



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 06:45 PM GMT

PDB ID : 4MMO  
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](mailto:validation@mail.wwpdb.org)  
A user guide is available at  
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467  
Mogul : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

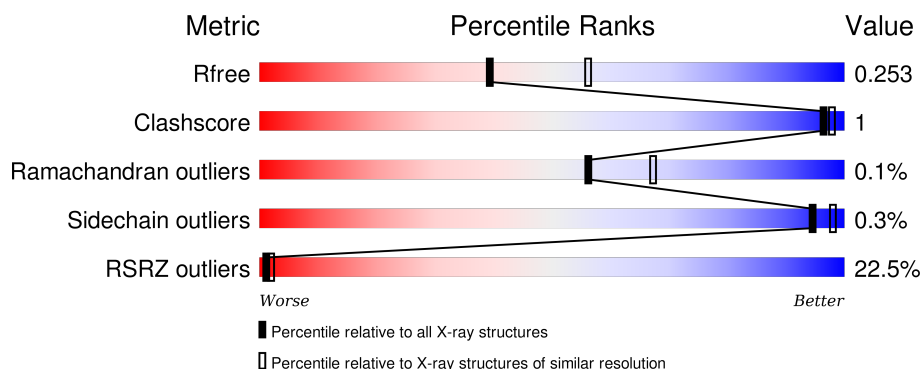
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

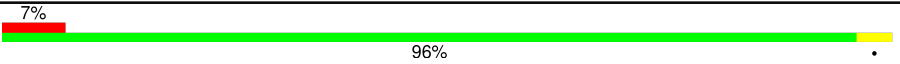

The reported resolution of this entry is 2.34 Å.

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))
$R_{free}$	91344	1406 (2.36-2.32)
Clashscore	102246	1509 (2.36-2.32)
Ramachandran outliers	100387	1490 (2.36-2.32)
Sidechain outliers	100360	1491 (2.36-2.32)
RSRZ outliers	91569	1412 (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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. 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	
1	B	437	

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
3	SO4	A	502	-	-	-	X
3	SO4	A	503	-	-	-	X
4	GOL	B	503	-	-	-	X

## 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 (three-letter code: ZN) (formula: Zn).

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

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



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 (three-letter code: 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		

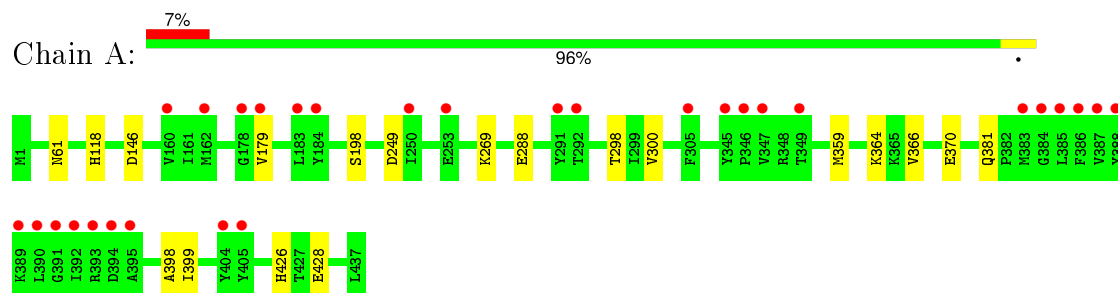
- Molecule 5 is water.

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

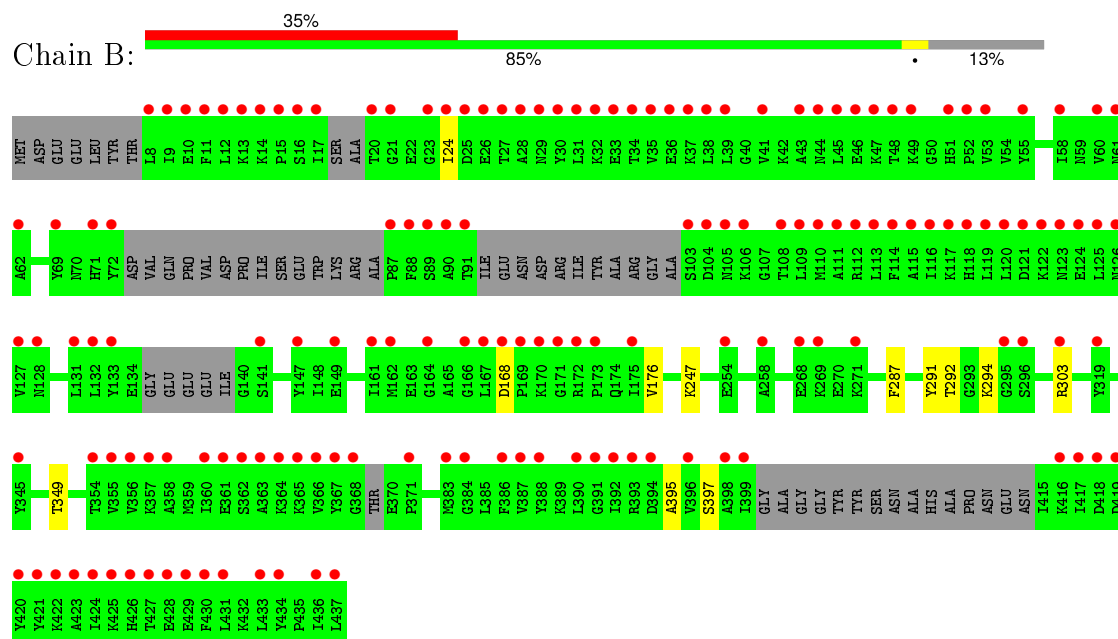
### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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, $\alpha$ , $\beta$ , $\gamma$	86.07Å 89.37Å 161.42Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.10 – 2.34 49.16 – 2.34	Depositor EDS
% Data completeness (in resolution range)	99.1 (46.10-2.34) 99.2 (49.16-2.34)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.00 (at 2.34Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.2_1309)	Depositor
R, $R_{free}$	0.206 , 0.253 0.205 , 0.253	Depositor DCC
$R_{free}$ test set	2651 reflections (5.00%)	DCC
Wilson B-factor (Å <sup>2</sup> )	46.7	Xtriage
Anisotropy	0.510	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.39 , 60.0	EDS
Estimated twinning fraction	0.018 for k,h,-l	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	1 of 53076 reflections (0.002%)	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	12814	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	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.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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: GOL, ZN, SO4

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	0.25	0/3479	0.44	0/4706
1	B	0.23	0/2885	0.42	0/3909
All	All	0.24	0/6364	0.43	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 [i](#)

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: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:B:247:LYS:NZ	5:B:673:HOH:O	2.45	0.42
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%)	52	61
1	B	368/437 (84%)	355 (96%)	13 (4%)	0	100	100
All	All	803/874 (92%)	783 (98%)	19 (2%)	1 (0%)	56	67

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%)	275 (99%)	2 (1%)	88	95
All	All	640/748 (86%)	638 (100%)	2 (0%)	94	98

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	168	ASP
1	B	287	PHE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

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

### 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 carbohydrates 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	502	-	4,4,4	0.21	0	6,6,6	0.35	0
3	SO4	A	503	-	4,4,4	0.16	0	6,6,6	0.08	0
3	SO4	A	504	-	4,4,4	0.18	0	6,6,6	0.10	0
3	SO4	B	501	-	4,4,4	0.20	0	6,6,6	0.10	0
3	SO4	B	502	-	4,4,4	0.20	0	6,6,6	0.10	0
4	GOL	B	503	-	5,5,5	0.36	0	5,5,5	0.33	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
3	SO4	A	502	-	-	0/0/0/0	0/0/0/0
3	SO4	A	503	-	-	0/0/0/0	0/0/0/0
3	SO4	A	504	-	-	0/0/0/0	0/0/0/0
3	SO4	B	501	-	-	0/0/0/0	0/0/0/0
3	SO4	B	502	-	-	0/0/0/0	0/0/0/0
4	GOL	B	503	-	-	0/4/4/4	0/0/0/0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	437/437 (100%)	0.65	30 (6%)	20 30	31, 47, 80, 131	0
1	B	382/437 (87%)	2.25	154 (40%)	0 0	32, 90, 172, 241	0
All	All	819/874 (93%)	1.40	184 (22%)	1 2	31, 53, 151, 241	0

All (184) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	39	LEU	15.6
1	B	38	LEU	11.7
1	B	120	LEU	11.1
1	B	17	ILE	10.8
1	B	31	LEU	10.5
1	B	114	PHE	10.3
1	B	398	ALA	9.8
1	B	418	ASP	9.2
1	B	111	ALA	9.1
1	B	52	PRO	8.6
1	B	53	VAL	8.4
1	B	16	SER	8.3
1	B	421	TYR	8.1
1	B	417	ILE	8.1
1	B	9	ILE	8.0
1	B	115	ALA	7.9
1	B	11	PHE	7.5
1	B	430	PHE	7.0
1	B	113	LEU	7.0
1	B	364	LYS	6.9
1	B	48	THR	6.7
1	B	366	VAL	6.6
1	B	29	ASN	6.5
1	B	362	SER	6.4

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Mol	Chain	Res	Type	RSRZ
1	B	124	GLU	6.4
1	B	45	LEU	6.3
1	B	125	LEU	6.3
1	B	360	ILE	6.2
1	B	399	ILE	6.2
1	B	43	ALA	6.1
1	B	167	LEU	6.1
1	B	126	ASN	6.0
1	B	30	TYR	5.9
1	B	426	HIS	5.7
1	B	87	PRO	5.7
1	B	169	PRO	5.7
1	B	387	VAL	5.7
1	B	10	GLU	5.6
1	A	405	TYR	5.6
1	B	41	VAL	5.6
1	B	27	THR	5.5
1	B	354	THR	5.5
1	B	371	PRO	5.5
1	B	51	HIS	5.4
1	B	35	VAL	5.4
1	B	431	LEU	5.3
1	B	71	HIS	5.3
1	B	131	LEU	5.3
1	B	26	GLU	5.2
1	B	173	PRO	5.2
1	B	388	TYR	5.2
1	A	404	TYR	5.1
1	B	24	ILE	5.1
1	B	425	LYS	5.0
1	A	388	TYR	5.0
1	B	12	LEU	5.0
1	B	88	PHE	4.9
1	B	429	GLU	4.9
1	B	72	TYR	4.8
1	B	109	LEU	4.8
1	B	422	LYS	4.8
1	B	437	LEU	4.8
1	B	13	LYS	4.8
1	B	28	ALA	4.8
1	B	44	ASN	4.8
1	B	34	THR	4.8

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Mol	Chain	Res	Type	RSRZ
1	B	367	TYR	4.7
1	B	58	ILE	4.7
1	B	365	LYS	4.7
1	B	36	GLU	4.6
1	B	15	PRO	4.6
1	B	108	THR	4.6
1	B	25	ASP	4.6
1	B	123	ASN	4.5
1	B	424	ILE	4.5
1	B	119	LEU	4.5
1	B	393	ARG	4.4
1	B	132	LEU	4.3
1	B	14	LYS	4.3
1	B	436	ILE	4.3
1	B	37	LYS	4.2
1	B	103	SER	4.1
1	A	392	ILE	4.1
1	B	166	GLY	4.0
1	B	127	VAL	4.0
1	B	61	ASN	4.0
1	B	368	GLY	4.0
1	B	121	ASP	4.0
1	B	112	ARG	3.9
1	B	32	LYS	3.9
1	B	8	LEU	3.8
1	B	110	MET	3.8
1	B	116	ILE	3.7
1	A	387	VAL	3.7
1	B	427	THR	3.7
1	B	55	TYR	3.6
1	B	164	GLY	3.6
1	B	122	LYS	3.6
1	B	141	SER	3.6
1	B	394	ASP	3.6
1	B	91	THR	3.5
1	B	392	ILE	3.5
1	A	395	ALA	3.5
1	B	105	ASN	3.5
1	B	433	LEU	3.5
1	A	345	TYR	3.5
1	B	420	TYR	3.5
1	B	33	GLU	3.5

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Mol	Chain	Res	Type	RSRZ
1	B	356	VAL	3.4
1	A	386	PHE	3.4
1	B	62	ALA	3.4
1	B	357	LYS	3.4
1	B	296	SER	3.4
1	B	391	GLY	3.3
1	A	305	PHE	3.3
1	B	423	ALA	3.3
1	B	133	TYR	3.3
1	B	358	ALA	3.3
1	B	168	ASP	3.3
1	B	254	GLU	3.2
1	B	90	ALA	3.2
1	B	361	GLU	3.2
1	B	69	TYR	3.1
1	A	349	THR	3.1
1	A	391	GLY	3.1
1	B	171	GLY	3.1
1	B	106	LYS	3.1
1	B	118	HIS	3.1
1	B	161	ILE	2.9
1	B	23	GLY	2.9
1	B	390	LEU	2.9
1	B	172	ARG	2.9
1	A	347	VAL	2.9
1	A	390	LEU	2.9
1	B	434	TYR	2.8
1	B	104	ASP	2.8
1	B	175	ILE	2.8
1	B	386	PHE	2.8
1	A	383	MET	2.8
1	B	46	GLU	2.8
1	A	160	VAL	2.7
1	B	128	ASN	2.7
1	B	47	LYS	2.7
1	B	258	ALA	2.7
1	A	385	LEU	2.7
1	B	89	SER	2.7
1	A	393	ARG	2.7
1	B	20	THR	2.7
1	B	170	LYS	2.7
1	B	345	TYR	2.6

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Mol	Chain	Res	Type	RSRZ
1	B	149	GLU	2.6
1	A	291	TYR	2.5
1	A	178	GLY	2.5
1	A	384	GLY	2.5
1	A	184	TYR	2.5
1	B	60	VAL	2.5
1	B	355	VAL	2.5
1	B	363	ALA	2.5
1	A	250	ILE	2.5
1	B	428	GLU	2.4
1	A	162	MET	2.4
1	B	117	LYS	2.4
1	B	384	GLY	2.3
1	A	346	PRO	2.3
1	B	419	ASP	2.3
1	B	295	GLY	2.3
1	A	292	THR	2.3
1	A	183	LEU	2.3
1	B	269	LYS	2.3
1	B	268	GLU	2.3
1	B	416	LYS	2.2
1	B	383	MET	2.1
1	A	389	LYS	2.1
1	A	179	VAL	2.1
1	B	271	LYS	2.1
1	A	394	ASP	2.1
1	B	162	MET	2.1
1	B	147	TYR	2.1
1	B	49	LYS	2.1
1	A	253	GLU	2.1
1	B	21	GLY	2.0
1	B	303	ARG	2.0
1	B	319	TYR	2.0
1	B	396	VAL	2.0

## 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 [i](#)

There are no carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> 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	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
3	SO4	A	502	5/5	0.71	0.34	3.56	74,99,111,113	0
4	GOL	B	503	6/6	0.86	0.20	2.56	36,62,84,90	0
3	SO4	A	503	5/5	0.95	0.20	2.23	64,78,96,98	0
3	SO4	B	501	5/5	0.95	0.15	-0.46	51,63,76,78	0
2	ZN	A	501	1/1	0.85	0.14	-1.44	31,31,31,31	1
3	SO4	A	504	5/5	0.93	0.14	-2.22	58,77,89,91	0
3	SO4	B	502	5/5	0.85	0.23	-	75,84,94,94	0

### 6.5 Other polymers [i](#)

There are no such residues in this entry.