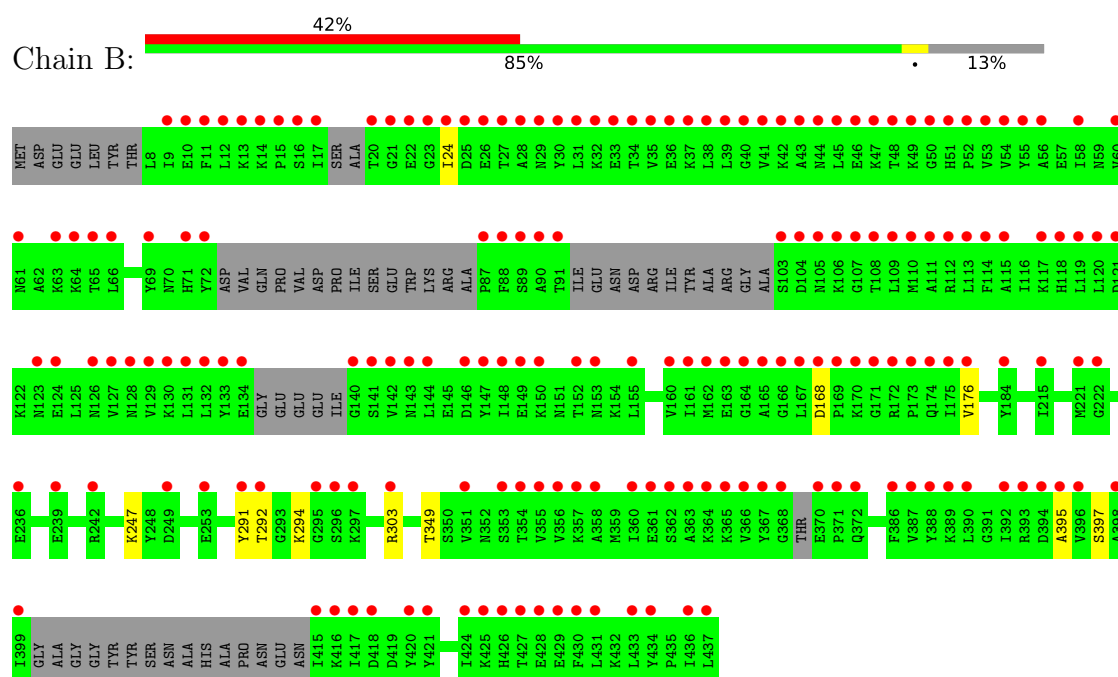
3 Residue-property plots

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: Sso-CP2 metallo-carboxypeptidase



• Molecule 1: Sso-CP2 metallo-carboxypeptidase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	86.07Å 89.37Å 161.42Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.10 – 2.34 46.10 – 2.34	Depositor EDS
% Data completeness (in resolution range)	99.1 (46.10-2.34) 99.2 (46.10-2.34)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.00 (at 2.34Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.2_1309)	Depositor
R, R_{free}	0.206 , 0.253 0.210 , 0.258	Depositor DCC
R_{free} test set	2654 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	46.7	Xtriage
Anisotropy	0.510	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.40 , 72.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.018 for k,h,-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	12814	wwPDB-VP
Average B, all atoms (Å ²)	73.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.37% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, SO4, 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	0.33	0/3479	0.64	0/4706
1	B	0.30	0/2885	0.63	0/3909
All	All	0.32	0/6364	0.64	0/8615

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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	3414	3431	3435	12	0
1	B	2840	2771	2761	7	0
2	A	1	0	0	0	0
3	A	15	0	0	0	0
3	B	10	0	0	0	0
4	B	6	8	8	0	0
5	A	188	0	0	2	0
5	B	130	0	0	3	0
All	All	6604	6210	6204	18	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 1.

All (18) 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:A:198:SER:OG	1:A:298:THR:OG1	2.09	0.69
1:A:61:ASN:ND2	5:A:705:HOH:O	2.32	0.63
1:B:291:TYR:OH	1:B:294:LYS:O	2.19	0.61
1:A:198:SER:HG	1:A:298:THR:HG1	1.49	0.60
1:A:364:LYS:NZ	1:A:370:GLU:OE1	2.38	0.56
1:A:249:ASP:OD1	1:A:269:LYS:NZ	2.40	0.55
1:B:303:ARG:NE	5:B:629:HOH:O	2.29	0.55
1:A:359:MET:HG2	1:A:398:ALA:HB3	1.93	0.51
1:B:247:LYS:NZ	5:B:673:HOH:O	2.45	0.49
1:A:146:ASP:OD1	5:A:677:HOH:O	2.20	0.46
1:A:198:SER:HA	1:A:300:VAL:HG23	1.97	0.46
1:B:24:ILE:N	5:B:627:HOH:O	2.46	0.44
1:A:179:VAL:HG11	1:A:381:GLN:HB3	2.00	0.43
1:A:288:GLU:HB2	1:B:292:THR:HG21	2.01	0.42
1:A:366:VAL:HG21	1:A:426:HIS:HA	2.02	0.41
1:A:118:HIS:ND1	1:A:428:GLU:OE2	2.48	0.41
1:B:176:VAL:HG13	1:B:397:SER:HB3	2.02	0.40
1:B:349:THR:HG21	1:B:395:ALA:H	1.85	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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	435/437 (100%)	428 (98%)	6 (1%)	1 (0%)	43	50
1	B	368/437 (84%)	355 (96%)	13 (4%)	0	100	100
All	All	803/874 (92%)	783 (98%)	19 (2%)	1 (0%)	48	57

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	399	ILE

5.3.2 Protein sidechains [i](#)

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	363/374 (97%)	363 (100%)	0	100	100
1	B	277/374 (74%)	276 (100%)	1 (0%)	84	89
All	All	640/748 (86%)	639 (100%)	1 (0%)	87	93

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	168	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	70	ASN
1	B	105	ASN
1	B	372	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 7 ligands modelled in this entry, 1 is monoatomic - leaving 6 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	$\# Z > 2$
3	SO4	A	503	-	4,4,4	0.24	0	6,6,6	0.08	0
3	SO4	B	502	-	4,4,4	0.25	0	6,6,6	0.10	0
3	SO4	B	501	-	4,4,4	0.22	0	6,6,6	0.07	0
3	SO4	A	502	-	4,4,4	0.29	0	6,6,6	0.58	0
4	GOL	B	503	-	5,5,5	0.37	0	5,5,5	0.33	0
3	SO4	A	504	-	4,4,4	0.24	0	6,6,6	0.10	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	GOL	B	503	-	-	4/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	B	503	GOL	O1-C1-C2-C3
4	B	503	GOL	C1-C2-C3-O3
4	B	503	GOL	O2-C2-C3-O3
4	B	503	GOL	O1-C1-C2-O2

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

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	437/437 (100%)	0.49	31 (7%)	22 26	33, 51, 92, 135	0
1	B	382/437 (87%)	2.10	184 (48%)	0 0	33, 97, 183, 259	0
All	All	819/874 (93%)	1.24	215 (26%)	1 1	33, 59, 162, 259	0

All (215) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	292	THR	9.0
1	B	106	LYS	8.8
1	B	11	PHE	8.2
1	B	17	ILE	8.0
1	B	89	SER	7.2
1	B	87	PRO	7.2
1	B	30	TYR	6.9
1	B	120	LEU	6.9
1	B	114	PHE	6.9
1	B	368	GLY	6.8
1	B	370	GLU	6.8
1	B	167	LEU	6.7
1	B	364	LYS	6.6
1	B	398	ALA	6.4
1	B	22	GLU	6.4
1	B	418	ASP	6.3
1	B	399	ILE	6.3
1	B	9	ILE	6.3
1	B	51	HIS	6.3
1	B	164	GLY	6.1
1	B	123	ASN	6.0
1	B	88	PHE	5.9
1	B	111	ALA	5.8
1	B	39	LEU	5.8

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Mol	Chain	Res	Type	RSRZ
1	B	16	SER	5.7
1	B	110	MET	5.6
1	B	173	PRO	5.6
1	A	103	SER	5.5
1	B	60	VAL	5.4
1	B	134	GLU	5.4
1	B	26	GLU	5.4
1	B	143	ASN	5.3
1	B	354	THR	5.3
1	B	31	LEU	5.3
1	B	172	ARG	5.2
1	B	133	TYR	5.2
1	B	358	ALA	5.1
1	B	170	LYS	5.1
1	B	142	VAL	5.1
1	A	405	TYR	5.1
1	B	50	GLY	5.0
1	B	14	LYS	5.0
1	B	71	HIS	5.0
1	B	372	GLN	5.0
1	B	367	TYR	4.9
1	B	127	VAL	4.9
1	B	46	GLU	4.8
1	B	52	PRO	4.8
1	B	430	PHE	4.7
1	A	404	TYR	4.7
1	B	53	VAL	4.7
1	B	417	ILE	4.7
1	B	38	LEU	4.7
1	B	10	GLU	4.7
1	B	29	ASN	4.6
1	B	113	LEU	4.6
1	B	393	ARG	4.6
1	B	48	THR	4.5
1	B	431	LEU	4.5
1	B	141	SER	4.4
1	B	119	LEU	4.4
1	B	115	ALA	4.4
1	B	108	THR	4.4
1	B	103	SER	4.4
1	B	168	ASP	4.3
1	B	147	TYR	4.3

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Mol	Chain	Res	Type	RSRZ
1	B	355	VAL	4.3
1	B	253	GLU	4.3
1	B	426	HIS	4.2
1	B	28	ALA	4.2
1	B	171	GLY	4.2
1	B	296	SER	4.2
1	B	104	ASP	4.1
1	B	169	PRO	4.1
1	B	124	GLU	4.1
1	B	132	LEU	4.0
1	B	175	ILE	4.0
1	A	293	GLY	4.0
1	B	25	ASP	4.0
1	B	149	GLU	3.9
1	B	45	LEU	3.9
1	B	165	ALA	3.9
1	B	415	ILE	3.8
1	B	425	LYS	3.8
1	B	109	LEU	3.8
1	B	166	GLY	3.8
1	B	366	VAL	3.8
1	B	360	ILE	3.8
1	B	140	GLY	3.8
1	B	428	GLU	3.7
1	B	69	TYR	3.7
1	A	47	LYS	3.7
1	B	12	LEU	3.7
1	A	296	SER	3.7
1	B	356	VAL	3.6
1	B	371	PRO	3.6
1	A	409	HIS	3.6
1	B	105	ASN	3.6
1	B	91	THR	3.6
1	B	295	GLY	3.6
1	B	129	VAL	3.6
1	B	434	TYR	3.5
1	B	436	ILE	3.5
1	B	392	ILE	3.5
1	B	21	GLY	3.5
1	B	126	ASN	3.5
1	B	176	VAL	3.5
1	A	406	SER	3.4

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Mol	Chain	Res	Type	RSRZ
1	B	390	LEU	3.4
1	B	15	PRO	3.4
1	B	107	GLY	3.4
1	B	155	LEU	3.3
1	B	20	THR	3.3
1	B	357	LYS	3.3
1	B	118	HIS	3.3
1	B	148	ILE	3.2
1	B	161	ILE	3.2
1	B	54	VAL	3.2
1	B	131	LEU	3.2
1	B	27	THR	3.2
1	B	362	SER	3.2
1	B	42	LYS	3.2
1	B	146	ASP	3.2
1	B	221	MET	3.1
1	A	408	ALA	3.1
1	B	32	LYS	3.0
1	B	49	LYS	3.0
1	B	34	THR	3.0
1	B	424	ILE	3.0
1	A	268	GLU	3.0
1	B	351	VAL	2.9
1	B	365	LYS	2.9
1	B	72	TYR	2.9
1	B	63	LYS	2.9
1	B	56	ALA	2.9
1	B	144	LEU	2.9
1	A	184	TYR	2.9
1	B	421	TYR	2.9
1	B	363	ALA	2.9
1	B	58	ILE	2.9
1	B	128	ASN	2.9
1	A	295	GLY	2.8
1	A	267	ASN	2.8
1	B	236	GLU	2.8
1	B	292	THR	2.8
1	B	66	LEU	2.8
1	B	174	GLN	2.7
1	B	353	SER	2.7
1	B	13	LYS	2.7
1	A	291	TYR	2.7

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Mol	Chain	Res	Type	RSRZ
1	B	386	PHE	2.7
1	A	253	GLU	2.7
1	B	429	GLU	2.7
1	B	395	ALA	2.7
1	B	388	TYR	2.7
1	A	209	ILE	2.7
1	B	130	LYS	2.6
1	B	160	VAL	2.6
1	B	47	LYS	2.6
1	A	239	GLU	2.6
1	A	50	GLY	2.6
1	B	420	TYR	2.6
1	A	330	GLN	2.6
1	B	162	MET	2.6
1	B	90	ALA	2.5
1	B	23	GLY	2.5
1	B	117	LYS	2.5
1	A	6	TYR	2.5
1	B	361	GLU	2.5
1	A	393	ARG	2.5
1	B	150	LYS	2.5
1	B	249	ASP	2.5
1	B	152	THR	2.4
1	B	61	ASN	2.4
1	B	222	GLY	2.4
1	B	416	LYS	2.4
1	A	287	PHE	2.4
1	B	121	ASP	2.3
1	B	37	LYS	2.3
1	B	437	LEU	2.3
1	A	342	GLY	2.3
1	B	43	ALA	2.3
1	B	433	LEU	2.3
1	B	24	ILE	2.3
1	B	396	VAL	2.3
1	A	22	GLU	2.2
1	B	55	TYR	2.2
1	B	64	LYS	2.2
1	B	389	LYS	2.2
1	B	153	ASN	2.2
1	B	427	THR	2.2
1	B	41	VAL	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	418	ASP	2.2
1	B	297	LYS	2.2
1	B	291	TYR	2.1
1	B	35	VAL	2.1
1	B	36	GLU	2.1
1	B	40	GLY	2.1
1	B	33	GLU	2.1
1	B	163	GLU	2.1
1	A	79	PRO	2.1
1	B	387	VAL	2.1
1	B	65	THR	2.1
1	B	44	ASN	2.1
1	B	242	ARG	2.1
1	A	45	LEU	2.1
1	B	112	ARG	2.1
1	B	303	ARG	2.1
1	A	364	LYS	2.0
1	A	337	GLU	2.0
1	B	239	GLU	2.0
1	B	394	ASP	2.0
1	B	184	TYR	2.0
1	A	1	MET	2.0
1	B	215	ILE	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

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.

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	SO4	A	502	5/5	0.62	0.22	74,99,111,113	0
3	SO4	B	502	5/5	0.75	0.13	75,84,94,94	0
4	GOL	B	503	6/6	0.81	0.17	36,62,84,90	0
3	SO4	A	503	5/5	0.83	0.12	64,78,96,98	0
3	SO4	A	504	5/5	0.87	0.10	58,77,89,91	0
3	SO4	B	501	5/5	0.91	0.11	51,63,76,78	0
2	ZN	A	501	1/1	0.93	0.07	31,31,31,31	1

6.5 Other polymers [i](#)

There are no such residues in this entry.