



Full wwPDB X-ray Structure Validation Report

Feb 27, 2014 – 04:46 AM GMT

PDB ID : 3C01
Title : Crystal structural of native SpaS C-terminal domain
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Deposited on : 2008-01-18
Resolution : 2.60 Å(reported)

This is a full wwPDB validation report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

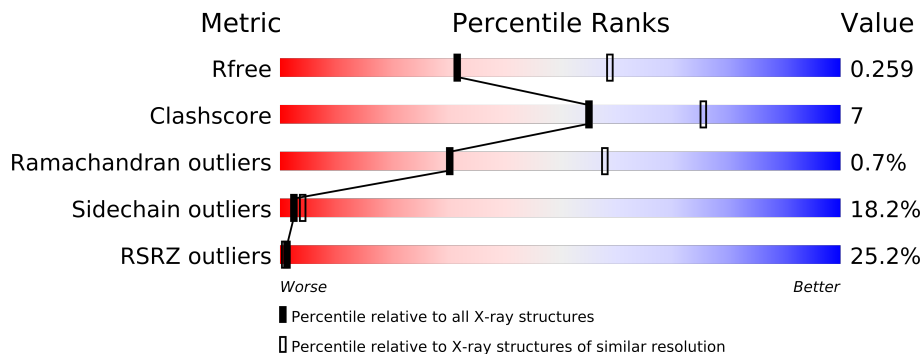
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : stable22639
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

The reported resolution of this entry is 2.60 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}	66092	1718 (2.60-2.60)
Clashscore	79885	2154 (2.60-2.60)
Ramachandran outliers	78287	2113 (2.60-2.60)
Sidechain outliers	78261	2113 (2.60-2.60)
RSRZ outliers	66119	1718 (2.60-2.60)

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 ≥ 3 , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	48	
1	B	48	
1	C	48	
1	D	48	
2	E	98	
2	F	98	
2	G	98	
2	H	98	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
3	SO4	E	66	-	X

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Mol	Type	Chain	Res	Geometry	Electron density
3	SO4	F	67	-	X
3	SO4	H	69	-	X
4	CYS	E	61	-	X
4	CYS	F	62	-	X

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 3554 atoms, of which 0 are hydrogen and 0 are deuterium.

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 Surface presentation of antigens protein spaS.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
1	A	20	Total	C	N	O	0	1	0
			164	100	27	37			
1	B	20	Total	C	N	O	0	0	0
			158	96	27	35			
1	C	19	Total	C	N	O	0	0	0
			149	91	26	32			
1	D	19	Total	C	N	O	0	0	0
			149	91	26	32			

- Molecule 2 is a protein called Surface presentation of antigens protein spaS.

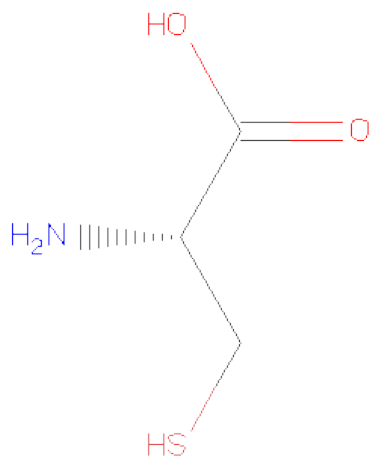
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	E	88	Total	C	N	O	S	0	0	0
			713	464	119	128	2			
2	F	87	Total	C	N	O	S	0	0	0
			706	459	118	127	2			
2	G	87	Total	C	N	O	S	0	1	0
			712	463	119	128	2			
2	H	87	Total	C	N	O	S	0	0	0
			706	459	118	127	2			

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



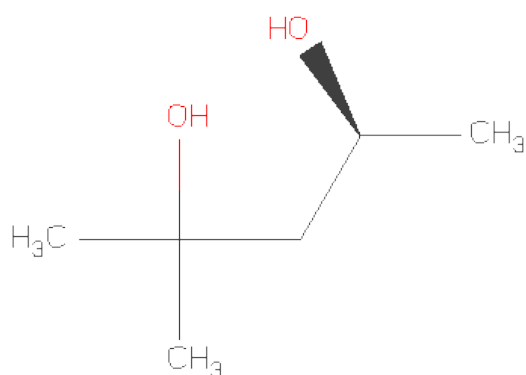
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	E	1	Total	O	S	0	0
			5	4	1		
3	F	1	Total	O	S	0	0
			5	4	1		
3	G	1	Total	O	S	0	0
			5	4	1		
3	H	1	Total	O	S	0	0
			5	4	1		
3	H	1	Total	O	S	0	0
			5	4	1		

- Molecule 4 is CYSTEINE (three-letter code: CYS) (formula: C₃H₇NO₂S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	E	1	Total	C	N	O	S	0	0
			7	3	1	2	1		
4	F	1	Total	C	N	O	S	0	0
			7	3	1	2	1		
4	G	1	Total	C	N	O	S	0	0
			7	3	1	2	1		
4	H	1	Total	C	N	O	S	0	0
			7	3	1	2	1		

- Molecule 5 is (4S)-2-METHYL-2,4-PENTANEDIOL (three-letter code: MPD) (formula: $C_6H_{14}O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	G	1	Total	C	O	0	0
			8	6	2		

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	8	Total	O	0	0
			8	8		
6	B	2	Total	O	0	0
			2	2		
6	C	3	Total	O	0	0
			3	3		
6	D	3	Total	O	0	0
			3	3		

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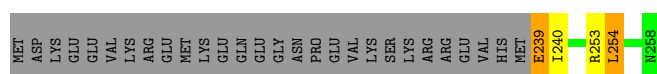
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	E	6	Total 6	O 6	0	0
6	F	5	Total 5	O 5	0	0
6	G	4	Total 4	O 4	0	0
6	H	5	Total 5	O 5	0	0

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.

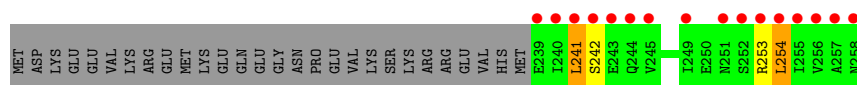
- Molecule 1: Surface presentation of antigens protein spaS

Chain A: 



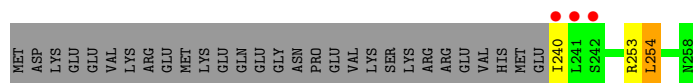
- Molecule 1: Surface presentation of antigens protein spaS

Chain B: 



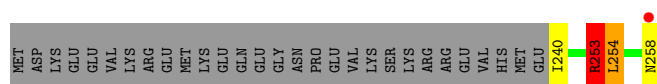
- Molecule 1: Surface presentation of antigens protein spaS

Chain C: 



- Molecule 1: Surface presentation of antigens protein spaS

Chain D: 



- Molecule 2: Surface presentation of antigens protein spaS

Chain E: 

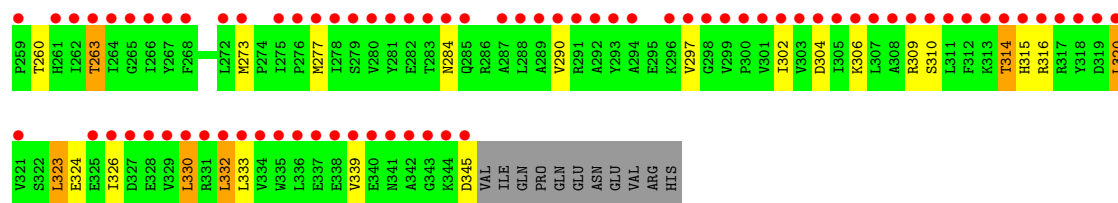


- Molecule 2: Surface presentation of antigens protein spaS

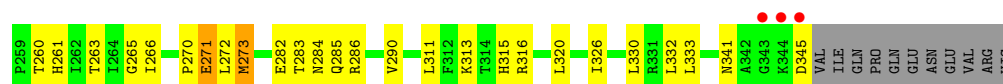
Chain F: 



Chain G:



Chain H:



4 Data and refinement statistics

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α , β , γ	96.66Å 96.66Å 217.51Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	83.62 – 2.60 40.22 – 2.60	Depositor EDS
% Data completeness (in resolution range)	99.4 (83.62-2.60) 99.5 (40.22-2.60)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.78 (at 2.61Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.223 , 0.254 0.229 , 0.259	Depositor DCC
R_{free} test set	1831 reflections (5.26%)	DCC
Wilson B-factor (Å ²)	60.5	Xtriage
Anisotropy	0.176	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 10.4	EDS
Estimated twinning fraction	0.024 for -h,-k,l	Xtriage
L-test for twinning	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 36671 reflections	Xtriage
F_o, F_c correlation	0.82	EDS
Total number of atoms	3554	wwPDB-VP
Average B, all atoms (Å ²)	24.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.24% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MPD, 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	0.93	0/166	0.95	1/221 (0.5%)
1	B	0.85	0/157	1.09	2/209 (1.0%)
1	C	0.85	0/148	0.86	0/197
1	D	0.80	0/148	1.00	1/197 (0.5%)
2	E	0.85	1/727 (0.1%)	0.86	2/987 (0.2%)
2	F	0.85	0/720	0.89	2/977 (0.2%)
2	G	0.84	0/729	0.80	1/989 (0.1%)
2	H	0.80	0/720	0.86	0/977
All	All	0.84	1/3515 (0.0%)	0.88	9/4754 (0.2%)

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

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

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	295	GLU	CG-CD	5.25	1.59	1.51

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	253	ARG	NE-CZ-NH2	6.67	123.64	120.30
2	F	304	ASP	CB-CG-OD1	6.14	123.83	118.30
2	E	291	ARG	NE-CZ-NH1	5.81	123.20	120.30
1	B	241	LEU	C-N-CA	5.75	136.08	121.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	316	ARG	NE-CZ-NH2	5.68	123.14	120.30
1	A	254	LEU	CA-CB-CG	5.37	127.65	115.30
2	G	304	ASP	CB-CG-OD1	5.36	123.12	118.30
2	F	343	GLY	N-CA-C	-5.30	99.86	113.10
1	B	254	LEU	CA-CB-CG	5.03	126.87	115.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	239	GLU	Peptide

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	164	0	166	0	0
1	B	158	0	160	0	0
1	C	149	0	154	1	0
1	D	149	0	154	4	0
2	E	713	0	743	12	0
2	F	706	0	734	9	0
2	G	712	0	742	14	0
2	H	706	0	734	11	0
3	E	5	0	0	1	0
3	F	5	0	0	0	0
3	G	5	0	0	0	0
3	H	10	0	0	0	0
4	E	7	0	4	0	0
4	F	7	0	4	0	0
4	G	7	0	4	0	0
4	H	7	0	4	0	0
5	G	8	0	14	0	0
6	A	8	0	0	0	0
6	B	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	C	3	0	0	0	0
6	D	3	0	0	0	0
6	E	6	0	0	0	0
6	F	5	0	0	0	0
6	G	4	0	0	0	0
6	H	5	0	0	0	0
All	All	3554	0	3617	48	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 7.

All (48) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:G:314:THR:HG22	2:G:315:HIS:ND1	1.82	0.94
2:G:314:THR:HG22	2:G:315:HIS:CE1	2.06	0.90
2:H:260:THR:HG23	2:H:284:ASN:ND2	1.96	0.80
2:G:339:VAL:O	2:H:273:MET:HE1	1.89	0.72
2:G:314:THR:CG2	2:G:315:HIS:CE1	2.75	0.69
2:G:323:LEU:HD12	2:G:323:LEU:H	1.62	0.64
2:E:302:ILE:HD13	2:E:332:LEU:HD21	1.80	0.62
2:E:302:ILE:HD13	2:E:332:LEU:CD2	2.34	0.57
2:G:326:ILE:HG13	2:G:330:LEU:HD22	1.89	0.55
2:H:260:THR:CG2	2:H:284:ASN:ND2	2.68	0.55
2:F:342:ALA:N	2:F:343:GLY:HA3	2.21	0.55
2:H:286:ARG:O	2:H:290:VAL:HG23	2.09	0.52
2:E:263:THR:HG22	2:E:263:THR:O	2.08	0.52
2:H:311:LEU:O	2:H:315:HIS:HB2	2.12	0.50
2:E:263:THR:HG21	2:E:290:VAL:HB	1.95	0.49
2:H:260:THR:CG2	2:H:284:ASN:HD21	2.26	0.49
2:E:329:VAL:HG12	2:E:333:LEU:HD22	1.94	0.49
2:G:263:THR:HG22	2:G:263:THR:O	2.12	0.49
2:E:263:THR:HG21	2:E:290:VAL:CB	2.43	0.48
2:G:260:THR:H	2:G:284:ASN:HD21	1.59	0.48
2:H:265:GLY:O	2:H:266:ILE:HD13	2.13	0.48
2:E:339:VAL:O	2:F:273:MET:HE1	2.13	0.48
2:E:296:LYS:NZ	3:E:66:SO4:S	2.87	0.47
2:E:263:THR:CG2	2:E:263:THR:O	2.62	0.47
2:H:270:PRO:C	2:H:272:LEU:H	2.18	0.47
2:G:323:LEU:CD1	2:G:323:LEU:H	2.27	0.46
2:H:273:MET:HB2	2:H:273:MET:HE2	1.88	0.46
1:D:258:ASN:HD21	2:H:261:HIS:HA	1.81	0.46
2:E:263:THR:CG2	2:E:290:VAL:HG11	2.46	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:D:254:LEU:CD2	1:D:254:LEU:C	2.85	0.45
1:D:240:ILE:O	1:D:240:ILE:HG23	2.16	0.45
2:F:297:VAL:O	2:F:297:VAL:HG13	2.16	0.44
2:F:283:THR:HG23	2:F:284:ASN:ND2	2.33	0.44
2:F:263:THR:HG21	2:F:290:VAL:HB	1.98	0.44
2:G:302:ILE:HD13	2:G:332:LEU:HD21	1.98	0.43
2:G:263:THR:CG2	2:G:290:VAL:HG11	2.49	0.43
1:C:254:LEU:CD2	1:C:254:LEU:C	2.87	0.43
2:F:326:ILE:HG13	2:F:330:LEU:HD22	2.02	0.42
2:E:330:LEU:HA	2:E:330:LEU:HD12	1.93	0.42
2:G:263:THR:HG21	2:G:290:VAL:HG11	2.02	0.41
2:F:273:MET:HB2	2:F:273:MET:HE2	1.70	0.41
1:D:253:ARG:HH21	1:D:253:ARG:HG3	1.85	0.41
2:E:263:THR:HG21	2:E:290:VAL:HG11	2.01	0.41
2:F:333:LEU:HA	2:F:333:LEU:HD12	1.86	0.41
2:G:320:LEU:HA	2:G:320:LEU:HD12	1.84	0.41
2:H:261:HIS:H	2:H:284:ASN:HD22	1.69	0.41
2:G:263:THR:HG21	2:G:290:VAL:HB	2.02	0.40
2:F:267:TYR:HB2	2:F:279:SER:HB3	2.02	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	19/48 (40%)	19 (100%)	0	0	100	100
1	B	18/48 (38%)	17 (94%)	0	1 (6%)	3	3
1	C	17/48 (35%)	17 (100%)	0	0	100	100
1	D	17/48 (35%)	17 (100%)	0	0	100	100
2	E	86/98 (88%)	85 (99%)	1 (1%)	0	100	100
2	F	85/98 (87%)	82 (96%)	2 (2%)	1 (1%)	19	39
2	G	86/98 (88%)	83 (96%)	3 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	H	85/98 (87%)	82 (96%)	2 (2%)	1 (1%)	19	39
All	All	413/584 (71%)	402 (97%)	8 (2%)	3 (1%)	30	58

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	242	SER
2	F	344	LYS
2	H	271	GLU

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	20/46 (44%)	16 (80%)	4 (20%)	2	3
1	B	19/46 (41%)	16 (84%)	3 (16%)	4	6
1	C	18/46 (39%)	15 (83%)	3 (17%)	3	5
1	D	18/46 (39%)	16 (89%)	2 (11%)	9	16
2	E	79/89 (89%)	68 (86%)	11 (14%)	5	9
2	F	78/89 (88%)	64 (82%)	14 (18%)	2	4
2	G	79/89 (89%)	63 (80%)	16 (20%)	2	3
2	H	78/89 (88%)	63 (81%)	15 (19%)	2	3
All	All	389/540 (72%)	321 (82%)	68 (18%)	2	4

All (68) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	239	GLU
1	A	240	ILE
1	A	253	ARG
1	A	254	LEU
2	E	260	THR
2	E	263	THR
2	E	272	LEU

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Mol	Chain	Res	Type
2	E	291	ARG
2	E	297	VAL
2	E	309	ARG
2	E	323	LEU
2	E	325	GLU
2	E	330	LEU
2	E	332	LEU
2	E	333	LEU
1	B	241	LEU
1	B	253	ARG
1	B	254	LEU
2	F	260	THR
2	F	263	THR
2	F	272	LEU
2	F	273	MET
2	F	283	THR
2	F	286	ARG
2	F	291	ARG
2	F	313	LYS
2	F	316	ARG
2	F	320	LEU
2	F	330	LEU
2	F	332	LEU
2	F	333	LEU
2	F	345	ASP
1	C	240	ILE
1	C	253	ARG
1	C	254	LEU
2	G	263	THR
2	G	273	MET
2	G	277	MET
2	G	297	VAL
2	G	306	LYS
2	G	309	ARG
2	G	310	SER
2	G	314	THR
2	G	316	ARG
2	G	320	LEU
2	G	323	LEU
2	G	324	GLU
2	G	330	LEU
2	G	332	LEU

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Mol	Chain	Res	Type
2	G	333	LEU
2	G	345	ASP
1	D	253	ARG
1	D	254	LEU
2	H	263	THR
2	H	271	GLU
2	H	273	MET
2	H	282	GLU
2	H	283	THR
2	H	285	GLN
2	H	313	LYS
2	H	316	ARG
2	H	320	LEU
2	H	326	ILE
2	H	330	LEU
2	H	332	LEU
2	H	333	LEU
2	H	341	ASN
2	H	345	ASP

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

Mol	Chain	Res	Type
2	G	284	ASN
2	H	284	ASN

5.3.3 RNA ⓘ

There are no RNA chains in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

10 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
4	CYS	E	61	-	6,6,6	1.22	1 (16%)	7,7,7	1.04	0
3	SO4	E	66	-	4,4,4	0.20	0	6,6,6	0.36	0
4	CYS	F	62	-	6,6,6	1.37	1 (16%)	7,7,7	1.52	1 (14%)
3	SO4	F	67	-	4,4,4	0.13	0	6,6,6	0.27	0
4	CYS	G	60	-	6,6,6	2.18	1 (16%)	7,7,7	2.19	2 (28%)
5	MPD	G	65	-	7,7,7	0.71	0	10,10,10	1.72	2 (20%)
3	SO4	G	68	-	4,4,4	0.09	0	6,6,6	0.35	0
4	CYS	H	63	-	6,6,6	0.86	0	7,7,7	1.33	1 (14%)
3	SO4	H	64	-	4,4,4	0.33	0	6,6,6	0.49	0
3	SO4	H	69	-	4,4,4	0.19	0	6,6,6	0.28	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	CYS	E	61	-	-	0/6/6/6	0/0/0/0
3	SO4	E	66	-	-	0/0/0/0	0/0/0/0
4	CYS	F	62	-	-	0/6/6/6	0/0/0/0
3	SO4	F	67	-	-	0/0/0/0	0/0/0/0
4	CYS	G	60	-	-	0/6/6/6	0/0/0/0
5	MPD	G	65	-	1/1/2/2	0/5/5/5	0/0/0/0
3	SO4	G	68	-	-	0/0/0/0	0/0/0/0
4	CYS	H	63	-	-	0/6/6/6	0/0/0/0
3	SO4	H	64	-	-	0/0/0/0	0/0/0/0
3	SO4	H	69	-	-	0/0/0/0	0/0/0/0

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	G	60	CYS	CB-SG	-4.61	1.70	1.81
4	F	62	CYS	CB-SG	-2.93	1.74	1.81
4	E	61	CYS	OXT-C	-2.12	1.22	1.30

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	G	60	CYS	CA-CB-SG	-4.01	102.44	115.14
5	G	65	MPD	CM-C2-C1	-3.52	102.32	110.11
4	F	62	CYS	C-CA-N	2.54	113.58	109.36
4	G	60	CYS	C-CA-N	2.15	112.93	109.36
5	G	65	MPD	O2-C2-C3	2.09	116.50	109.16
4	H	63	CYS	OXT-C-CA	2.01	121.38	116.88

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
5	G	65	MPD	C4

There are no torsion outliers.

There are no ring outliers.

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	20/48 (41%)	0.25	0 100 100	11, 16, 23, 28	0
1	B	20/48 (41%)	5.86	16 (80%) 0 0	17, 19, 34, 36	0
1	C	19/48 (39%)	0.61	3 (15%) 3 2	19, 22, 31, 33	0
1	D	19/48 (39%)	-0.05	1 (5%) 25 22	15, 20, 25, 26	0
2	E	88/98 (89%)	-0.04	3 (3%) 43 39	9, 20, 39, 44	0
2	F	87/98 (88%)	-0.07	2 (2%) 57 54	16, 22, 32, 40	0
2	G	87/98 (88%)	3.88	77 (88%) 0 0	13, 26, 33, 43	0
2	H	87/98 (88%)	0.36	3 (3%) 43 39	17, 25, 38, 39	0
All	All	427/584 (73%)	1.15	105 (24%) 1 1	9, 23, 36, 44	0

All (105) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	257	ALA	12.5
1	B	241	LEU	11.9
1	B	242	SER	10.7
1	B	243	GLU	9.1
1	B	256	VAL	8.9
1	B	244	GLN	8.9
1	B	258	ASN	8.5
2	G	341	ASN	8.1
1	B	255	ILE	8.0
2	G	302	ILE	7.8
2	G	264	ILE	7.2
2	G	301	VAL	7.1
1	B	254	LEU	7.1
2	G	300	PRO	6.9
2	G	342	ALA	6.9
2	G	328	GLU	6.7

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Mol	Chain	Res	Type	RSRZ
2	G	304	ASP	6.6
2	G	338	GLU	6.5
2	G	327	ASP	6.3
2	G	343	GLY	6.2
2	G	339	VAL	6.2
2	G	298	GLY	6.0
2	G	337	GLU	6.0
2	G	305	ILE	5.8
2	G	266	ILE	5.6
2	G	335	TRP	5.5
2	G	280	VAL	5.3
1	B	240	ILE	5.3
2	G	340	GLU	5.1
2	G	262	ILE	4.9
1	B	252	SER	4.8
2	G	307	LEU	4.7
2	G	303	VAL	4.7
2	G	326	ILE	4.7
2	G	277	MET	4.6
2	G	263	THR	4.6
2	G	333	LEU	4.5
2	G	336	LEU	4.4
2	G	318	TYR	4.4
1	B	253	ARG	4.4
2	G	265	GLY	4.4
2	G	261	HIS	4.3
2	G	279	SER	4.3
2	G	281	TYR	4.3
2	G	329	VAL	4.2
2	G	331	ARG	4.2
2	G	330	LEU	4.2
2	G	276	PRO	4.1
2	G	345	ASP	4.1
2	G	312	PHE	4.1
2	G	297	VAL	4.0
2	G	308	ALA	4.0
2	G	332	LEU	3.9
2	G	285[A]	GLN	3.9
2	G	290	VAL	3.8
2	G	289	ALA	3.8
2	G	334	VAL	3.8
2	G	320	LEU	3.7

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Mol	Chain	Res	Type	RSRZ
2	H	343	GLY	3.7
2	G	299	VAL	3.7
2	F	345	ASP	3.6
2	G	291	ARG	3.5
2	G	325	GLU	3.5
2	G	278	ILE	3.4
2	G	267	TYR	3.4
2	G	311	LEU	3.4
2	G	316	ARG	3.4
2	G	294	ALA	3.3
1	B	239	GLU	3.2
2	G	288	LEU	3.2
2	G	315	HIS	3.2
1	B	249	ILE	3.2
2	G	344	LYS	3.2
1	C	241	LEU	3.1
2	G	321	VAL	3.1
2	G	310	SER	3.0
2	G	296	LYS	3.0
2	G	292	ALA	2.9
2	G	272	LEU	2.9
2	G	293	TYR	2.9
2	G	259	PRO	2.9
2	G	287	ALA	2.8
1	B	245	VAL	2.8
2	G	306	LYS	2.8
2	G	319	ASP	2.7
2	G	283	THR	2.7
2	E	344	LYS	2.7
2	G	309	ARG	2.7
2	F	344	LYS	2.6
2	G	268	PHE	2.6
2	G	317	ARG	2.6
2	E	345	ASP	2.5
2	G	275	ILE	2.5
2	E	346	VAL	2.5
1	B	251	ASN	2.5
2	G	273	MET	2.4
1	C	240	ILE	2.4
2	G	313	LYS	2.3
2	H	345	ASP	2.2
2	G	314	THR	2.2

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Mol	Chain	Res	Type	RSRZ
1	D	258	ASN	2.1
2	G	282	GLU	2.1
1	C	242	SER	2.1
2	H	344	LYS	2.0
2	G	284	ASN	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 ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. 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, 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	RSR	LLDF	B-factors(Å ²)	Q<0.9
3	SO4	H	69	5/5	0.45	17.59	57,58,59,59	5
3	SO4	F	67	5/5	0.48	13.38	75,75,76,77	5
4	CYS	F	62	7/7	0.30	7.20	91,92,92,92	0
4	CYS	E	61	7/7	0.34	3.14	84,86,87,87	0
3	SO4	E	66	5/5	0.32	2.14	63,64,64,65	5
3	SO4	H	64	5/5	0.25	1.84	89,89,90,92	0
5	MPD	G	65	8/8	0.32	0.76	76,78,81,82	0
4	CYS	G	60	7/7	0.31	-0.12	75,77,78,81	0
4	CYS	H	63	7/7	0.22	-0.51	90,91,91,91	0
3	SO4	G	68	5/5	0.29	-6.81	79,80,80,81	5

6.5 Other polymers ⓘ

There are no such residues in this entry.