



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 07:48 PM UTC

PDB ID : 4MCM / pdb_00004mcm
Title : Human SOD1 C57S Mutant, As-isolated
Authors : Sea, K.; Sohn, S.H.; Durazo, A.; Sheng, Y.; Shaw, B.; Cao, X.; Taylor, A.B.; Whitson, L.J.; Holloway, S.P.; Hart, P.J.; Cabelli, D.E.; Gralla, E.B.; Valentine, J.S.
Deposited on : 2013-08-21
Resolution : 2.20 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

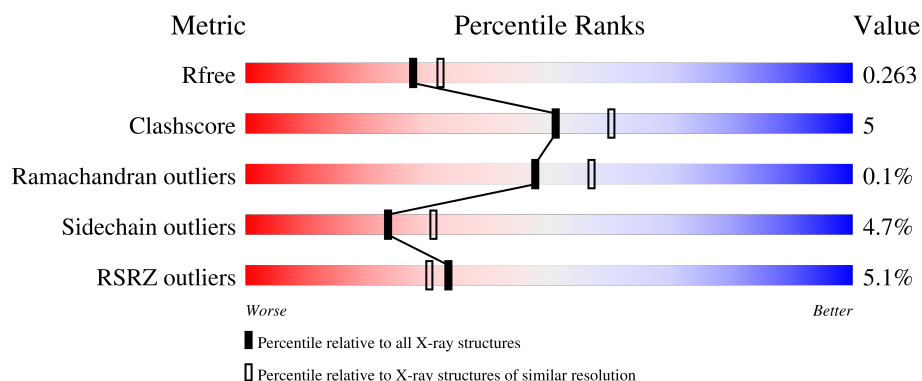
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

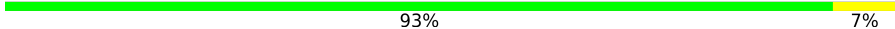
The reported resolution of this entry is 2.20 Å.

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	6164 (2.20-2.20)
Clashscore	190562	6851 (2.20-2.20)
Ramachandran outliers	187476	6768 (2.20-2.20)
Sidechain outliers	187428	6769 (2.20-2.20)
RSRZ outliers	180081	6166 (2.20-2.20)

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	153	
1	B	153	
1	C	153	
1	D	153	
1	E	153	

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Mol	Chain	Length	Quality of chain
1	F	153	
1	G	153	
1	H	153	
1	I	153	
1	J	153	
1	K	153	
1	L	153	

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	C	203	-	-	X	-

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 14503 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	153	Total	C	N	O	S	0	1	0
			1115	682	203	227	3			
1	B	153	Total	C	N	O	S	0	0	0
			1110	679	203	225	3			
1	C	152	Total	C	N	O	S	0	0	0
			1105	676	202	224	3			
1	D	153	Total	C	N	O	S	0	0	0
			1110	679	203	225	3			
1	E	152	Total	C	N	O	S	0	0	0
			1105	676	202	224	3			
1	F	153	Total	C	N	O	S	0	0	0
			1110	679	203	225	3			
1	G	153	Total	C	N	O	S	0	0	0
			1110	679	203	225	3			
1	H	153	Total	C	N	O	S	0	0	0
			1110	679	203	225	3			
1	I	153	Total	C	N	O	S	0	0	0
			1110	679	203	225	3			
1	J	153	Total	C	N	O	S	0	0	0
			1110	679	203	225	3			
1	K	153	Total	C	N	O	S	0	0	0
			1110	679	203	225	3			
1	L	153	Total	C	N	O	S	0	0	0
			1110	679	203	225	3			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	57	SER	CYS	engineered mutation	UNP P00441
B	57	SER	CYS	engineered mutation	UNP P00441
C	57	SER	CYS	engineered mutation	UNP P00441
D	57	SER	CYS	engineered mutation	UNP P00441
E	57	SER	CYS	engineered mutation	UNP P00441

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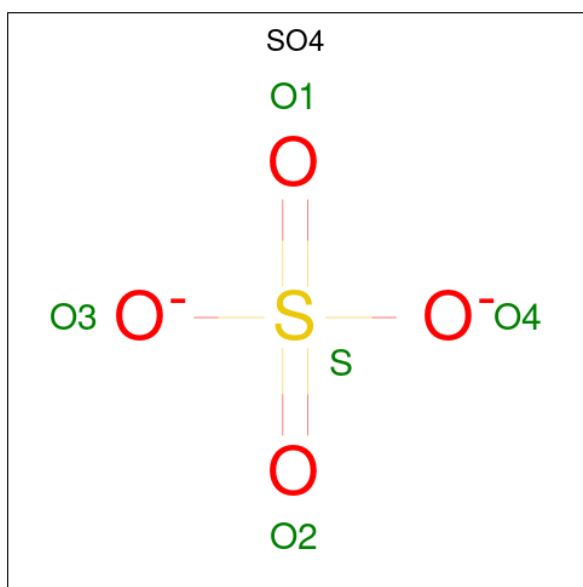
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Chain	Residue	Modelled	Actual	Comment	Reference
F	57	SER	CYS	engineered mutation	UNP P00441
G	57	SER	CYS	engineered mutation	UNP P00441
H	57	SER	CYS	engineered mutation	UNP P00441
I	57	SER	CYS	engineered mutation	UNP P00441
J	57	SER	CYS	engineered mutation	UNP P00441
K	57	SER	CYS	engineered mutation	UNP P00441
L	57	SER	CYS	engineered mutation	UNP P00441

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	2	Total	Zn	0	0
			2	2		
2	B	2	Total	Zn	0	0
			2	2		
2	C	2	Total	Zn	0	0
			2	2		
2	D	2	Total	Zn	0	0
			2	2		
2	E	2	Total	Zn	0	0
			2	2		
2	F	2	Total	Zn	0	0
			2	2		
2	G	2	Total	Zn	0	0
			2	2		
2	H	2	Total	Zn	0	0
			2	2		
2	I	2	Total	Zn	0	0
			2	2		
2	J	2	Total	Zn	0	0
			2	2		
2	K	2	Total	Zn	0	0
			2	2		
2	L	2	Total	Zn	0	0
			2	2		

- 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		
3	B	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		
3	C	1	Total	O	S	0	0
			5	4	1		
3	D	1	Total	O	S	0	0
			5	4	1		
3	E	1	Total	O	S	0	0
			5	4	1		
3	F	1	Total	O	S	0	0
			5	4	1		
3	G	1	Total	O	S	0	0
			5	4	1		
3	H	1	Total	O	S	0	0
			5	4	1		
3	H	1	Total	O	S	0	0
			5	4	1		
3	I	1	Total	O	S	0	0
			5	4	1		
3	J	1	Total	O	S	0	0
			5	4	1		
3	K	1	Total	O	S	0	0
			5	4	1		
3	L	1	Total	O	S	0	0
			5	4	1		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	142	Total 142	O 142	0	0
4	B	155	Total 155	O 155	0	0
4	C	21	Total 21	O 21	0	0
4	D	93	Total 93	O 93	0	0
4	E	37	Total 37	O 37	0	0
4	F	87	Total 87	O 87	0	0
4	G	137	Total 137	O 137	0	0
4	H	160	Total 160	O 160	0	0
4	I	52	Total 52	O 52	0	0
4	J	100	Total 100	O 100	0	0
4	K	33	Total 33	O 33	0	0
4	L	77	Total 77	O 77	0	0

3 Residue-property plots [i](#)

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]

Chain A:  93% 7%



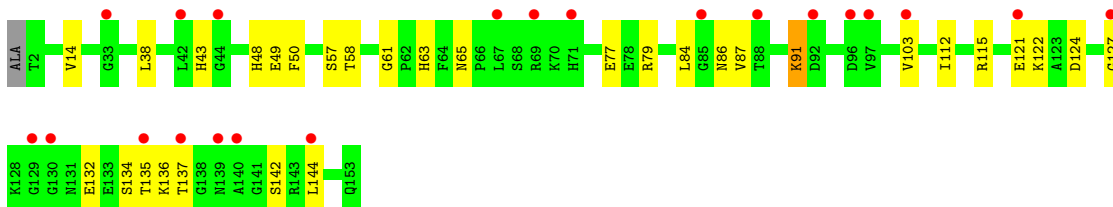
- Molecule 1: Superoxide dismutase [Cu-Zn]

Chain B:  92% 7%



- Molecule 1: Superoxide dismutase [Cu-Zn]

Chain C:  14% 79% 20%



- Molecule 1: Superoxide dismutase [Cu-Zn]

Chain D:  91% 9%

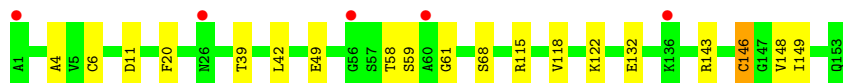
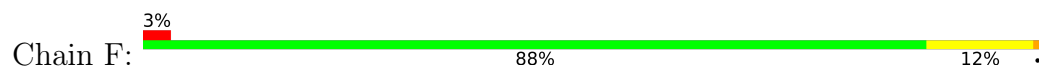


- Molecule 1: Superoxide dismutase [Cu-Zn]

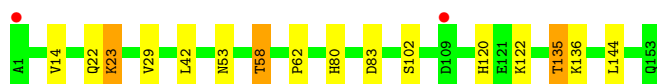
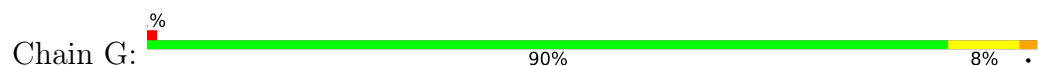
Chain E:  4% 88% 10%



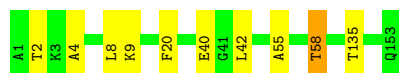
- Molecule 1: Superoxide dismutase [Cu-Zn]



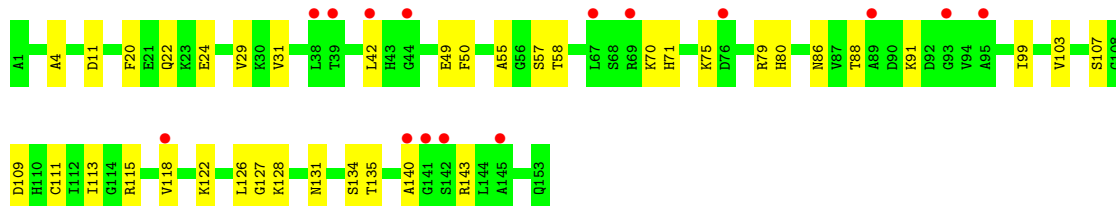
- Molecule 1: Superoxide dismutase [Cu-Zn]



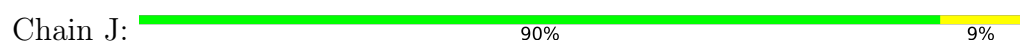
- Molecule 1: Superoxide dismutase [Cu-Zn]



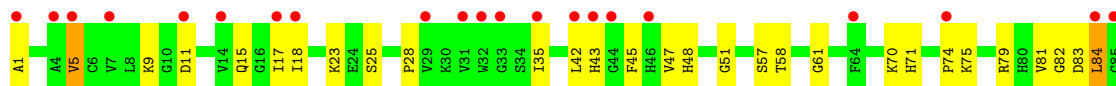
- Molecule 1: Superoxide dismutase [Cu-Zn]

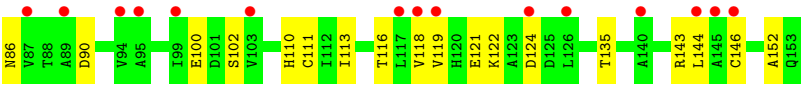


- Molecule 1: Superoxide dismutase [Cu-Zn]

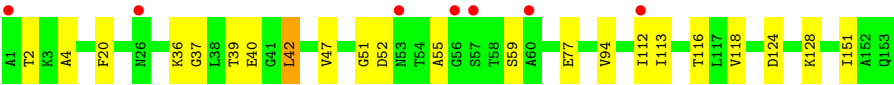
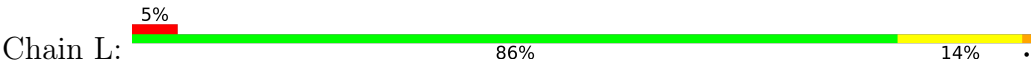


- Molecule 1: Superoxide dismutase [Cu-Zn]





• Molecule 1: Superoxide dismutase [Cu-Zn]



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	74.53Å 163.88Å 174.14Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.84 – 2.20 29.84 – 2.20	Depositor EDS
% Data completeness (in resolution range)	98.2 (29.84-2.20) 98.1 (29.84-2.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.36 (at 2.20Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.1_1161)	Depositor
R, R_{free}	0.210 , 0.262 0.213 , 0.263	Depositor DCC
R_{free} test set	5325 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å ²)	32.9	Xtriage
Anisotropy	0.329	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 39.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	14503	wwPDB-VP
Average B, all atoms (Å ²)	31.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.16% 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

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	0.57	0/1136	0.87	2/1531 (0.1%)
1	B	0.60	0/1128	0.88	2/1520 (0.1%)
1	C	0.40	0/1123	0.84	0/1513
1	D	0.52	0/1128	0.86	1/1520 (0.1%)
1	E	0.45	0/1123	0.87	1/1513 (0.1%)
1	F	0.55	0/1128	0.88	0/1520
1	G	0.58	0/1128	0.84	0/1520
1	H	0.61	0/1128	0.85	0/1520
1	I	0.45	0/1128	0.85	0/1520
1	J	0.54	0/1128	0.89	0/1520
1	K	0.40	0/1128	0.81	1/1520 (0.1%)
1	L	0.54	0/1128	0.86	0/1520
All	All	0.52	0/13534	0.86	7/18237 (0.0%)

There are no bond length outliers.

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	K	110	HIS	N-CA-C	-7.17	103.63	112.88
1	D	49	GLU	N-CA-C	5.81	117.29	111.07
1	A	12	GLY	CA-C-N	5.39	125.86	120.04
1	A	12	GLY	C-N-CA	5.39	125.86	120.04
1	B	27	GLY	CA-C-N	5.20	125.10	119.85
1	B	27	GLY	C-N-CA	5.20	125.10	119.85
1	E	120	HIS	N-CA-C	5.07	117.96	110.46

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	1115	0	1083	3	0
1	B	1110	0	1079	6	0
1	C	1105	0	1071	18	0
1	D	1110	0	1079	9	0
1	E	1105	0	1071	12	0
1	F	1110	0	1079	9	0
1	G	1110	0	1079	10	0
1	H	1110	0	1079	5	0
1	I	1110	0	1079	20	0
1	J	1110	0	1079	9	0
1	K	1110	0	1079	25	0
1	L	1110	0	1079	17	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
2	C	2	0	0	0	0
2	D	2	0	0	0	0
2	E	2	0	0	0	0
2	F	2	0	0	0	0
2	G	2	0	0	0	0
2	H	2	0	0	0	0
2	I	2	0	0	0	0
2	J	2	0	0	0	0
2	K	2	0	0	0	0
2	L	2	0	0	0	0
3	A	5	0	0	0	0
3	B	10	0	0	0	0
3	C	5	0	0	2	0
3	D	5	0	0	0	0
3	E	5	0	0	0	0
3	F	5	0	0	0	0
3	G	5	0	0	1	0
3	H	10	0	0	0	0
3	I	5	0	0	1	0
3	J	5	0	0	1	0
3	K	5	0	0	0	0
3	L	5	0	0	0	0
4	A	142	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	B	155	0	0	2	0
4	C	21	0	0	2	0
4	D	93	0	0	1	0
4	E	37	0	0	3	0
4	F	87	0	0	2	0
4	G	137	0	0	6	0
4	H	160	0	0	2	0
4	I	52	0	0	2	0
4	J	100	0	0	2	0
4	K	33	0	0	2	0
4	L	77	0	0	6	0
All	All	14503	0	12936	138	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.

All (138) 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:K:5:VAL:HG23	1:K:152:ALA:HB2	1.74	0.69
1:E:42:LEU:HB3	1:E:123:ALA:HB2	1.73	0.69
1:K:9:LYS:HD2	1:K:15:GLN:HB2	1.73	0.69
1:K:45:PHE:HD2	1:K:84:LEU:HD11	1.59	0.68
1:L:55:ALA:HB3	1:L:59:SER:HB3	1.75	0.68
1:L:39:THR:HB	4:L:349:HOH:O	1.95	0.66
1:E:6:CYS:HB2	1:E:149:ILE:HG22	1.78	0.65
1:F:49:GLU:O	1:F:115:ARG:NH1	2.30	0.63
1:E:2:THR:N	1:E:22:GLN:O	2.32	0.63
1:K:5:VAL:HG22	4:K:330:HOH:O	1.99	0.63
1:K:79:ARG:NH2	1:K:83:ASP:O	2.31	0.63
1:C:121:GLU:HG2	1:C:142:SER:H	1.65	0.62
1:J:136:LYS:NZ	4:J:371:HOH:O	2.22	0.61
1:I:91:LYS:HD3	1:I:91:LYS:H	1.64	0.61
1:I:55:ALA:O	1:I:58:THR:HG22	2.01	0.60
1:C:50:PHE:CZ	1:D:153:GLN:HB3	2.37	0.59
1:K:48:HIS:ND1	1:K:61:GLY:O	2.35	0.59
1:D:153:GLN:NE2	4:D:360:HOH:O	2.32	0.59
1:I:49:GLU:O	1:I:115:ARG:NH1	2.34	0.59
1:K:45:PHE:CD2	1:K:84:LEU:HD11	2.37	0.59
1:D:53:ASN:ND2	1:D:53:ASN:O	2.37	0.58
1:K:121:GLU:HA	1:K:144:LEU:HD11	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:135:THR:HA	4:G:432:HOH:O	2.06	0.55
1:I:50:PHE:CZ	1:J:153:GLN:HB3	2.41	0.55
1:K:118:VAL:HG11	1:K:143:ARG:HG2	1.90	0.54
1:C:14:VAL:HG21	1:C:144:LEU:HD13	1.90	0.54
1:E:55:ALA:O	1:E:58:THR:OG1	2.24	0.53
1:F:39:THR:HG22	1:J:37:GLY:HA2	1.90	0.52
1:C:87:VAL:HA	4:C:314:HOH:O	2.08	0.52
1:K:48:HIS:HD2	1:K:118:VAL:HB	1.74	0.52
1:B:71:HIS:HB2	1:B:80:HIS:CE1	2.44	0.52
1:L:113:ILE:HD13	1:L:151:ILE:HG12	1.92	0.51
1:C:91:LYS:HD3	1:C:91:LYS:H	1.76	0.51
1:J:143:ARG:NE	3:J:203:SO4:O4	2.44	0.51
1:K:81:VAL:HG13	4:K:328:HOH:O	2.12	0.50
1:C:121:GLU:HG3	1:C:122:LYS:H	1.76	0.50
1:C:49:GLU:O	1:C:115:ARG:HD3	2.11	0.50
1:B:55:ALA:O	1:B:58:THR:HG23	2.11	0.50
1:J:75:LYS:HE2	1:L:128:LYS:HE3	1.94	0.49
1:E:36:LYS:HB3	4:E:327:HOH:O	2.11	0.49
1:I:126:LEU:HB2	1:I:128:LYS:HE2	1.93	0.49
1:C:63:HIS:NE2	3:C:203:SO4:O3	2.44	0.49
1:C:79:ARG:CZ	1:C:103:VAL:HG11	2.43	0.49
1:I:127:GLY:HA2	1:I:134:SER:O	2.12	0.49
1:L:47:VAL:HG11	1:L:112:ILE:HD11	1.93	0.49
1:C:48:HIS:ND1	1:C:61:GLY:O	2.44	0.49
1:F:4:ALA:HB3	1:F:20:PHE:HB2	1.94	0.49
1:J:71:HIS:HB2	1:J:80:HIS:CE1	2.48	0.49
1:B:132:GLU:CD	1:B:132:GLU:H	2.20	0.48
1:G:136:LYS:NZ	4:G:402:HOH:O	2.45	0.48
1:L:40:GLU:N	4:L:349:HOH:O	2.46	0.48
1:K:28:PRO:HB3	1:K:102:SER:HB3	1.95	0.48
1:K:43:HIS:HA	1:K:122:LYS:O	2.13	0.48
1:C:121:GLU:HG2	1:C:142:SER:N	2.29	0.48
1:F:6:CYS:HB2	1:F:149:ILE:HA	1.96	0.48
1:K:71:HIS:NE2	1:K:124:ASP:OD1	2.45	0.47
1:E:153:GLN:HB2	4:E:310:HOH:O	2.14	0.47
1:A:71:HIS:HB2	1:A:80:HIS:CE1	2.50	0.47
1:G:58:THR:HG22	4:G:385:HOH:O	2.15	0.47
1:I:143:ARG:NH2	3:I:203:SO4:O2	2.46	0.47
1:H:4:ALA:HB3	1:H:20:PHE:HB2	1.97	0.47
1:J:52:ASP:HB3	1:J:59:SER:O	2.15	0.47
1:E:55:ALA:HB3	1:E:59:SER:HB3	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:74:PRO:HG2	1:K:75:LYS:HD2	1.97	0.47
1:L:42:LEU:HD22	4:L:356:HOH:O	2.15	0.47
1:L:4:ALA:HB3	1:L:20:PHE:HB2	1.97	0.46
1:C:86:ASN:OD1	1:C:124:ASP:N	2.48	0.46
1:C:127:GLY:HA2	1:C:134:SER:O	2.16	0.45
1:D:113:ILE:HD13	1:D:151:ILE:HG12	1.99	0.45
1:D:121:GLU:HA	1:D:144:LEU:HD11	1.98	0.45
1:E:153:GLN:HG2	4:E:301:HOH:O	2.16	0.45
1:F:118:VAL:HG22	1:F:146:CYS:HB2	1.97	0.45
1:K:1:ALA:HA	1:K:23:LYS:HA	1.97	0.45
1:E:22:GLN:HG2	1:E:24:GLU:O	2.16	0.45
1:K:57:SER:O	1:K:143:ARG:NH1	2.46	0.45
1:C:112:ILE:HA	1:C:115:ARG:HG3	1.97	0.45
1:I:79:ARG:CZ	1:I:103:VAL:HG11	2.46	0.45
1:E:14:VAL:HG21	1:E:144:LEU:HD13	1.99	0.45
1:K:47:VAL:HB	1:K:82:GLY:HA2	1.97	0.45
1:I:111:CYS:HA	4:I:333:HOH:O	2.16	0.44
1:I:71:HIS:HB2	1:I:80:HIS:CE1	2.52	0.44
1:K:18:ILE:HD13	1:K:45:PHE:HZ	1.82	0.44
1:F:39:THR:HG21	4:J:321:HOH:O	2.17	0.44
1:F:61:GLY:O	1:F:143:ARG:NH2	2.49	0.44
1:B:153:GLN:O	4:B:433:HOH:O	2.21	0.44
1:E:14:VAL:HG21	1:E:144:LEU:HB3	1.99	0.44
1:L:47:VAL:HG11	1:L:112:ILE:HG13	1.97	0.44
1:L:47:VAL:HG11	1:L:112:ILE:CD1	2.48	0.44
1:L:47:VAL:HG11	1:L:112:ILE:CG1	2.47	0.44
1:G:120:HIS:HE1	3:G:203:SO4:O2	2.01	0.44
1:H:58:THR:HG22	4:H:458:HOH:O	2.18	0.44
1:I:118:VAL:HG11	1:I:143:ARG:HG2	2.00	0.44
1:F:132:GLU:HB3	4:F:387:HOH:O	2.18	0.44
1:G:22:GLN:HB2	1:G:29:VAL:HG22	1.99	0.44
1:L:124:ASP:OD2	4:L:320:HOH:O	2.21	0.44
1:J:80:HIS:HB2	1:J:83:ASP:CG	2.43	0.43
1:D:108:GLY:O	1:D:111:CYS:HB2	2.19	0.43
1:I:70:LYS:NZ	4:I:345:HOH:O	2.40	0.43
1:K:75:LYS:HD2	1:K:75:LYS:N	2.33	0.43
1:H:8:LEU:O	1:H:9:LYS:HD3	2.18	0.43
1:D:80:HIS:HB2	1:D:83:ASP:CG	2.44	0.43
1:I:42:LEU:HB2	1:I:86:ASN:HB3	2.01	0.42
1:I:131:ASN:OD1	1:I:134:SER:N	2.50	0.42
1:H:55:ALA:O	1:H:58:THR:HG23	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:36:LYS:HE3	4:B:320:HOH:O	2.19	0.42
1:K:5:VAL:HG21	1:L:52:ASP:OD2	2.20	0.42
1:C:121:GLU:HG3	1:C:122:LYS:N	2.34	0.42
1:I:22:GLN:HB2	1:I:29:VAL:HG22	2.02	0.42
1:I:75:LYS:HD3	1:I:75:LYS:HA	1.78	0.42
1:L:51:GLY:HA2	1:L:116:THR:OG1	2.19	0.42
1:A:121:GLU:HB2	1:A:142:SER:HB2	2.01	0.42
1:G:14:VAL:HG21	1:G:144:LEU:HD13	2.02	0.42
1:A:31:VAL:HB	1:A:99:ILE:HB	2.02	0.42
1:C:38:LEU:HD13	1:C:43:HIS:CD2	2.55	0.42
1:L:116:THR:HG22	1:L:118:VAL:HG23	2.01	0.42
1:G:53:ASN:ND2	4:G:386:HOH:O	2.42	0.41
1:G:80:HIS:HB2	1:G:83:ASP:CG	2.45	0.41
1:J:55:ALA:O	1:J:58:THR:HG23	2.20	0.41
1:L:77:GLU:HG3	4:L:308:HOH:O	2.19	0.41
1:I:31:VAL:HB	1:I:99:ILE:HB	2.01	0.41
1:I:4:ALA:HB3	1:I:20:PHE:HB2	2.02	0.41
1:I:122:LYS:N	1:I:140:ALA:O	2.44	0.41
1:K:42:LEU:HD22	1:K:86:ASN:HB3	2.01	0.41
1:C:137:THR:HB	3:C:203:SO4:O4	2.20	0.41
1:K:48:HIS:N	1:K:116:THR:O	2.47	0.41
1:C:65:ASN:HA	4:C:302:HOH:O	2.21	0.41
1:D:105:SER:O	1:D:111:CYS:HA	2.21	0.41
1:F:148:VAL:HB	4:F:385:HOH:O	2.20	0.41
1:K:70:LYS:HE3	1:K:135:THR:HB	2.03	0.41
1:G:23:LYS:NZ	4:G:414:HOH:O	2.53	0.41
1:H:40:GLU:HB3	4:H:425:HOH:O	2.21	0.41
1:B:132:GLU:CD	1:B:132:GLU:N	2.79	0.41
1:L:37:GLY:O	4:L:337:HOH:O	2.22	0.41
1:I:42:LEU:HA	1:I:88:THR:HA	2.03	0.41
1:D:26:ASN:OD1	1:D:26:ASN:N	2.54	0.40
1:G:62:PRO:HA	4:G:341:HOH:O	2.19	0.40
1:E:51:GLY:HA2	1:E:116:THR:OG1	2.22	0.40
1:K:51:GLY:HA2	1:K:116:THR:OG1	2.21	0.40

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	152/153 (99%)	149 (98%)	3 (2%)	0	100	100
1	B	151/153 (99%)	149 (99%)	2 (1%)	0	100	100
1	C	150/153 (98%)	139 (93%)	11 (7%)	0	100	100
1	D	151/153 (99%)	149 (99%)	2 (1%)	0	100	100
1	E	150/153 (98%)	143 (95%)	7 (5%)	0	100	100
1	F	151/153 (99%)	145 (96%)	6 (4%)	0	100	100
1	G	151/153 (99%)	147 (97%)	4 (3%)	0	100	100
1	H	151/153 (99%)	148 (98%)	3 (2%)	0	100	100
1	I	151/153 (99%)	142 (94%)	9 (6%)	0	100	100
1	J	151/153 (99%)	150 (99%)	1 (1%)	0	100	100
1	K	151/153 (99%)	141 (93%)	9 (6%)	1 (1%)	18	19
1	L	151/153 (99%)	146 (97%)	5 (3%)	0	100	100
All	All	1811/1836 (99%)	1748 (96%)	62 (3%)	1 (0%)	48	57

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	K	90	ASP

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	119/118 (101%)	116 (98%)	3 (2%)	42	56
1	B	118/118 (100%)	112 (95%)	6 (5%)	21	27
1	C	118/118 (100%)	110 (93%)	8 (7%)	14	17
1	D	118/118 (100%)	117 (99%)	1 (1%)	73	85
1	E	118/118 (100%)	114 (97%)	4 (3%)	32	44
1	F	118/118 (100%)	111 (94%)	7 (6%)	18	22
1	G	118/118 (100%)	112 (95%)	6 (5%)	21	27
1	H	118/118 (100%)	114 (97%)	4 (3%)	32	44
1	I	118/118 (100%)	111 (94%)	7 (6%)	18	22
1	J	118/118 (100%)	114 (97%)	4 (3%)	32	44
1	K	118/118 (100%)	106 (90%)	12 (10%)	7	7
1	L	118/118 (100%)	114 (97%)	4 (3%)	32	44
All	All	1417/1416 (100%)	1351 (95%)	66 (5%)	23	31

All (66) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	58	THR
1	A	91	LYS
1	A	133	GLU
1	B	2	THR
1	B	24	GLU
1	B	42	LEU
1	B	58	THR
1	B	77	GLU
1	B	132	GLU
1	C	57	SER
1	C	58	THR
1	C	77	GLU
1	C	84	LEU
1	C	91	LYS
1	C	132	GLU
1	C	135	THR
1	C	136	LYS
1	D	42	LEU
1	E	2	THR
1	E	21	GLU
1	E	149	ILE
1	E	153	GLN

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Mol	Chain	Res	Type
1	F	11	ASP
1	F	42	LEU
1	F	58	THR
1	F	59	SER
1	F	68	SER
1	F	122	LYS
1	F	146	CYS
1	G	23	LYS
1	G	42	LEU
1	G	58	THR
1	G	102	SER
1	G	122	LYS
1	G	135	THR
1	H	2	THR
1	H	42	LEU
1	H	58	THR
1	H	135	THR
1	I	11	ASP
1	I	24	GLU
1	I	57	SER
1	I	107	SER
1	I	109	ASP
1	I	113	ILE
1	I	135	THR
1	J	2	THR
1	J	34	SER
1	J	42	LEU
1	J	58	THR
1	K	5	VAL
1	K	11	ASP
1	K	17	ILE
1	K	25	SER
1	K	35	ILE
1	K	58	THR
1	K	84	LEU
1	K	100	GLU
1	K	111	CYS
1	K	113	ILE
1	K	119	VAL
1	K	146	CYS
1	L	2	THR
1	L	36	LYS

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Mol	Chain	Res	Type
1	L	42	LEU
1	L	94	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	15	GLN
1	C	131	ASN
1	C	139	ASN
1	E	53	ASN
1	F	26	ASN
1	F	53	ASN
1	G	53	ASN
1	I	15	GLN
1	I	53	ASN
1	K	53	ASN
1	L	15	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 [i](#)

Of 38 ligands modelled in this entry, 24 are monoatomic - leaving 14 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	F	203	-	4,4,4	0.30	0	6,6,6	0.17	0
3	SO4	G	203	2	4,4,4	0.22	0	6,6,6	0.30	0
3	SO4	E	203	2	4,4,4	0.25	0	6,6,6	0.24	0
3	SO4	H	203	2	4,4,4	0.20	0	6,6,6	0.46	0
3	SO4	I	203	2	4,4,4	0.27	0	6,6,6	0.28	0
3	SO4	K	203	2	4,4,4	0.26	0	6,6,6	0.20	0
3	SO4	B	204	-	4,4,4	0.38	0	6,6,6	0.27	0
3	SO4	C	203	2	4,4,4	0.24	0	6,6,6	0.23	0
3	SO4	D	203	-	4,4,4	0.25	0	6,6,6	0.20	0
3	SO4	H	204	-	4,4,4	0.33	0	6,6,6	0.30	0
3	SO4	J	203	2	4,4,4	0.30	0	6,6,6	0.37	0
3	SO4	L	203	2	4,4,4	0.23	0	6,6,6	0.07	0
3	SO4	B	203	2	4,4,4	0.18	0	6,6,6	0.46	0
3	SO4	A	203	2	4,4,4	0.25	0	6,6,6	0.37	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.

4 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	G	203	SO4	1	0
3	I	203	SO4	1	0
3	C	203	SO4	2	0
3	J	203	SO4	1	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	153/153 (100%)	-0.43	0 100 100	9, 17, 29, 38	1 (0%)
1	B	153/153 (100%)	-0.54	2 (1%) 75 73	7, 14, 28, 36	0
1	C	152/153 (99%)	1.13	21 (13%) 6 5	26, 50, 72, 84	0
1	D	153/153 (100%)	-0.22	0 100 100	13, 25, 45, 51	0
1	E	152/153 (99%)	0.92	6 (3%) 43 40	27, 42, 64, 72	0
1	F	153/153 (100%)	0.29	5 (3%) 49 46	13, 27, 47, 57	0
1	G	153/153 (100%)	-0.40	2 (1%) 75 73	9, 19, 32, 42	0
1	H	153/153 (100%)	-0.58	0 100 100	7, 14, 28, 46	0
1	I	153/153 (100%)	0.92	15 (9%) 13 10	25, 43, 63, 76	0
1	J	153/153 (100%)	-0.24	0 100 100	10, 22, 40, 48	0
1	K	153/153 (100%)	1.43	36 (23%) 2 1	36, 57, 76, 82	0
1	L	153/153 (100%)	0.37	7 (4%) 37 34	17, 31, 54, 72	0
All	All	1834/1836 (99%)	0.22	94 (5%) 33 30	7, 28, 63, 84	1 (0%)

All (94) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	135	THR	4.1
1	E	150	GLY	3.7
1	K	94	VAL	3.6
1	K	17	ILE	3.5
1	K	144	LEU	3.5
1	F	60	ALA	3.4
1	K	35	ILE	3.4
1	K	145	ALA	3.4
1	L	1	ALA	3.4
1	C	85	GLY	3.4
1	L	56	GLY	3.4

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Mol	Chain	Res	Type	RSRZ
1	K	18	ILE	3.2
1	L	53	ASN	3.2
1	E	152	ALA	3.1
1	I	140	ALA	3.1
1	K	95	ALA	3.0
1	C	129	GLY	3.0
1	K	126	LEU	3.0
1	G	1	ALA	3.0
1	K	146	CYS	3.0
1	L	57	SER	2.9
1	K	42	LEU	2.9
1	E	149	ILE	2.9
1	K	11	ASP	2.9
1	C	140	ALA	2.9
1	I	42	LEU	2.9
1	K	64	PHE	2.9
1	K	84	LEU	2.8
1	I	95	ALA	2.8
1	K	32	TRP	2.8
1	B	26	ASN	2.7
1	G	109	ASP	2.7
1	L	112	ILE	2.7
1	C	44	GLY	2.6
1	K	74	PRO	2.6
1	K	46	HIS	2.6
1	K	89	ALA	2.6
1	C	69	ARG	2.6
1	K	99	ILE	2.6
1	I	93	GLY	2.6
1	K	29	VAL	2.5
1	C	139	ASN	2.5
1	I	89	ALA	2.5
1	K	44	GLY	2.5
1	K	7	VAL	2.5
1	K	87	VAL	2.5
1	C	42	LEU	2.5
1	I	67	LEU	2.5
1	C	127	GLY	2.5
1	C	130	GLY	2.5
1	I	44	GLY	2.5
1	C	97	VAL	2.5
1	K	118	VAL	2.5

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Mol	Chain	Res	Type	RSRZ
1	C	92	ASP	2.4
1	B	1	ALA	2.4
1	K	85	GLY	2.4
1	F	56	GLY	2.4
1	K	103	VAL	2.4
1	F	26	ASN	2.3
1	L	26	ASN	2.3
1	I	145	ALA	2.3
1	C	121	GLU	2.3
1	E	5	VAL	2.3
1	K	119	VAL	2.3
1	E	30	LYS	2.3
1	K	33	GLY	2.3
1	K	1	ALA	2.3
1	I	141	GLY	2.2
1	C	71	HIS	2.2
1	C	88	THR	2.2
1	K	43	HIS	2.2
1	L	60	ALA	2.2
1	E	110	HIS	2.2
1	K	14	VAL	2.2
1	K	140	ALA	2.2
1	F	1	ALA	2.2
1	I	118	VAL	2.1
1	C	137	THR	2.1
1	I	142	SER	2.1
1	I	38	LEU	2.1
1	C	33	GLY	2.1
1	C	144	LEU	2.1
1	I	76	ASP	2.1
1	K	5	VAL	2.1
1	K	31	VAL	2.1
1	I	39	THR	2.1
1	C	96	ASP	2.1
1	K	124	ASP	2.1
1	C	103	VAL	2.1
1	K	4	ALA	2.0
1	C	67	LEU	2.0
1	K	117	LEU	2.0
1	F	136	LYS	2.0
1	I	69	ARG	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.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	SO4	H	204	5/5	0.53	0.18	33,48,50,70	5
3	SO4	B	204	5/5	0.63	0.13	42,44,49,67	0
3	SO4	C	203	5/5	0.80	0.16	54,56,63,69	5
3	SO4	D	203	5/5	0.86	0.13	27,32,34,38	5
3	SO4	I	203	5/5	0.87	0.10	42,42,54,58	5
3	SO4	F	203	5/5	0.89	0.12	31,33,40,42	5
3	SO4	K	203	5/5	0.90	0.12	46,49,56,60	5
3	SO4	J	203	5/5	0.92	0.10	17,20,22,25	5
3	SO4	B	203	5/5	0.93	0.09	14,22,23,26	5
3	SO4	H	203	5/5	0.93	0.10	11,15,22,23	5
3	SO4	E	203	5/5	0.93	0.10	24,34,37,37	5
2	ZN	C	201	1/1	0.94	0.06	62,62,62,62	1
3	SO4	L	203	5/5	0.94	0.09	26,30,37,37	5
2	ZN	C	202	1/1	0.95	0.06	49,49,49,49	1
2	ZN	E	201	1/1	0.96	0.04	36,36,36,36	1
2	ZN	F	201	1/1	0.96	0.04	40,40,40,40	0
2	ZN	K	202	1/1	0.96	0.04	46,46,46,46	1
2	ZN	J	201	1/1	0.97	0.04	26,26,26,26	1
2	ZN	K	201	1/1	0.97	0.04	58,58,58,58	0
2	ZN	D	201	1/1	0.97	0.05	32,32,32,32	1
2	ZN	I	201	1/1	0.98	0.03	45,45,45,45	1
2	ZN	I	202	1/1	0.98	0.04	32,32,32,32	0
2	ZN	E	202	1/1	0.98	0.03	28,28,28,28	0
2	ZN	B	201	1/1	0.98	0.03	21,21,21,21	1
2	ZN	F	202	1/1	0.98	0.03	23,23,23,23	0
3	SO4	A	203	5/5	0.98	0.07	15,16,21,22	5
2	ZN	H	201	1/1	0.99	0.02	23,23,23,23	1

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	ZN	B	202	1/1	0.99	0.02	13,13,13,13	0
2	ZN	L	201	1/1	0.99	0.02	36,36,36,36	1
2	ZN	A	201	1/1	0.99	0.02	22,22,22,22	1
2	ZN	G	201	1/1	0.99	0.02	20,20,20,20	1
3	SO4	G	203	5/5	0.99	0.04	16,21,23,25	5
2	ZN	H	202	1/1	1.00	0.02	12,12,12,12	0
2	ZN	A	202	1/1	1.00	0.02	13,13,13,13	0
2	ZN	G	202	1/1	1.00	0.03	15,15,15,15	0
2	ZN	L	202	1/1	1.00	0.03	20,20,20,20	0
2	ZN	D	202	1/1	1.00	0.03	15,15,15,15	0
2	ZN	J	202	1/1	1.00	0.01	12,12,12,12	0

6.5 Other polymers [i](#)

There are no such residues in this entry.