



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 09:58 AM GMT

PDB ID : 3KCM  
Title : The crystal structure of thioredoxin protein from *Geobacter metallireducens*  
Authors : Zhang, Z.; Burley, S.K.; Swaminathan, S.; New York SGX Research Center  
for Structural Genomics (NYSGXRC)  
Deposited on : 2009-10-21  
Resolution : 2.45 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

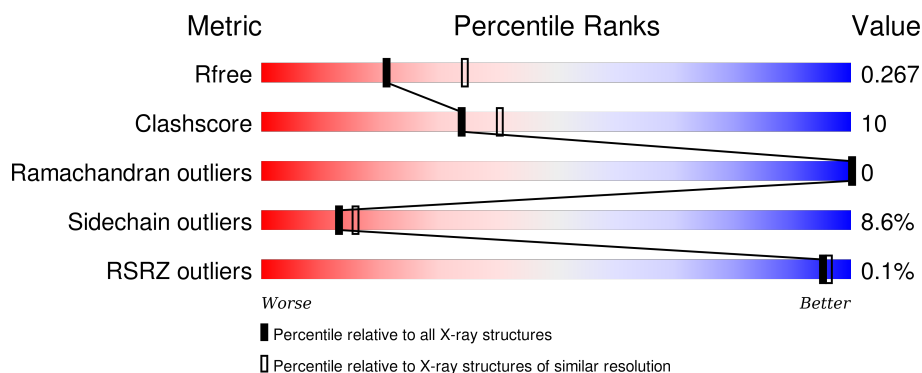
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.45 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	4776 (2.50-2.42)
Clashscore	102246	1030 (2.48-2.44)
Ramachandran outliers	100387	1024 (2.48-2.44)
Sidechain outliers	100360	1024 (2.48-2.44)
RSRZ outliers	91569	4787 (2.50-2.42)

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	154	
1	B	154	
1	C	154	
1	D	154	
1	E	154	

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Mol	Chain	Length	Quality of chain
1	F	154	 A horizontal bar chart showing the quality of the chain. The bar is divided into three segments: green (63%), yellow (25%), and orange (10%). The segments are labeled with their respective percentages: 63%, 25%, and 10%.

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 6720 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 Thioredoxin family protein.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	139	Total	C	N	O	S	Se	0	0	0
			1081	698	179	196	3	5			
1	B	141	Total	C	N	O	S	Se	0	0	0
			1088	704	180	196	3	5			
1	C	139	Total	C	N	O	S	Se	0	0	0
			1075	695	177	195	3	5			
1	D	142	Total	C	N	O	S	Se	0	0	0
			1091	705	181	197	3	5			
1	E	141	Total	C	N	O	S	Se	0	0	0
			1094	706	184	196	3	5			
1	F	138	Total	C	N	O	S	Se	0	0	0
			1063	687	176	192	3	5			

There are 66 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	25	MSE	-	expression tag	UNP Q39SU7
A	26	SER	-	expression tag	UNP Q39SU7
A	27	LEU	-	expression tag	UNP Q39SU7
A	171	GLU	-	expression tag	UNP Q39SU7
A	172	GLY	-	expression tag	UNP Q39SU7
A	173	HIS	-	expression tag	UNP Q39SU7
A	174	HIS	-	expression tag	UNP Q39SU7
A	175	HIS	-	expression tag	UNP Q39SU7
A	176	HIS	-	expression tag	UNP Q39SU7
A	177	HIS	-	expression tag	UNP Q39SU7
A	178	HIS	-	expression tag	UNP Q39SU7
B	25	MSE	-	expression tag	UNP Q39SU7
B	26	SER	-	expression tag	UNP Q39SU7
B	27	LEU	-	expression tag	UNP Q39SU7
B	171	GLU	-	expression tag	UNP Q39SU7
B	172	GLY	-	expression tag	UNP Q39SU7
B	173	HIS	-	expression tag	UNP Q39SU7

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Chain	Residue	Modelled	Actual	Comment	Reference
B	174	HIS	-	expression tag	UNP Q39SU7
B	175	HIS	-	expression tag	UNP Q39SU7
B	176	HIS	-	expression tag	UNP Q39SU7
B	177	HIS	-	expression tag	UNP Q39SU7
B	178	HIS	-	expression tag	UNP Q39SU7
C	25	MSE	-	expression tag	UNP Q39SU7
C	26	SER	-	expression tag	UNP Q39SU7
C	27	LEU	-	expression tag	UNP Q39SU7
C	171	GLU	-	expression tag	UNP Q39SU7
C	172	GLY	-	expression tag	UNP Q39SU7
C	173	HIS	-	expression tag	UNP Q39SU7
C	174	HIS	-	expression tag	UNP Q39SU7
C	175	HIS	-	expression tag	UNP Q39SU7
C	176	HIS	-	expression tag	UNP Q39SU7
C	177	HIS	-	expression tag	UNP Q39SU7
C	178	HIS	-	expression tag	UNP Q39SU7
D	25	MSE	-	expression tag	UNP Q39SU7
D	26	SER	-	expression tag	UNP Q39SU7
D	27	LEU	-	expression tag	UNP Q39SU7
D	171	GLU	-	expression tag	UNP Q39SU7
D	172	GLY	-	expression tag	UNP Q39SU7
D	173	HIS	-	expression tag	UNP Q39SU7
D	174	HIS	-	expression tag	UNP Q39SU7
D	175	HIS	-	expression tag	UNP Q39SU7
D	176	HIS	-	expression tag	UNP Q39SU7
D	177	HIS	-	expression tag	UNP Q39SU7
D	178	HIS	-	expression tag	UNP Q39SU7
E	25	MSE	-	expression tag	UNP Q39SU7
E	26	SER	-	expression tag	UNP Q39SU7
E	27	LEU	-	expression tag	UNP Q39SU7
E	171	GLU	-	expression tag	UNP Q39SU7
E	172	GLY	-	expression tag	UNP Q39SU7
E	173	HIS	-	expression tag	UNP Q39SU7
E	174	HIS	-	expression tag	UNP Q39SU7
E	175	HIS	-	expression tag	UNP Q39SU7
E	176	HIS	-	expression tag	UNP Q39SU7
E	177	HIS	-	expression tag	UNP Q39SU7
E	178	HIS	-	expression tag	UNP Q39SU7
F	25	MSE	-	expression tag	UNP Q39SU7
F	26	SER	-	expression tag	UNP Q39SU7
F	27	LEU	-	expression tag	UNP Q39SU7
F	171	GLU	-	expression tag	UNP Q39SU7

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Chain	Residue	Modelled	Actual	Comment	Reference
F	172	GLY	-	expression tag	UNP Q39SU7
F	173	HIS	-	expression tag	UNP Q39SU7
F	174	HIS	-	expression tag	UNP Q39SU7
F	175	HIS	-	expression tag	UNP Q39SU7
F	176	HIS	-	expression tag	UNP Q39SU7
F	177	HIS	-	expression tag	UNP Q39SU7
F	178	HIS	-	expression tag	UNP Q39SU7

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		
2	D	1	Total	O	S	0	0
			5	4	1		
2	E	1	Total	O	S	0	0
			5	4	1		
2	F	1	Total	O	S	0	0
			5	4	1		

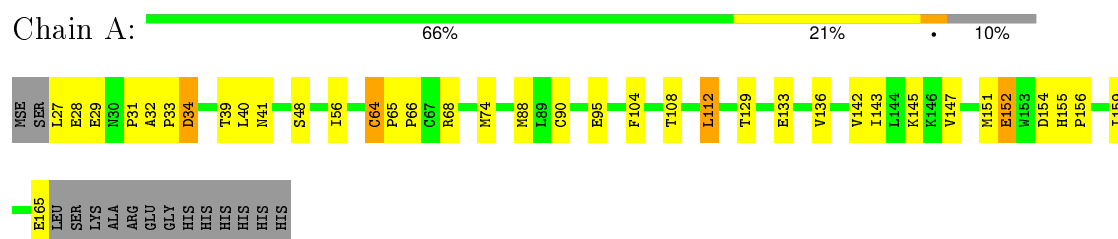
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	39	Total 39	O 39	0	0
3	B	28	Total 28	O 28	0	0
3	C	27	Total 27	O 27	0	0
3	D	37	Total 37	O 37	0	0
3	E	39	Total 39	O 39	0	0
3	F	28	Total 28	O 28	0	0

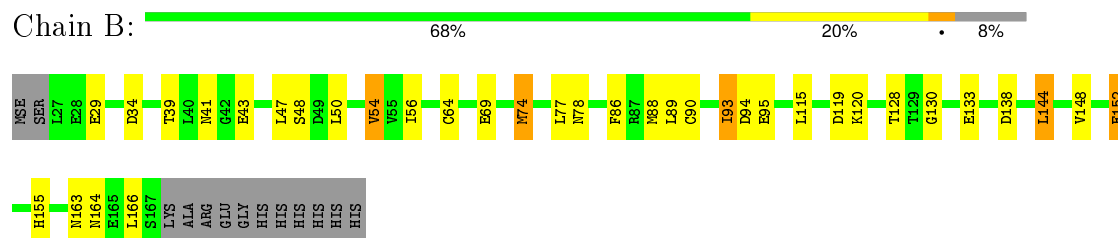
### 3 Residue-property plots

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.

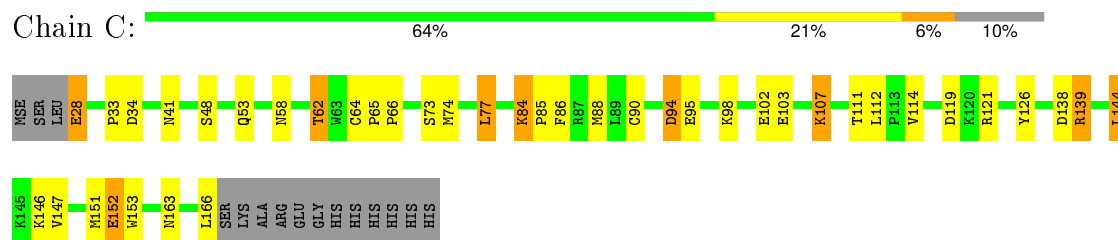
#### • Molecule 1: Thioredoxin family protein



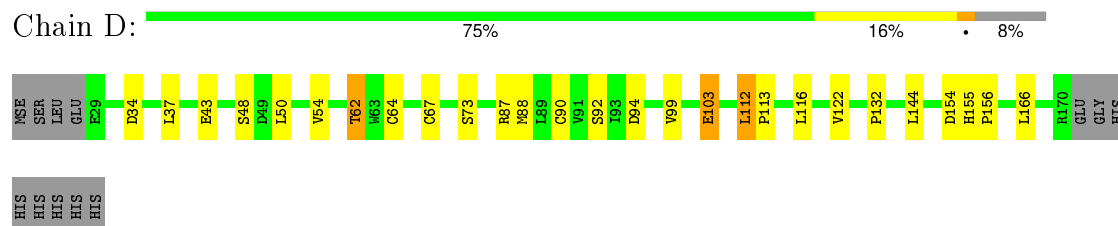
#### • Molecule 1: Thioredoxin family protein



#### • Molecule 1: Thioredoxin family protein

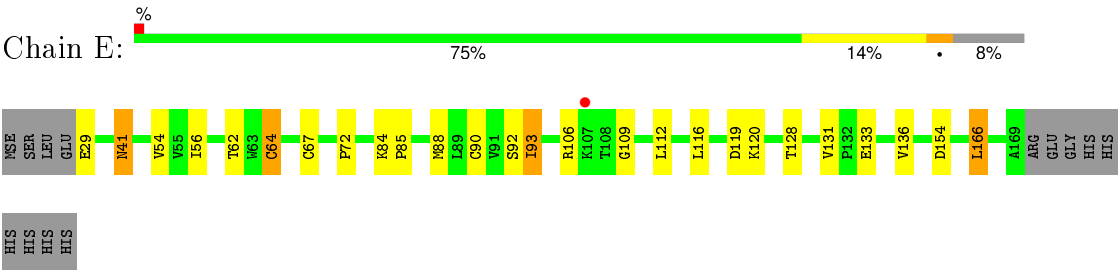


#### • Molecule 1: Thioredoxin family protein

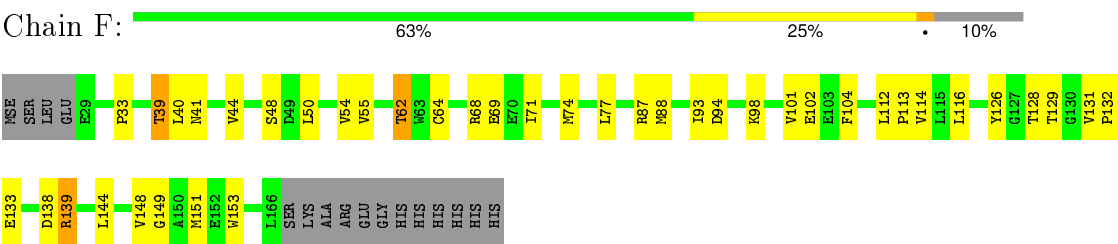




● Molecule 1: Thioredoxin family protein



● Molecule 1: Thioredoxin family protein



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	51.99Å 74.56Å 82.41Å 100.66° 109.05° 99.07°	Depositor
Resolution (Å)	75.36 – 2.45 75.36 – 2.45	Depositor EDS
% Data completeness (in resolution range)	94.4 (75.36-2.45) 86.8 (75.36-2.45)	Depositor EDS
$R_{merge}$	0.10	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.77 (at 2.45Å)	Xtriage
Refinement program	REFMAC 5.5.0072	Depositor
R, $R_{free}$	0.214 , 0.270 0.214 , 0.267	Depositor DCC
$R_{free}$ test set	1953 reflections (5.30%)	DCC
Wilson B-factor (Å <sup>2</sup> )	37.0	Xtriage
Anisotropy	0.050	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 40.6	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.30$	Xtriage
Outliers	0 of 38797 reflections	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	6720	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	23.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.82% 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: 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	0.90	0/1101	0.85	2/1487 (0.1%)
1	B	0.91	0/1108	0.89	0/1498
1	C	0.81	0/1095	0.85	0/1480
1	D	0.93	0/1111	0.91	1/1501 (0.1%)
1	E	0.97	0/1114	0.88	1/1503 (0.1%)
1	F	0.88	1/1083 (0.1%)	0.85	0/1464
All	All	0.90	1/6612 (0.0%)	0.87	4/8933 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	F	101	VAL	CB-CG2	-5.37	1.41	1.52

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	112	LEU	CA-CB-CG	5.67	128.34	115.30
1	A	34	ASP	CB-CG-OD1	5.47	123.22	118.30
1	E	154	ASP	CB-CG-OD2	5.36	123.12	118.30
1	A	112	LEU	CA-CB-CG	5.15	127.14	115.30

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	1081	0	1081	27	0
1	B	1088	0	1083	19	0
1	C	1075	0	1072	28	0
1	D	1091	0	1091	18	0
1	E	1094	0	1107	16	0
1	F	1063	0	1057	27	0
2	A	5	0	0	0	0
2	B	5	0	0	0	0
2	C	5	0	0	1	0
2	D	5	0	0	0	0
2	E	5	0	0	0	0
2	F	5	0	0	0	0
3	A	39	0	0	3	0
3	B	28	0	0	1	0
3	C	27	0	0	2	0
3	D	37	0	0	0	0
3	E	39	0	0	3	0
3	F	28	0	0	1	0
All	All	6720	0	6491	132	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 10.

All (132) 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:D:88:MSE:HE1	1:D:112:LEU:HD22	1.28	1.09
1:D:88:MSE:HE3	1:D:90:CYS:SG	2.03	0.98
1:D:88:MSE:CE	1:D:112:LEU:HD22	1.96	0.96
1:B:95:GLU:HG3	3:B:231:HOH:O	1.73	0.88
1:F:139:ARG:HE	1:F:139:ARG:H	1.22	0.88
1:A:39:THR:HG21	3:A:204:HOH:O	1.72	0.87
1:A:88:MSE:HE3	1:A:90:CYS:SG	2.16	0.85
1:C:139:ARG:HG2	3:C:247:HOH:O	1.76	0.85
1:C:28:GLU:OE1	1:C:146:LYS:HB2	1.80	0.81
1:A:88:MSE:CE	1:A:112:LEU:HD22	2.14	0.78
1:F:62:THR:HB	1:F:94:ASP:OD1	1.88	0.74
1:A:88:MSE:HE1	1:A:112:LEU:HD22	1.68	0.73
1:A:165:GLU:HG3	3:A:197:HOH:O	1.88	0.73
1:B:138:ASP:HB3	1:B:144:LEU:HD23	1.72	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:62:THR:HB	1:C:94:ASP:OD1	1.90	0.71
1:E:88:MSE:CE	1:E:112:LEU:HD22	2.21	0.71
1:C:95:GLU:HB2	2:C:6:SO4:O4	1.91	0.71
1:C:138:ASP:HB3	1:C:144:LEU:HD22	1.74	0.70
1:F:138:ASP:HB2	1:F:139:ARG:HH21	1.59	0.68
1:E:88:MSE:HE1	1:E:112:LEU:HD22	1.75	0.67
1:F:71:ILE:HA	1:F:74:MSE:HE2	1.77	0.67
1:D:88:MSE:HE1	1:D:112:LEU:CD2	2.14	0.67
1:C:84:LYS:HB3	1:C:85:PRO:HD2	1.78	0.65
1:B:133:GLU:HG2	1:B:148:VAL:HG12	1.78	0.64
1:C:163:ASN:HA	1:C:166:LEU:HD12	1.80	0.63
1:F:98:LYS:HG2	1:F:102:GLU:OE2	1.99	0.63
1:C:84:LYS:HE3	1:C:163:ASN:OD1	1.99	0.62
1:D:88:MSE:CE	1:D:90:CYS:SG	2.86	0.62
1:F:55:VAL:HA	1:F:87:ARG:O	2.01	0.60
1:A:152:GLU:HA	1:A:152:GLU:OE1	2.02	0.60
1:C:28:GLU:OE1	1:C:146:LYS:CB	2.50	0.59
1:C:77:LEU:HD13	1:C:153:TRP:O	2.02	0.59
1:F:93:ILE:HD13	1:F:131:VAL:HG11	1.84	0.59
1:C:74:MSE:CE	1:C:90:CYS:SG	2.90	0.59
1:B:74:MSE:HG2	1:B:88:MSE:SE	2.53	0.58
1:F:39:THR:HG23	1:F:41:ASN:H	1.67	0.58
1:F:133:GLU:HG3	1:F:148:VAL:HG12	1.85	0.58
1:A:88:MSE:CE	1:A:90:CYS:SG	2.91	0.58
1:A:154:ASP:OD2	1:A:155:HIS:CD2	2.57	0.58
1:F:88:MSE:HE3	1:F:113:PRO:CD	2.36	0.56
1:A:147:VAL:HG11	1:A:151:MSE:HG3	1.88	0.55
1:F:132:PRO:HD2	1:F:149:GLY:HA2	1.89	0.55
1:A:39:THR:HG22	1:A:40:LEU:N	2.22	0.55
1:C:98:LYS:O	1:C:102:GLU:HG2	2.07	0.54
1:C:84:LYS:HB3	1:C:85:PRO:CD	2.38	0.54
1:E:128:THR:HA	1:E:133:GLU:OE2	2.08	0.53
1:C:88:MSE:CE	1:C:112:LEU:HD22	2.39	0.53
1:A:31:PRO:HA	1:A:142:VAL:HA	1.91	0.53
1:B:89:LEU:HD22	1:B:115:LEU:HD11	1.91	0.53
1:F:138:ASP:HB2	1:F:139:ARG:NH2	2.22	0.53
1:A:39:THR:CG2	3:A:204:HOH:O	2.44	0.52
1:B:93:ILE:O	1:B:120:LYS:NZ	2.42	0.52
1:D:37:LEU:HD22	1:D:116:LEU:O	2.09	0.52
1:C:152:GLU:OE1	1:C:152:GLU:HA	2.10	0.52
1:C:34:ASP:OD2	1:C:48:SER:OG	2.28	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:72:PRO:HD2	3:E:197:HOH:O	2.11	0.51
1:A:129:THR:HG23	1:D:87:ARG:NH2	2.26	0.50
1:E:54:VAL:HG13	1:E:54:VAL:O	2.11	0.50
1:A:155:HIS:O	1:A:159:ILE:HG12	2.12	0.50
1:F:151:MSE:HE3	3:F:211:HOH:O	2.11	0.50
1:D:88:MSE:HE2	1:D:113:PRO:HD2	1.93	0.50
1:F:40:LEU:HG	1:F:114:VAL:HB	1.94	0.50
1:F:139:ARG:H	1:F:139:ARG:NE	1.99	0.50
1:B:34:ASP:OD2	1:B:48:SER:OG	2.28	0.50
1:B:130:GLY:O	1:B:133:GLU:HG3	2.13	0.49
1:F:68:ARG:HG2	1:F:104:PHE:CZ	2.47	0.49
1:C:88:MSE:HE3	1:C:112:LEU:HD22	1.94	0.49
1:E:54:VAL:HG12	1:E:166:LEU:HD11	1.94	0.49
1:B:48:SER:C	1:B:50:LEU:H	2.15	0.49
1:E:84:LYS:HB3	1:E:85:PRO:HD2	1.95	0.48
1:D:112:LEU:HB3	1:D:113:PRO:HD2	1.96	0.48
1:F:88:MSE:HE3	1:F:113:PRO:HD2	1.96	0.48
1:A:136:VAL:HB	1:A:145:LYS:HB3	1.96	0.48
1:F:128:THR:HG22	1:F:133:GLU:CD	2.34	0.47
1:D:67:CYS:SG	1:D:132:PRO:HG3	2.54	0.47
1:E:88:MSE:HE3	1:E:90:CYS:SG	2.54	0.47
1:E:109:GLY:HA2	3:E:186:HOH:O	2.14	0.47
1:A:39:THR:HG22	1:A:41:ASN:H	1.79	0.47
1:D:62:THR:HB	1:D:94:ASP:OD1	2.14	0.47
1:F:68:ARG:HG2	1:F:104:PHE:HZ	1.80	0.47
1:C:65:PRO:HB2	1:C:66:PRO:HD3	1.97	0.47
1:C:147:VAL:HG11	1:C:151:MSE:HG3	1.97	0.47
1:B:74:MSE:HE3	1:B:90:CYS:SG	2.55	0.46
1:A:32:ALA:HB2	1:A:143:ILE:HG13	1.96	0.46
1:B:47:LEU:O	1:B:50:LEU:HB2	2.15	0.46
1:E:64:CYS:O	1:E:67:CYS:HB2	2.15	0.46
1:A:39:THR:CG2	1:A:40:LEU:N	2.79	0.46
1:B:54:VAL:HG12	1:B:166:LEU:HD23	1.98	0.45
1:D:73:SER:HB2	1:D:154:ASP:OD2	2.17	0.45
1:A:104:PHE:O	1:A:108:THR:HG23	2.17	0.45
1:A:28:GLU:O	1:A:29:GLU:HB2	2.18	0.44
1:E:56:ILE:HD13	1:E:136:VAL:HG22	2.00	0.44
1:B:29:GLU:HA	1:B:29:GLU:OE1	2.18	0.44
1:E:54:VAL:CG1	1:E:166:LEU:HD11	2.48	0.44
1:F:71:ILE:HG12	1:F:112:LEU:HD11	1.98	0.44
1:C:58:ASN:ND2	1:C:74:MSE:HE1	2.32	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:39:THR:CG2	1:F:41:ASN:H	2.29	0.44
1:C:111:THR:O	1:C:112:LEU:HD23	2.18	0.43
1:A:88:MSE:HE1	1:A:112:LEU:CD2	2.42	0.43
1:E:93:ILE:O	1:E:120:LYS:NZ	2.44	0.43
1:F:128:THR:HA	1:F:133:GLU:OE2	2.18	0.43
1:B:163:ASN:O	1:B:164:ASN:C	2.53	0.43
1:A:65:PRO:HB2	1:A:66:PRO:HD3	2.00	0.43
1:F:128:THR:HG22	1:F:133:GLU:OE2	2.18	0.43
1:B:43:GLU:OE2	1:F:133:GLU:OE1	2.37	0.43
1:F:33:PRO:HD2	1:F:126:TYR:CZ	2.54	0.43
1:B:152:GLU:HB2	1:B:155:HIS:CD2	2.53	0.42
1:D:34:ASP:OD2	1:D:48:SER:OG	2.35	0.42
1:A:34:ASP:OD2	1:A:48:SER:OG	2.32	0.42
1:F:71:ILE:HA	1:F:74:MSE:CE	2.47	0.42
1:E:41:ASN:ND2	3:E:185:HOH:O	2.52	0.42
1:D:54:VAL:CG2	1:D:166:LEU:HD12	2.49	0.42
1:C:112:LEU:O	1:C:114:VAL:HG23	2.20	0.42
1:A:155:HIS:HB3	1:A:156:PRO:CD	2.51	0.41
1:C:138:ASP:HB3	1:C:144:LEU:CD2	2.48	0.41
1:C:90:CYS:SG	1:C:112:LEU:HD13	2.61	0.41
1:D:37:LEU:HD11	1:D:122:VAL:HG21	2.02	0.41
1:B:78:ASN:OD1	1:B:88:MSE:HE2	2.20	0.41
1:E:56:ILE:CD1	1:E:136:VAL:HG22	2.50	0.41
1:D:99:VAL:O	1:D:103:GLU:HG2	2.20	0.41
1:B:128:THR:HG22	1:B:133:GLU:OE2	2.21	0.41
1:A:32:ALA:HA	1:A:33:PRO:HD2	1.96	0.41
1:C:103:GLU:O	1:C:107:LYS:HD3	2.20	0.41
1:C:119:ASP:OD2	1:C:121:ARG:HB3	2.20	0.41
1:B:119:ASP:C	1:B:120:LYS:HG2	2.41	0.41
1:E:119:ASP:C	1:E:120:LYS:HG2	2.41	0.41
1:C:73:SER:HB3	3:C:235:HOH:O	2.19	0.41
1:C:33:PRO:HD2	1:C:126:TYR:CZ	2.56	0.41
1:F:77:LEU:HD22	1:F:153:TRP:HB3	2.01	0.40
1:A:64:CYS:O	1:A:68:ARG:HG3	2.21	0.40
1:D:155:HIS:HA	1:D:156:PRO:HD3	1.98	0.40
1:A:133:GLU:OE1	1:D:43:GLU:OE2	2.39	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	137/154 (89%)	129 (94%)	8 (6%)	0	100	100
1	B	139/154 (90%)	132 (95%)	7 (5%)	0	100	100
1	C	137/154 (89%)	128 (93%)	9 (7%)	0	100	100
1	D	140/154 (91%)	134 (96%)	6 (4%)	0	100	100
1	E	139/154 (90%)	135 (97%)	4 (3%)	0	100	100
1	F	136/154 (88%)	130 (96%)	6 (4%)	0	100	100
All	All	828/924 (90%)	788 (95%)	40 (5%)	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	117/126 (93%)	111 (95%)	6 (5%)	29	41
1	B	116/126 (92%)	103 (89%)	13 (11%)	7	7
1	C	116/126 (92%)	103 (89%)	13 (11%)	7	7
1	D	117/126 (93%)	111 (95%)	6 (5%)	29	41
1	E	119/126 (94%)	109 (92%)	10 (8%)	14	17
1	F	114/126 (90%)	102 (90%)	12 (10%)	8	9
All	All	699/756 (92%)	639 (91%)	60 (9%)	13	16



All (60) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	27	LEU
1	A	56	ILE
1	A	64	CYS
1	A	74	MSE
1	A	95	GLU
1	A	152	GLU
1	B	39	THR
1	B	41	ASN
1	B	54	VAL
1	B	56	ILE
1	B	64	CYS
1	B	69	GLU
1	B	74	MSE
1	B	77	LEU
1	B	86	PHE
1	B	93	ILE
1	B	94	ASP
1	B	144	LEU
1	B	152	GLU
1	C	28	GLU
1	C	41	ASN
1	C	53	GLN
1	C	62	THR
1	C	64	CYS
1	C	77	LEU
1	C	84	LYS
1	C	86	PHE
1	C	94	ASP
1	C	107	LYS
1	C	139	ARG
1	C	144	LEU
1	C	152	GLU
1	D	50	LEU
1	D	62	THR
1	D	64	CYS
1	D	92	SER
1	D	103	GLU
1	D	144	LEU
1	E	29	GLU
1	E	41	ASN
1	E	62	THR
1	E	64	CYS

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Mol	Chain	Res	Type
1	E	92	SER
1	E	93	ILE
1	E	106	ARG
1	E	116	LEU
1	E	131	VAL
1	E	166	LEU
1	F	39	THR
1	F	44	VAL
1	F	48	SER
1	F	50	LEU
1	F	54	VAL
1	F	62	THR
1	F	64	CYS
1	F	69	GLU
1	F	116	LEU
1	F	129	THR
1	F	139	ARG
1	F	144	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	38	ASN
1	A	53	GLN
1	A	58	ASN
1	A	155	HIS
1	B	58	ASN
1	B	155	HIS
1	C	38	ASN
1	C	53	GLN
1	C	58	ASN
1	D	58	ASN
1	E	41	ASN
1	F	53	GLN
1	F	58	ASN

### 5.3.3 RNA ⓘ

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 [i](#)

6 ligands are modelled in this entry.

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	$\# Z  > 2$
2	SO4	A	1	-	4,4,4	0.26	0	6,6,6	0.44	0
2	SO4	B	2	-	4,4,4	0.23	0	6,6,6	0.21	0
2	SO4	C	6	-	4,4,4	0.41	0	6,6,6	0.16	0
2	SO4	D	3	-	4,4,4	0.64	0	6,6,6	0.39	0
2	SO4	E	4	-	4,4,4	0.50	0	6,6,6	0.39	0
2	SO4	F	5	-	4,4,4	0.58	0	6,6,6	0.40	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
2	SO4	A	1	-	-	0/0/0/0	0/0/0/0
2	SO4	B	2	-	-	0/0/0/0	0/0/0/0
2	SO4	C	6	-	-	0/0/0/0	0/0/0/0
2	SO4	D	3	-	-	0/0/0/0	0/0/0/0
2	SO4	E	4	-	-	0/0/0/0	0/0/0/0
2	SO4	F	5	-	-	0/0/0/0	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.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	6	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 [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

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	134/154 (87%)	-0.32	0	100	100	12, 21, 36, 49	0
1	B	136/154 (88%)	-0.27	0	100	100	12, 22, 40, 47	0
1	C	134/154 (87%)	-0.29	0	100	100	12, 21, 38, 51	0
1	D	137/154 (88%)	-0.35	0	100	100	12, 20, 33, 39	0
1	E	136/154 (88%)	-0.25	1 (0%)	89	90	13, 21, 39, 46	0
1	F	133/154 (86%)	-0.28	0	100	100	13, 23, 40, 47	0
All	All	810/924 (87%)	-0.29	1 (0%)	95	96	12, 21, 39, 51	0

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	107	LYS	2.1

### 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 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
2	SO4	F	5	5/5	0.99	0.16	1.32	24,25,25,26	0
2	SO4	C	6	5/5	0.99	0.16	0.85	27,28,28,31	0
2	SO4	D	3	5/5	0.99	0.15	0.64	26,26,29,29	0
2	SO4	B	2	5/5	0.99	0.13	-0.44	22,24,25,25	0
2	SO4	A	1	5/5	0.99	0.12	-0.75	19,20,22,25	0
2	SO4	E	4	5/5	0.97	0.10	-1.48	24,25,26,27	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.