



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 11:50 AM GMT

PDB ID : 3Q6N
Title : Crystal Structure of Human MC-HSP90 in P21 space group
Authors : Lee, C.C.; Lin, T.W.; Ko, T.P.; Wang, A.H.-J.
Deposited on : 2011-01-03
Resolution : 3.05 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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

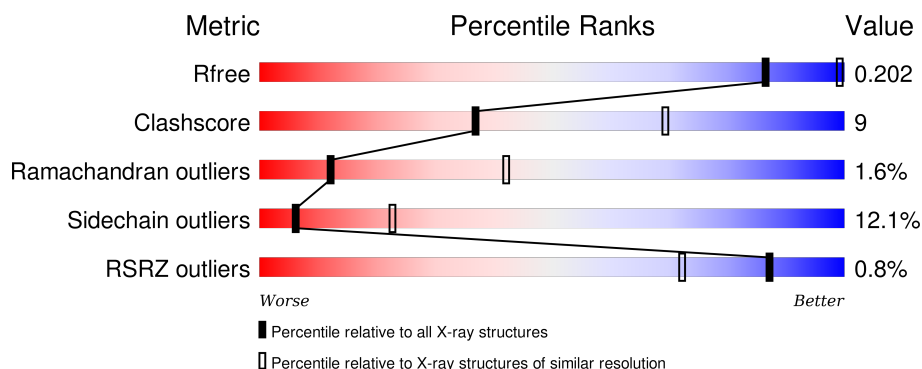
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.05 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	1191 (3.10-3.02)
Clashscore	102246	1303 (3.10-3.02)
Ramachandran outliers	100387	1254 (3.10-3.02)
Sidechain outliers	100360	1254 (3.10-3.02)
RSRZ outliers	91569	1197 (3.10-3.02)

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. 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	448	<div> <div>62%</div> <div>14%</div> <div>•</div> <div>20%</div> </div>
1	B	448	<div> <div>58%</div> <div>18%</div> <div>• •</div> <div>19%</div> </div>
1	C	448	<div> <div>59%</div> <div>15%</div> <div>5%</div> <div>21%</div> </div>
1	D	448	<div> <div>58%</div> <div>19%</div> <div>•</div> <div>20%</div> </div>
1	E	448	<div> <div>59%</div> <div>17%</div> <div>•</div> <div>20%</div> </div>

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Mol	Chain	Length	Quality of chain				
1	F	448	 A horizontal bar chart showing the quality of chain F. The bar is divided into three segments: green (63%), yellow (15%), and grey (19%). A small black dot is located on the yellow segment. <table><tr><td>63%</td><td>15%</td><td>•</td><td>19%</td></tr></table>	63%	15%	•	19%
63%	15%	•	19%				

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 18134 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 Heat shock protein HSP 90-alpha.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	360	Total	C	N	O	S	0	0	0
			2974	1894	499	567	14			
1	B	362	Total	C	N	O	S	0	0	0
			2990	1904	502	570	14			
1	C	354	Total	C	N	O	S	0	0	0
			2927	1867	493	553	14			
1	D	360	Total	C	N	O	S	0	0	0
			2971	1895	501	561	14			
1	E	360	Total	C	N	O	S	0	0	0
			2971	1889	500	568	14			
1	F	363	Total	C	N	O	S	0	0	0
			2994	1910	506	563	15			

There are 48 discrepancies between the modelled and reference sequences:

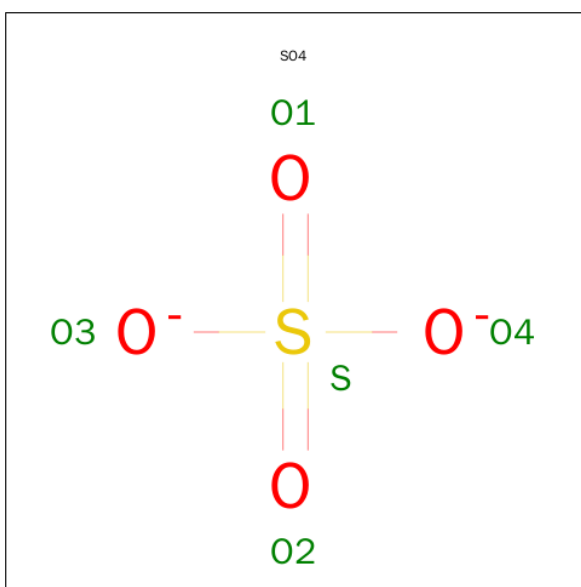
Chain	Residue	Modelled	Actual	Comment	Reference
A	291	ALA	-	EXPRESSION TAG	UNP P07900
A	292	ALA	-	EXPRESSION TAG	UNP P07900
A	733	HIS	-	EXPRESSION TAG	UNP P07900
A	734	HIS	-	EXPRESSION TAG	UNP P07900
A	735	HIS	-	EXPRESSION TAG	UNP P07900
A	736	HIS	-	EXPRESSION TAG	UNP P07900
A	737	HIS	-	EXPRESSION TAG	UNP P07900
A	738	HIS	-	EXPRESSION TAG	UNP P07900
B	291	ALA	-	EXPRESSION TAG	UNP P07900
B	292	ALA	-	EXPRESSION TAG	UNP P07900
B	733	HIS	-	EXPRESSION TAG	UNP P07900
B	734	HIS	-	EXPRESSION TAG	UNP P07900
B	735	HIS	-	EXPRESSION TAG	UNP P07900
B	736	HIS	-	EXPRESSION TAG	UNP P07900
B	737	HIS	-	EXPRESSION TAG	UNP P07900
B	738	HIS	-	EXPRESSION TAG	UNP P07900
C	291	ALA	-	EXPRESSION TAG	UNP P07900

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Chain	Residue	Modelled	Actual	Comment	Reference
C	292	ALA	-	EXPRESSION TAG	UNP P07900
C	733	HIS	-	EXPRESSION TAG	UNP P07900
C	734	HIS	-	EXPRESSION TAG	UNP P07900
C	735	HIS	-	EXPRESSION TAG	UNP P07900
C	736	HIS	-	EXPRESSION TAG	UNP P07900
C	737	HIS	-	EXPRESSION TAG	UNP P07900
C	738	HIS	-	EXPRESSION TAG	UNP P07900
D	291	ALA	-	EXPRESSION TAG	UNP P07900
D	292	ALA	-	EXPRESSION TAG	UNP P07900
D	733	HIS	-	EXPRESSION TAG	UNP P07900
D	734	HIS	-	EXPRESSION TAG	UNP P07900
D	735	HIS	-	EXPRESSION TAG	UNP P07900
D	736	HIS	-	EXPRESSION TAG	UNP P07900
D	737	HIS	-	EXPRESSION TAG	UNP P07900
D	738	HIS	-	EXPRESSION TAG	UNP P07900
E	291	ALA	-	EXPRESSION TAG	UNP P07900
E	292	ALA	-	EXPRESSION TAG	UNP P07900
E	733	HIS	-	EXPRESSION TAG	UNP P07900
E	734	HIS	-	EXPRESSION TAG	UNP P07900
E	735	HIS	-	EXPRESSION TAG	UNP P07900
E	736	HIS	-	EXPRESSION TAG	UNP P07900
E	737	HIS	-	EXPRESSION TAG	UNP P07900
E	738	HIS	-	EXPRESSION TAG	UNP P07900
F	291	ALA	-	EXPRESSION TAG	UNP P07900
F	292	ALA	-	EXPRESSION TAG	UNP P07900
F	733	HIS	-	EXPRESSION TAG	UNP P07900
F	734	HIS	-	EXPRESSION TAG	UNP P07900
F	735	HIS	-	EXPRESSION TAG	UNP P07900
F	736	HIS	-	EXPRESSION TAG	UNP P07900
F	737	HIS	-	EXPRESSION TAG	UNP P07900
F	738	HIS	-	EXPRESSION TAG	UNP P07900

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O₄S).




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.

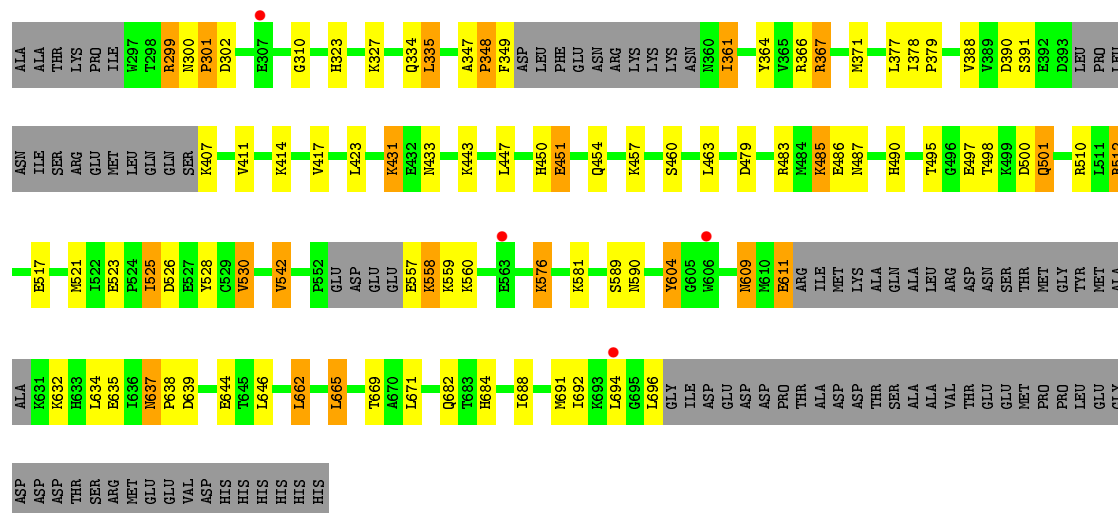
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	33	Total	O	0	0
			33	33		
3	B	57	Total	O	0	0
			57	57		
3	C	45	Total	O	0	0
			45	45		
3	D	46	Total	O	0	0
			46	46		
3	E	46	Total	O	0	0
			46	46		
3	F	50	Total	O	0	0
			50	50		

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.

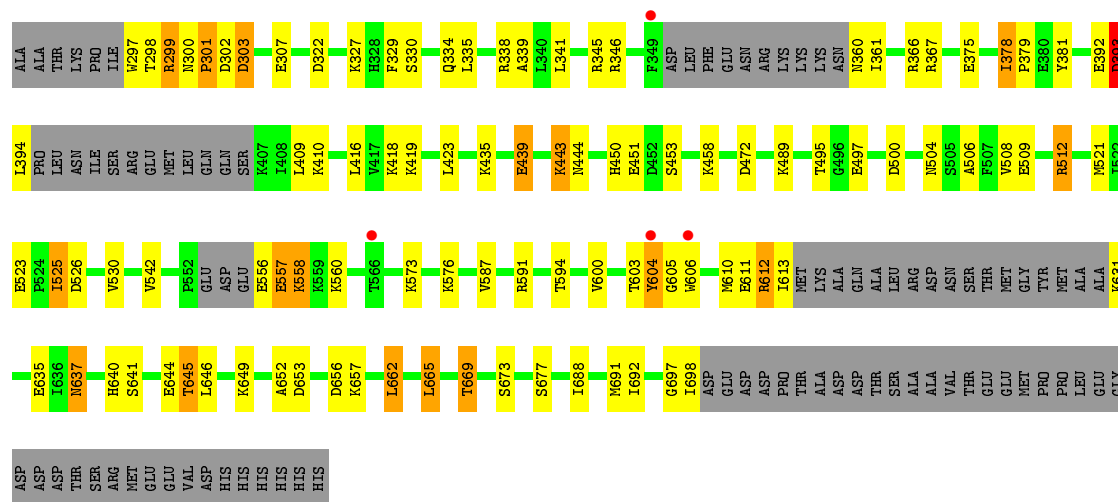
- Chain A: 

- Chain B:
-
- 58% 18% 19%
- | Position | Amino Acid | Information Content (bits) |
|----------|------------|----------------------------|
| 1 | GLY | 0.2 |
| 2 | ASP | 0.1 |
| 3 | ASP | 0.1 |
| 4 | ASP | 0.1 |
| 5 | ASP | 0.1 |
| 6 | THR | 0.1 |
| 7 | SER | 0.1 |
| 8 | ARG | 0.1 |
| 9 | MET | 0.1 |
| 10 | GLU | 0.1 |
| 11 | GLU | 0.1 |
| 12 | VAL | 0.1 |
| 13 | ASP | 0.1 |
| 14 | HIS | 0.1 |
| 15 | HIS | 0.1 |
| 16 | HIS | 0.1 |
| 17 | HIS | 0.1 |
| 18 | HIS | 0.1 |
| 19 | HIS | 0.1 |
| 20 | ALA | 0.1 |
| 21 | THR | 0.1 |
| 22 | PRO | 0.1 |
| 23 | PRO | 0.1 |
| 24 | ILE | 0.1 |
| 25 | K297 | 0.1 |
| 26 | T298 | 0.1 |
| 27 | T299 | 0.1 |
| 28 | N300 | 0.1 |
| 29 | N301 | 0.1 |
| 30 | D302 | 0.1 |
| 31 | D303 | 0.1 |
| 32 | T304 | 0.1 |
| 33 | E307 | 0.1 |
| 34 | F312 | 0.1 |
| 35 | H323 | 0.1 |
| 36 | F329 | 0.1 |
| 37 | Q334 | 0.1 |
| 38 | L335 | 0.1 |
| 39 | A339 | 0.1 |
| 40 | L340 | 0.1 |
| 41 | L341 | 0.1 |
| 42 | R346 | 0.1 |
| 43 | A347 | 0.1 |
| 44 | P348 | 0.1 |
| 45 | F349 | 0.1 |
| 46 | ASP | 0.1 |
| 47 | LEU | 0.1 |
| 48 | PHE | 0.1 |
| 49 | GLU | 0.1 |
| 50 | ASN | 0.1 |
| 51 | ARG | 0.1 |
| 52 | LYS | 0.1 |
| 53 | LYS | 0.1 |
| 54 | K358 | 0.1 |
| 55 | N359 | 0.1 |
| 56 | N360 | 0.1 |
| 57 | R366 | 0.1 |
| 58 | R367 | 0.1 |
| 59 | M371 | 0.1 |
| 60 | D372 | 0.1 |
| 61 | N373 | 0.1 |
| 62 | E376 | 0.1 |
| 63 | L377 | 0.1 |
| 64 | L378 | 0.1 |
| 65 | P379 | 0.1 |
| 66 | D390 | 0.1 |
| 67 | D393 | 0.1 |
| 68 | L394 | 0.1 |
| 69 | PRO | 0.1 |
| 70 | LEU | 0.1 |
| 71 | ASN | 0.1 |
| 72 | ILE | 0.1 |
| 73 | SER | 0.1 |
| 74 | ARG | 0.1 |
| 75 | GLU | 0.1 |
| 76 | MET | 0.1 |
| 77 | LEU | 0.1 |
| 78 | GLN | 0.1 |
| 79 | SER | 0.1 |
| 80 | LYS | 0.1 |
| 81 | I408 | 0.1 |
| 82 | L409 | 0.1 |
| 83 | K410 | 0.1 |
| 84 | R413 | 0.1 |
| 85 | L416 | 0.1 |
| 86 | K435 | 0.1 |
| 87 | E439 | 0.1 |
| 88 | K443 | 0.1 |
| 89 | L447 | 0.1 |
| 90 | E451 | 0.1 |
| 91 | Y465 | 0.1 |
| 92 | K485 | 0.1 |
| 93 | E486 | 0.1 |
| 94 | N487 | 0.1 |
| 95 | Q488 | 0.1 |
| 96 | K489 | 0.1 |
| 97 | T495 | 0.1 |
| 98 | G496 | 0.1 |
| 99 | E497 | 0.1 |
| 100 | A506 | 0.1 |
| 101 | F507 | 0.1 |
| 102 | V508 | 0.1 |
| 103 | E509 | 0.1 |
| 104 | R512 | 0.1 |
| 105 | G515 | 0.1 |
| 106 | M521 | 0.1 |
| 107 | L522 | 0.1 |
| 108 | E523 | 0.1 |
| 109 | P524 | 0.1 |
| 110 | S525 | 0.1 |
| 111 | K631 | 0.1 |
| 112 | K632 | 0.1 |

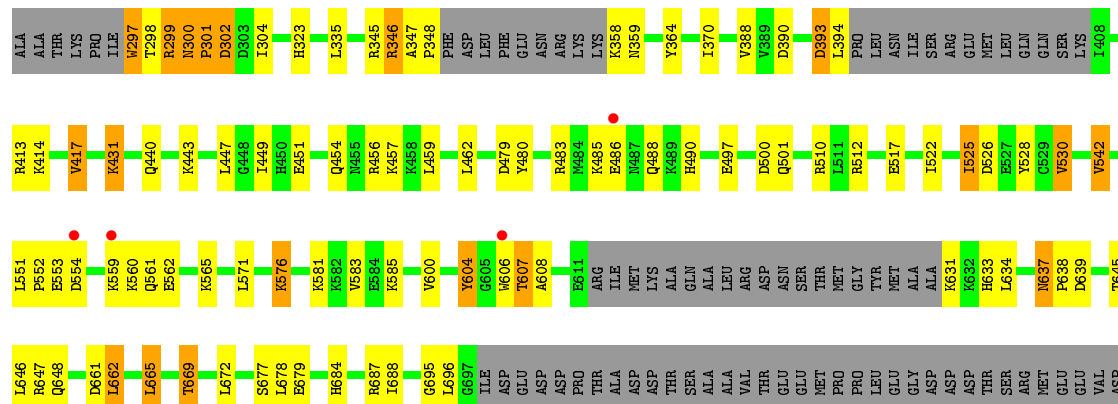
- Chain C: 



• Molecule 1: Heat shock protein HSP 90-alpha

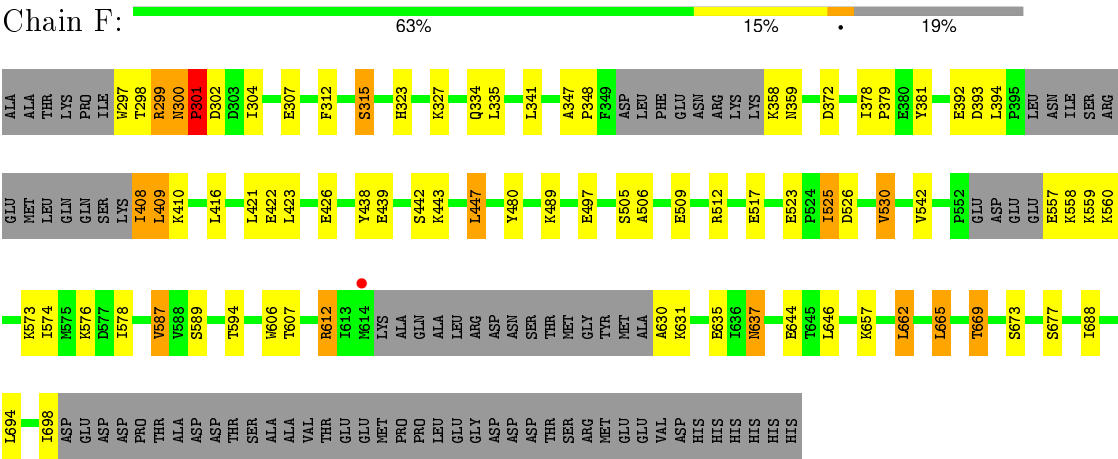


• Molecule 1: Heat shock protein HSP 90-alpha



HIS
HIS
HIS
HIS
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HIS

● Molecule 1: Heat shock protein HSP 90-alpha



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	157.90 Å 90.87 Å 167.09 Å 90.00° 115.85° 90.00°	Depositor
Resolution (Å)	30.00 – 3.05 29.75 – 3.02	Depositor EDS
% Data completeness (in resolution range)	98.7 (30.00-3.05) 94.4 (29.75-3.02)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.21 (at 3.00 Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.204 , 0.259 0.200 , 0.202	Depositor DCC
R_{free} test set	4051 reflections (5.48%)	DCC
Wilson B-factor (Å ²)	73.3	Xtriage
Anisotropy	0.348	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 57.9	EDS
Estimated twinning fraction	0.034 for h,-k,-h-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Outliers	0 of 82268 reflections	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	18134	wwPDB-VP
Average B, all atoms (Å ²)	85.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.90% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: 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	0.63	0/3023	0.68	0/4058
1	B	0.64	0/3039	0.70	1/4080 (0.0%)
1	C	0.64	0/2975	0.68	0/3992
1	D	0.62	0/3019	0.70	0/4052
1	E	0.62	0/3019	0.70	1/4053 (0.0%)
1	F	0.61	0/3043	0.70	0/4084
All	All	0.63	0/18118	0.69	2/24319 (0.0%)

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	B	0	1
1	D	0	1
1	F	0	1
All	All	0	3

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	302	ASP	N-CA-C	5.21	125.07	111.00
1	B	304	ILE	N-CA-C	-5.21	96.93	111.00

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	301	PRO	Peptide
1	D	303	ASP	Peptide
1	F	301	PRO	Peptide

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	2974	0	3000	52	0
1	B	2990	0	3017	64	0
1	C	2927	0	2963	66	0
1	D	2971	0	3007	62	0
1	E	2971	0	2997	63	0
1	F	2994	0	3039	44	0
2	A	5	0	0	0	0
2	B	5	0	0	0	0
2	C	5	0	0	0	0
2	D	5	0	0	0	0
2	E	5	0	0	0	0
2	F	5	0	0	0	0
3	A	33	0	0	1	0
3	B	57	0	0	3	0
3	C	45	0	0	2	0
3	D	46	0	0	5	0
3	E	46	0	0	1	0
3	F	50	0	0	1	0
All	All	18134	0	18023	337	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 9.

All (337) 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:B:525:ILE:HD13	1:B:525:ILE:H	1.00	1.14
1:F:299:ARG:HH11	1:F:299:ARG:HB3	1.10	1.10
1:C:512:ARG:HG2	1:C:512:ARG:HH11	1.11	1.10

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:525:ILE:HD13	1:A:525:ILE:H	1.17	1.09
1:D:525:ILE:H	1:D:525:ILE:HD13	1.16	1.06
1:D:393:ASP:CG	1:D:394:LEU:H	1.61	1.04
1:F:525:ILE:H	1:F:525:ILE:HD13	1.22	1.02
1:D:612:ARG:HA	1:D:613:ILE:C	1.82	0.99
1:B:525:ILE:CD1	1:B:525:ILE:H	1.75	0.99
1:B:646:LEU:HD13	1:B:662:LEU:HD12	1.45	0.98
1:C:497:GLU:H	1:C:501:GLN:HE22	1.08	0.95
1:E:299:ARG:HG2	1:E:299:ARG:HH11	1.29	0.93
1:A:366:ARG:NH1	1:A:392:GLU:O	2.03	0.92
1:F:665:LEU:O	1:F:669:THR:HG23	1.70	0.91
1:B:525:ILE:HD13	1:B:525:ILE:N	1.85	0.91
1:C:512:ARG:NH1	1:C:512:ARG:HG2	1.83	0.90
1:F:299:ARG:NH1	1:F:299:ARG:HB3	1.88	0.89
1:C:525:ILE:H	1:C:525:ILE:HD13	1.36	0.88
1:D:665:LEU:O	1:D:669:THR:HG23	1.74	0.86
1:A:512:ARG:HH11	1:A:512:ARG:HG2	1.38	0.85
1:F:525:ILE:HD13	1:F:525:ILE:N	1.91	0.85
1:E:299:ARG:CG	1:E:299:ARG:HH11	1.88	0.85
1:D:646:LEU:HD13	1:D:662:LEU:HD12	1.58	0.85
1:D:299:ARG:HB3	1:D:299:ARG:HH11	1.41	0.85
1:E:665:LEU:O	1:E:669:THR:HG23	1.77	0.83
1:B:665:LEU:O	1:B:669:THR:HG23	1.78	0.83
1:D:393:ASP:CG	1:D:394:LEU:N	2.32	0.83
1:D:525:ILE:CD1	1:D:525:ILE:H	1.91	0.82
1:C:646:LEU:HD13	1:C:662:LEU:HD12	1.61	0.82
1:D:301:PRO:CG	3:D:744:HOH:O	2.26	0.82
1:D:301:PRO:HG3	3:D:744:HOH:O	1.80	0.81
1:E:497:GLU:H	1:E:501:GLN:HE22	1.28	0.81
1:F:299:ARG:CB	1:F:299:ARG:HH11	1.90	0.81
1:D:525:ILE:N	1:D:525:ILE:HD13	1.95	0.80
1:A:497:GLU:H	1:A:501:GLN:HE22	1.30	0.79
1:E:497:GLU:H	1:E:501:GLN:NE2	1.81	0.78
1:B:299:ARG:HH11	1:B:299:ARG:HB3	1.48	0.78
1:A:299:ARG:HH11	1:A:299:ARG:HB3	1.49	0.77
1:C:431:LYS:HA	1:C:431:LYS:HE3	1.68	0.75
1:E:688:ILE:HG21	1:F:669:THR:HG21	1.67	0.74
1:A:665:LEU:O	1:A:669:THR:HG23	1.87	0.73
1:A:525:ILE:N	1:A:525:ILE:HD13	1.99	0.72
1:F:526:ASP:O	1:F:530:VAL:HG22	1.89	0.71
1:C:526:ASP:O	1:C:530:VAL:HG22	1.90	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:346:ARG:HH11	1:E:346:ARG:HG2	1.57	0.69
1:D:301:PRO:HG2	3:D:744:HOH:O	1.92	0.69
1:E:323:HIS:CD2	1:E:323:HIS:H	2.11	0.69
1:A:669:THR:HG21	1:B:688:ILE:HG21	1.75	0.69
1:A:637:ASN:HD22	1:A:637:ASN:C	1.96	0.69
1:C:637:ASN:ND2	1:C:639:ASP:H	1.92	0.68
1:A:525:ILE:CD1	1:A:525:ILE:H	1.92	0.67
1:E:297:TRP:O	1:E:301:PRO:HD2	1.93	0.67
1:C:497:GLU:N	1:C:501:GLN:HE22	1.86	0.67
1:C:665:LEU:O	1:C:669:THR:HG23	1.94	0.67
1:B:297:TRP:HA	1:B:297:TRP:CE3	2.29	0.66
1:F:525:ILE:CD1	1:F:525:ILE:H	1.91	0.66
1:E:669:THR:HG21	1:F:688:ILE:HG21	1.77	0.66
1:D:302:ASP:OD1	1:D:303:ASP:N	2.28	0.66
1:A:512:ARG:NH1	1:A:512:ARG:HG2	2.06	0.65
1:E:637:ASN:HD22	1:E:637:ASN:C	1.99	0.65
1:E:646:LEU:HD13	1:E:662:LEU:CD1	2.27	0.65
1:C:696:LEU:HD21	1:D:649:LYS:HE3	1.79	0.65
1:E:646:LEU:HD13	1:E:662:LEU:HD12	1.79	0.64
1:C:637:ASN:C	1:C:637:ASN:HD22	2.00	0.64
1:B:378:ILE:HG13	1:B:379:PRO:HD2	1.79	0.64
1:D:443:LYS:HE2	1:D:525:ILE:HD11	1.78	0.64
1:C:323:HIS:CD2	1:C:323:HIS:H	2.12	0.64
1:A:576:LYS:O	1:A:576:LYS:HD3	1.98	0.64
1:A:637:ASN:ND2	1:A:639:ASP:H	1.96	0.63
1:D:300:ASN:HD21	1:D:367:ARG:HE	1.44	0.63
1:C:414:LYS:NZ	1:C:454:GLN:HE22	1.97	0.63
1:D:556:GLU:HG3	1:D:558:LYS:HE3	1.81	0.63
1:A:323:HIS:CD2	1:A:323:HIS:H	2.14	0.62
1:E:526:ASP:O	1:E:530:VAL:HG22	1.97	0.62
1:C:498:THR:H	1:C:501:GLN:HE21	1.48	0.62
1:C:684:HIS:NE2	1:C:688:ILE:HD11	2.14	0.62
1:B:600:VAL:HG23	1:B:633:HIS:HB2	1.80	0.61
1:E:346:ARG:HH11	1:E:346:ARG:CG	2.13	0.61
1:B:323:HIS:H	1:B:323:HIS:CD2	2.17	0.61
1:F:646:LEU:HD13	1:F:662:LEU:HD12	1.82	0.61
1:C:299:ARG:HH11	1:C:299:ARG:HB3	1.65	0.60
1:B:587:VAL:CG2	1:B:635:GLU:HG2	2.30	0.60
1:B:302:ASP:OD1	1:B:303:ASP:N	2.34	0.60
1:D:523:GLU:O	1:D:526:ASP:HB2	2.02	0.60
1:F:301:PRO:HD2	1:F:304:ILE:HD11	1.82	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:346:ARG:HG2	1:E:346:ARG:NH1	2.17	0.59
1:B:297:TRP:HA	1:B:297:TRP:HE3	1.67	0.59
1:D:450:HIS:ND1	1:D:451:GLU:OE1	2.30	0.59
1:C:691:MET:SD	1:D:691:MET:HB3	2.42	0.59
1:E:299:ARG:CG	1:E:299:ARG:NH1	2.53	0.58
1:D:329:PHE:CE1	1:D:419:LYS:HG3	2.38	0.58
1:B:646:LEU:HD13	1:B:662:LEU:CD1	2.26	0.58
1:F:612:ARG:HG3	1:F:612:ARG:HH11	1.69	0.58
1:F:574:ILE:O	1:F:578:ILE:HG13	2.03	0.58
1:D:506:ALA:HA	1:D:509:GLU:OE2	2.02	0.58
1:D:298:THR:O	1:D:301:PRO:HD2	2.04	0.57
1:F:315:SER:HA	3:F:950:HOH:O	2.04	0.57
1:F:323:HIS:H	1:F:323:HIS:CD2	2.20	0.57
1:D:653:ASP:OD1	1:D:656:ASP:HB2	2.03	0.57
1:C:366:ARG:HA	1:C:367:ARG:NH1	2.19	0.57
1:B:600:VAL:CG2	1:B:633:HIS:HB2	2.34	0.57
1:C:512:ARG:CG	1:C:512:ARG:HH11	1.97	0.57
1:E:661:ASP:OD2	1:E:687:ARG:HG3	2.05	0.56
1:E:576:LYS:HD3	1:E:576:LYS:O	2.05	0.56
1:B:506:ALA:HA	1:B:509:GLU:OE2	2.04	0.56
1:D:591:ARG:CZ	1:D:600:VAL:HG11	2.36	0.56
1:D:443:LYS:HE2	1:D:525:ILE:CD1	2.36	0.56
1:C:604:TYR:HD2	1:C:604:TYR:H	1.53	0.55
1:C:523:GLU:O	1:C:526:ASP:HB2	2.07	0.55
1:C:443:LYS:HE3	1:C:525:ILE:HD12	1.89	0.55
1:F:612:ARG:HG3	1:F:612:ARG:NH1	2.22	0.55
1:E:695:GLY:O	1:E:696:LEU:HD12	2.07	0.54
1:C:348:PRO:O	1:C:349:PHE:HB2	2.06	0.54
1:B:554:ASP:O	1:B:556:GLU:N	2.39	0.54
1:D:610:MET:C	1:D:612:ARG:H	2.10	0.54
1:A:688:ILE:HG21	1:B:669:THR:HG21	1.90	0.54
1:A:298:THR:HG21	1:A:312:PHE:CD1	2.43	0.54
1:E:302:ASP:OD1	1:E:302:ASP:O	2.25	0.54
1:D:508:VAL:O	1:D:512:ARG:HB2	2.08	0.54
1:C:589:SER:HB2	1:C:635:GLU:HB3	1.89	0.54
1:C:457:LYS:HD2	3:C:909:HOH:O	2.07	0.54
1:E:483:ARG:NH2	1:E:517:GLU:OE2	2.40	0.54
1:B:358:LYS:HB2	1:B:373:ASN:OD1	2.07	0.53
1:A:637:ASN:ND2	1:A:637:ASN:C	2.61	0.53
1:F:637:ASN:C	1:F:637:ASN:HD22	2.11	0.53
1:A:556:GLU:HB3	1:A:559:LYS:HG2	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:692:ILE:HD11	1:D:665:LEU:HD13	1.92	0.52
1:F:612:ARG:HA	1:F:612:ARG:HH11	1.75	0.52
1:B:523:GLU:O	1:B:526:ASP:HB2	2.10	0.52
1:C:557:GLU:O	1:C:560:LYS:HB2	2.10	0.52
1:D:612:ARG:CA	1:D:613:ILE:C	2.70	0.52
1:A:665:LEU:HD13	1:B:692:ILE:HD11	1.91	0.52
1:F:589:SER:HB2	1:F:635:GLU:HB3	1.92	0.52
1:B:435:LYS:HG2	3:B:830:HOH:O	2.08	0.52
1:B:525:ILE:N	1:B:525:ILE:CD1	2.54	0.51
1:E:684:HIS:NE2	1:E:688:ILE:HD11	2.25	0.51
1:F:297:TRP:O	1:F:300:ASN:HB2	2.11	0.51
1:B:376:GLU:O	1:B:413:ARG:HD2	2.10	0.51
1:B:608:ALA:C	1:B:610:MET:H	2.14	0.51
1:E:301:PRO:HB2	1:E:304:ILE:HD11	1.91	0.51
1:B:335:LEU:HD13	1:B:393:ASP:OD1	2.09	0.51
1:C:682:GLN:NE2	1:D:504:ASN:O	2.43	0.50
1:E:637:ASN:HD22	1:E:638:PRO:N	2.09	0.50
1:B:637:ASN:ND2	1:B:639:ASP:H	2.09	0.50
1:A:498:THR:H	1:A:501:GLN:HE21	1.59	0.50
1:E:490:HIS:HB3	1:E:542:VAL:HG13	1.94	0.50
1:D:641:SER:O	1:D:645:THR:HG23	2.11	0.50
1:B:298:THR:HG21	1:B:312:PHE:CD1	2.46	0.50
1:C:665:LEU:HD13	1:D:692:ILE:HD11	1.94	0.50
1:D:652:ALA:O	1:D:653:ASP:HB3	2.12	0.50
1:D:366:ARG:NH2	1:D:393:ASP:O	2.45	0.49
1:A:589:SER:HB2	1:A:635:GLU:HB3	1.94	0.49
1:A:297:TRP:HB2	1:A:300:ASN:ND2	2.28	0.49
1:E:510:ARG:HH12	1:E:551:LEU:HD11	1.78	0.49
1:B:408:ILE:HG13	3:B:762:HOH:O	2.12	0.49
1:C:495:THR:HG22	1:C:521:MET:HB2	1.95	0.49
1:D:329:PHE:CZ	1:D:419:LYS:HG3	2.47	0.49
1:B:608:ALA:O	1:B:610:MET:N	2.45	0.49
1:A:576:LYS:C	1:A:576:LYS:HD3	2.33	0.49
1:C:632:LYS:HE3	1:C:671:LEU:HD21	1.94	0.49
1:D:378:ILE:HG13	1:D:379:PRO:HD2	1.93	0.49
1:E:637:ASN:ND2	1:E:637:ASN:C	2.66	0.49
1:A:684:HIS:NE2	1:A:688:ILE:HD11	2.28	0.48
1:E:480:TYR:CE1	1:E:517:GLU:HB3	2.48	0.48
1:C:637:ASN:C	1:C:637:ASN:ND2	2.66	0.48
1:F:480:TYR:CE1	1:F:517:GLU:HB3	2.48	0.48
1:A:487:ASN:N	1:A:487:ASN:OD1	2.33	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:561:GLN:O	1:E:565:LYS:HB2	2.13	0.48
1:A:299:ARG:HD2	1:A:390:ASP:HB2	1.94	0.48
1:C:637:ASN:HD22	1:C:639:ASP:H	1.61	0.48
1:C:576:LYS:HD2	1:C:576:LYS:O	2.14	0.48
1:C:510:ARG:HD3	1:C:590:ASN:O	2.13	0.48
1:C:323:HIS:HD2	1:C:323:HIS:H	1.61	0.48
1:F:300:ASN:H	1:F:301:PRO:HD3	1.78	0.48
1:A:607:THR:OG1	1:A:608:ALA:N	2.46	0.48
1:E:299:ARG:H	1:E:299:ARG:HG3	1.47	0.48
1:A:646:LEU:HD13	1:A:662:LEU:CD1	2.43	0.48
1:D:557:GLU:OE1	1:D:557:GLU:HA	2.13	0.48
1:C:310:GLY:HA2	1:C:323:HIS:CD2	2.49	0.48
1:B:637:ASN:HD22	1:B:639:ASP:H	1.61	0.48
1:E:637:ASN:ND2	1:E:639:ASP:H	2.11	0.48
1:D:418:LYS:HD2	3:D:776:HOH:O	2.14	0.48
1:A:656:ASP:OD2	1:A:658:SER:HB2	2.14	0.47
1:C:637:ASN:HD22	1:C:638:PRO:N	2.12	0.47
1:B:366:ARG:O	1:B:367:ARG:HB2	2.14	0.47
1:C:364:TYR:O	1:C:390:ASP:HA	2.15	0.47
1:E:300:ASN:HB2	1:E:301:PRO:HD3	1.97	0.47
1:C:414:LYS:HZ1	1:C:454:GLN:HE22	1.61	0.47
1:E:645:THR:HA	1:E:648:GLN:HE21	1.79	0.47
1:B:465:TYR:CE1	1:B:521:MET:HG2	2.50	0.47
1:E:431:LYS:O	1:E:431:LYS:HE3	2.15	0.46
1:E:335:LEU:HD11	1:E:393:ASP:OD2	2.14	0.46
1:D:587:VAL:CG2	1:D:635:GLU:HG2	2.46	0.46
1:D:298:THR:C	1:D:300:ASN:H	2.19	0.46
1:A:637:ASN:HD22	1:A:638:PRO:N	2.13	0.46
1:C:323:HIS:N	1:C:323:HIS:CD2	2.83	0.46
1:F:587:VAL:HG22	1:F:635:GLU:HG2	1.98	0.46
1:E:413:ARG:O	1:E:417:VAL:HG12	2.16	0.46
1:E:585:LYS:HD2	1:E:633:HIS:CE1	2.50	0.46
1:E:600:VAL:HG23	1:E:633:HIS:HB2	1.98	0.46
1:E:335:LEU:HD12	1:E:335:LEU:HA	1.76	0.46
1:B:652:ALA:O	1:B:653:ASP:HB3	2.15	0.46
1:C:361:ILE:HD12	1:C:377:LEU:HD13	1.98	0.46
1:C:497:GLU:H	1:C:501:GLN:NE2	1.92	0.46
1:D:594:THR:O	1:D:640:HIS:CD2	2.69	0.46
1:C:366:ARG:HA	1:C:367:ARG:HH11	1.81	0.46
1:A:297:TRP:O	1:A:297:TRP:CG	2.68	0.46
1:E:414:LYS:NZ	1:E:454:GLN:HE22	2.14	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:364:TYR:HB3	1:E:390:ASP:OD1	2.16	0.46
1:C:691:MET:SD	1:D:691:MET:CB	3.04	0.45
1:F:327:LYS:HD3	1:F:423:LEU:HB2	1.97	0.45
1:F:525:ILE:CD1	1:F:525:ILE:N	2.60	0.45
1:D:322:ASP:OD1	1:D:345:ARG:NH1	2.50	0.45
1:F:298:THR:HG21	1:F:312:PHE:CG	2.51	0.45
1:C:498:THR:H	1:C:501:GLN:NE2	2.11	0.45
1:A:408:ILE:HD12	1:A:408:ILE:HA	1.82	0.45
1:D:495:THR:HG22	1:D:521:MET:HB2	1.99	0.45
1:D:594:THR:O	1:D:640:HIS:HD2	2.00	0.45
1:C:609:ASN:HA	1:C:609:ASN:HD22	1.61	0.45
1:D:637:ASN:C	1:D:637:ASN:HD22	2.20	0.45
1:F:341:LEU:HD11	1:F:416:LEU:HD22	1.99	0.45
1:B:299:ARG:HD2	1:B:390:ASP:HB2	1.99	0.45
1:B:298:THR:O	1:B:301:PRO:HD2	2.17	0.45
1:A:301:PRO:HG2	3:A:862:HOH:O	2.17	0.45
1:F:347:ALA:HA	1:F:348:PRO:HD3	1.87	0.45
1:A:298:THR:C	1:A:300:ASN:H	2.21	0.44
1:E:607:THR:OG1	1:E:608:ALA:N	2.50	0.44
1:A:297:TRP:HE3	1:A:300:ASN:HD22	1.64	0.44
1:E:571:LEU:HD11	1:E:646:LEU:HG	1.99	0.44
1:B:637:ASN:C	1:B:637:ASN:HD22	2.21	0.44
1:E:449:ILE:HG23	1:E:456:ARG:HG3	2.00	0.44
1:D:297:TRP:O	1:D:300:ASN:HB2	2.18	0.44
1:A:299:ARG:HD2	1:A:390:ASP:CB	2.48	0.44
1:B:589:SER:HB2	1:B:635:GLU:HB3	1.99	0.44
1:F:297:TRP:O	1:F:300:ASN:N	2.51	0.44
1:F:523:GLU:O	1:F:526:ASP:HB2	2.17	0.44
1:F:297:TRP:O	1:F:298:THR:C	2.55	0.44
1:D:587:VAL:HG23	1:D:635:GLU:HG2	1.99	0.44
1:C:327:LYS:HD3	1:C:423:LEU:HB2	1.98	0.44
1:F:438:TYR:CZ	1:F:442:SER:HB2	2.52	0.44
1:E:672:LEU:HD11	1:E:678:LEU:HD11	1.99	0.44
1:A:646:LEU:HD13	1:A:662:LEU:HD12	1.99	0.44
1:B:587:VAL:HG22	1:B:635:GLU:HG2	1.99	0.44
1:B:495:THR:HA	1:B:521:MET:O	2.18	0.43
1:A:485:LYS:H	1:A:485:LYS:HG2	1.38	0.43
1:E:345:ARG:O	1:E:440:GLN:HG3	2.18	0.43
1:C:669:THR:HG21	1:D:688:ILE:HG21	1.99	0.43
1:E:576:LYS:HD3	1:E:576:LYS:C	2.37	0.43
1:C:487:ASN:OD1	1:C:487:ASN:N	2.48	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:600:VAL:CG2	1:E:633:HIS:HB2	2.48	0.43
1:E:604:TYR:N	1:E:604:TYR:CD2	2.87	0.43
1:C:378:ILE:CG1	1:C:379:PRO:HD2	2.47	0.43
1:A:498:THR:OG1	1:A:501:GLN:HB2	2.18	0.43
1:F:612:ARG:CG	1:F:612:ARG:HH11	2.31	0.43
1:E:645:THR:HA	1:E:648:GLN:NE2	2.32	0.43
1:F:381:TYR:HB3	1:F:447:LEU:HD23	2.01	0.43
1:B:508:VAL:O	1:B:512:ARG:HB2	2.19	0.43
1:F:378:ILE:HG13	1:F:379:PRO:HD2	2.01	0.43
1:F:408:ILE:HD12	1:F:408:ILE:O	2.19	0.43
1:B:569:GLU:HA	1:B:569:GLU:OE1	2.19	0.43
1:F:323:HIS:N	1:F:323:HIS:CD2	2.87	0.43
1:C:460:SER:HA	1:C:463:LEU:HD12	2.00	0.43
1:E:604:TYR:N	1:E:604:TYR:HD2	2.17	0.42
1:C:450:HIS:HD2	1:C:451:GLU:OE2	2.02	0.42
1:B:555:GLU:HG2	1:B:555:GLU:H	1.67	0.42
1:F:698:ILE:H	1:F:698:ILE:HG13	1.53	0.42
1:C:300:ASN:HB2	1:C:301:PRO:HD3	2.01	0.42
1:F:630:ALA:HA	1:F:631:LYS:HA	1.65	0.42
1:B:346:ARG:NH2	3:B:804:HOH:O	2.50	0.42
1:B:553:GLU:H	1:B:553:GLU:HG2	1.64	0.42
1:B:443:LYS:HG3	1:B:525:ILE:HG13	2.00	0.42
1:D:697:GLY:O	1:D:698:ILE:C	2.58	0.42
1:D:327:LYS:HB2	1:D:423:LEU:HD22	2.02	0.42
1:A:480:TYR:CE1	1:A:517:GLU:HB3	2.55	0.42
1:B:589:SER:CB	1:B:592:LEU:HD12	2.49	0.42
1:B:297:TRP:O	1:B:299:ARG:N	2.52	0.42
1:E:346:ARG:NH1	1:E:346:ARG:CG	2.79	0.42
1:D:509:GLU:OE1	1:D:594:THR:N	2.49	0.42
1:E:443:LYS:HG3	1:E:525:ILE:HG13	2.02	0.42
1:C:490:HIS:HB3	1:C:542:VAL:HG13	2.02	0.42
1:F:506:ALA:HA	1:F:509:GLU:OE2	2.19	0.42
1:C:483:ARG:NH2	1:C:517:GLU:OE2	2.33	0.42
1:A:443:LYS:HG3	1:A:525:ILE:HG13	2.02	0.42
1:D:435:LYS:O	1:D:439:GLU:HB2	2.19	0.42
1:F:509:GLU:OE1	1:F:594:THR:N	2.53	0.41
1:C:611:GLU:HB3	3:C:878:HOH:O	2.19	0.41
1:F:422:GLU:O	1:F:426:GLU:HG3	2.20	0.41
1:F:409:LEU:H	1:F:409:LEU:HD13	1.85	0.41
1:A:692:ILE:HD11	1:B:665:LEU:HD13	2.01	0.41
1:C:347:ALA:HA	1:C:348:PRO:HD3	1.68	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:366:ARG:HH21	1:D:394:LEU:HA	1.85	0.41
1:E:571:LEU:HD13	1:E:647:ARG:HA	2.02	0.41
1:D:329:PHE:CZ	1:D:339:ALA:HB3	2.55	0.41
1:A:583:VAL:HG21	1:A:634:LEU:HB2	2.02	0.41
1:A:328:HIS:HB2	1:A:340:LEU:HD13	2.02	0.41
1:C:501:GLN:HE21	1:C:501:GLN:HB3	1.50	0.41
1:E:297:TRP:HA	1:E:300:ASN:ND2	2.35	0.41
1:E:485:LYS:O	1:E:488:GLN:HB3	2.20	0.41
1:D:381:TYR:O	1:D:444:ASN:HB3	2.20	0.41
1:D:341:LEU:HD11	1:D:416:LEU:HD22	2.03	0.41
1:B:341:LEU:HD11	1:B:416:LEU:HD22	2.03	0.41
1:C:431:LYS:HA	1:C:431:LYS:CE	2.46	0.41
1:D:330:SER:HB3	1:D:338:ARG:HG2	2.03	0.41
1:D:646:LEU:HD13	1:D:662:LEU:CD1	2.41	0.41
1:B:637:ASN:HD22	1:B:638:PRO:HD2	1.85	0.41
1:E:585:LYS:HD2	1:E:633:HIS:HE1	1.86	0.41
1:C:327:LYS:HD2	1:C:327:LYS:HA	1.93	0.41
1:B:559:LYS:O	1:B:563:GLU:HG3	2.20	0.41
1:B:632:LYS:HE3	1:B:671:LEU:HD21	2.03	0.41
1:B:435:LYS:O	1:B:439:GLU:HB2	2.21	0.41
1:B:672:LEU:HD21	1:B:678:LEU:HG	2.02	0.41
1:E:459:LEU:HA	1:E:462:LEU:HD12	2.02	0.41
1:E:485:LYS:HA	3:E:926:HOH:O	2.20	0.40
1:C:485:LYS:HG2	1:C:485:LYS:H	1.44	0.40
1:A:581:LYS:HB3	1:A:581:LYS:HE2	1.95	0.40
1:B:329:PHE:CE2	1:B:339:ALA:HB3	2.55	0.40
1:A:377:LEU:O	1:A:413:ARG:HA	2.20	0.40
1:E:604:TYR:HD2	1:E:604:TYR:H	1.69	0.40
1:C:378:ILE:HG12	1:C:379:PRO:HD2	2.04	0.40
1:B:447:LEU:O	1:B:451:GLU:HG2	2.20	0.40
1:C:302:ASP:O	1:C:302:ASP:OD1	2.40	0.40
1:B:485:LYS:HE3	1:B:515:GLY:O	2.22	0.40
1:C:335:LEU:HD23	1:C:411:VAL:CG1	2.51	0.40
1:A:557:GLU:O	1:A:560:LYS:HB2	2.22	0.40
1:A:692:ILE:HD11	1:B:665:LEU:CD1	2.51	0.40
1:A:407:LYS:HA	1:A:407:LYS:HE2	2.02	0.40
1:A:329:PHE:CE1	1:A:419:LYS:HG3	2.57	0.40
1:D:610:MET:HE1	3:D:793:HOH:O	2.21	0.40
1:E:299:ARG:NH1	1:E:299:ARG:HG2	2.07	0.40
1:A:637:ASN:HD22	1:A:639:ASP:H	1.67	0.40
1:B:585:LYS:HB2	1:B:633:HIS:CD2	2.57	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:298:THR:HG21	1:B:312:PHE:CG	2.56	0.40
1:D:604:TYR:HD2	1:D:605:GLY:N	2.20	0.40
1:B:557:GLU:HG3	1:B:560:LYS:HE3	2.03	0.40
1:E:347:ALA:HA	1:E:348:PRO:HD3	1.74	0.40
1:B:487:ASN:OD1	1:B:487:ASN:N	2.33	0.40
1:A:345:ARG:O	1:A:440:GLN:HG3	2.21	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	352/448 (79%)	327 (93%)	17 (5%)	8 (2%)	8	32
1	B	354/448 (79%)	331 (94%)	14 (4%)	9 (2%)	7	30
1	C	344/448 (77%)	315 (92%)	25 (7%)	4 (1%)	16	50
1	D	350/448 (78%)	327 (93%)	18 (5%)	5 (1%)	14	46
1	E	352/448 (79%)	328 (93%)	21 (6%)	3 (1%)	21	58
1	F	353/448 (79%)	327 (93%)	22 (6%)	4 (1%)	17	53
All	All	2105/2688 (78%)	1955 (93%)	117 (6%)	33 (2%)	12	42

All (33) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	609	ASN
1	C	334	GLN
1	D	393	ASP
1	F	334	GLN
1	F	394	LEU
1	A	334	GLN

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Mol	Chain	Res	Type
1	B	553	GLU
1	B	555	GLU
1	B	697	GLY
1	C	348	PRO
1	E	606	TRP
1	A	555	GLU
1	B	334	GLN
1	C	558	LYS
1	D	334	GLN
1	F	301	PRO
1	A	301	PRO
1	A	606	TRP
1	D	301	PRO
1	D	611	GLU
1	E	301	PRO
1	B	653	ASP
1	C	301	PRO
1	A	302	ASP
1	A	552	PRO
1	D	375	GLU
1	A	300	ASN
1	A	548	GLY
1	F	300	ASN
1	B	300	ASN
1	B	301	PRO
1	B	348	PRO
1	E	552	PRO

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	335/412 (81%)	297 (89%)	38 (11%)	7	27
1	B	337/412 (82%)	296 (88%)	41 (12%)	6	22
1	C	330/412 (80%)	294 (89%)	36 (11%)	8	29

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	D	334/412 (81%)	292 (87%)	42 (13%)	5	21
1	E	335/412 (81%)	292 (87%)	43 (13%)	5	20
1	F	337/412 (82%)	294 (87%)	43 (13%)	5	20
All	All	2008/2472 (81%)	1765 (88%)	243 (12%)	6	23

All (243) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	299	ARG
1	A	302	ASP
1	A	360	ASN
1	A	371	MET
1	A	388	VAL
1	A	417	VAL
1	A	421	LEU
1	A	431	LYS
1	A	447	LEU
1	A	478	LYS
1	A	479	ASP
1	A	485	LYS
1	A	486	GLU
1	A	500	ASP
1	A	501	GLN
1	A	512	ARG
1	A	525	ILE
1	A	528	TYR
1	A	542	VAL
1	A	545	THR
1	A	554	ASP
1	A	555	GLU
1	A	557	GLU
1	A	559	LYS
1	A	562	GLU
1	A	576	LYS
1	A	581	LYS
1	A	604	TYR
1	A	607	THR
1	A	611	GLU
1	A	634	LEU
1	A	637	ASN
1	A	662	LEU

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Mol	Chain	Res	Type
1	A	665	LEU
1	A	669	THR
1	A	679	GLU
1	A	682	GLN
1	A	698	ILE
1	B	297	TRP
1	B	299	ARG
1	B	300	ASN
1	B	303	ASP
1	B	307	GLU
1	B	335	LEU
1	B	358	LYS
1	B	360	ASN
1	B	371	MET
1	B	378	ILE
1	B	408	ILE
1	B	409	LEU
1	B	410	LYS
1	B	439	GLU
1	B	443	LYS
1	B	489	LYS
1	B	497	GLU
1	B	512	ARG
1	B	525	ILE
1	B	540	THR
1	B	542	VAL
1	B	553	GLU
1	B	557	GLU
1	B	558	LYS
1	B	559	LYS
1	B	560	LYS
1	B	573	LYS
1	B	576	LYS
1	B	603	THR
1	B	604	TYR
1	B	637	ASN
1	B	644	GLU
1	B	645	THR
1	B	653	ASP
1	B	657	LYS
1	B	662	LEU
1	B	665	LEU

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Mol	Chain	Res	Type
1	B	677	SER
1	B	694	LEU
1	B	696	LEU
1	B	698	ILE
1	C	299	ARG
1	C	335	LEU
1	C	361	ILE
1	C	367	ARG
1	C	371	MET
1	C	388	VAL
1	C	391	SER
1	C	407	LYS
1	C	417	VAL
1	C	431	LYS
1	C	433	ASN
1	C	447	LEU
1	C	451	GLU
1	C	479	ASP
1	C	485	LYS
1	C	486	GLU
1	C	500	ASP
1	C	501	GLN
1	C	512	ARG
1	C	525	ILE
1	C	528	TYR
1	C	530	VAL
1	C	542	VAL
1	C	558	LYS
1	C	559	LYS
1	C	576	LYS
1	C	581	LYS
1	C	604	TYR
1	C	609	ASN
1	C	611	GLU
1	C	634	LEU
1	C	637	ASN
1	C	644	GLU
1	C	662	LEU
1	C	665	LEU
1	C	694	LEU
1	D	299	ARG
1	D	307	GLU

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Mol	Chain	Res	Type
1	D	335	LEU
1	D	346	ARG
1	D	360	ASN
1	D	361	ILE
1	D	378	ILE
1	D	392	GLU
1	D	393	ASP
1	D	409	LEU
1	D	410	LYS
1	D	439	GLU
1	D	443	LYS
1	D	453	SER
1	D	458	LYS
1	D	472	ASP
1	D	489	LYS
1	D	497	GLU
1	D	500	ASP
1	D	512	ARG
1	D	525	ILE
1	D	530	VAL
1	D	542	VAL
1	D	557	GLU
1	D	558	LYS
1	D	560	LYS
1	D	573	LYS
1	D	576	LYS
1	D	603	THR
1	D	604	TYR
1	D	606	TRP
1	D	612	ARG
1	D	631	LYS
1	D	637	ASN
1	D	644	GLU
1	D	645	THR
1	D	657	LYS
1	D	662	LEU
1	D	665	LEU
1	D	669	THR
1	D	673	SER
1	D	677	SER
1	E	297	TRP
1	E	298	THR

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Mol	Chain	Res	Type
1	E	299	ARG
1	E	300	ASN
1	E	346	ARG
1	E	358	LYS
1	E	359	ASN
1	E	370	ILE
1	E	388	VAL
1	E	393	ASP
1	E	394	LEU
1	E	417	VAL
1	E	431	LYS
1	E	447	LEU
1	E	451	GLU
1	E	457	LYS
1	E	479	ASP
1	E	486	GLU
1	E	500	ASP
1	E	512	ARG
1	E	522	ILE
1	E	525	ILE
1	E	528	TYR
1	E	530	VAL
1	E	542	VAL
1	E	553	GLU
1	E	554	ASP
1	E	559	LYS
1	E	560	LYS
1	E	562	GLU
1	E	576	LYS
1	E	581	LYS
1	E	583	VAL
1	E	604	TYR
1	E	607	THR
1	E	631	LYS
1	E	634	LEU
1	E	637	ASN
1	E	662	LEU
1	E	665	LEU
1	E	669	THR
1	E	677	SER
1	E	679	GLU
1	F	299	ARG

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Mol	Chain	Res	Type
1	F	302	ASP
1	F	307	GLU
1	F	315	SER
1	F	335	LEU
1	F	358	LYS
1	F	359	ASN
1	F	372	ASP
1	F	392	GLU
1	F	393	ASP
1	F	408	ILE
1	F	409	LEU
1	F	410	LYS
1	F	421	LEU
1	F	439	GLU
1	F	443	LYS
1	F	447	LEU
1	F	489	LYS
1	F	497	GLU
1	F	505	SER
1	F	512	ARG
1	F	525	ILE
1	F	530	VAL
1	F	542	VAL
1	F	557	GLU
1	F	558	LYS
1	F	559	LYS
1	F	560	LYS
1	F	573	LYS
1	F	576	LYS
1	F	587	VAL
1	F	606	TRP
1	F	607	THR
1	F	612	ARG
1	F	637	ASN
1	F	644	GLU
1	F	657	LYS
1	F	662	LEU
1	F	665	LEU
1	F	669	THR
1	F	673	SER
1	F	677	SER
1	F	694	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (44) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	323	HIS
1	A	501	GLN
1	A	637	ASN
1	A	648	GLN
1	A	682	GLN
1	A	686	ASN
1	B	323	HIS
1	B	334	GLN
1	B	454	GLN
1	B	531	GLN
1	B	637	ASN
1	B	686	ASN
1	C	323	HIS
1	C	360	ASN
1	C	450	HIS
1	C	501	GLN
1	C	504	ASN
1	C	609	ASN
1	C	633	HIS
1	C	637	ASN
1	C	648	GLN
1	C	682	GLN
1	C	686	ASN
1	D	300	ASN
1	D	323	HIS
1	D	360	ASN
1	D	454	GLN
1	D	504	ASN
1	D	637	ASN
1	D	686	ASN
1	E	300	ASN
1	E	323	HIS
1	E	373	ASN
1	E	501	GLN
1	E	504	ASN
1	E	637	ASN
1	E	648	GLN
1	E	686	ASN
1	F	323	HIS
1	F	334	GLN
1	F	454	GLN

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Mol	Chain	Res	Type
1	F	531	GLN
1	F	609	ASN
1	F	637	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 [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	2	-	4,4,4	0.34	0	6,6,6	0.27	0
2	SO4	B	3	-	4,4,4	0.23	0	6,6,6	0.22	0
2	SO4	C	5	-	4,4,4	0.31	0	6,6,6	0.39	0
2	SO4	D	4	-	4,4,4	0.27	0	6,6,6	0.47	0
2	SO4	E	6	-	4,4,4	0.24	0	6,6,6	0.08	0
2	SO4	F	1	-	4,4,4	0.26	0	6,6,6	0.18	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	2	-	-	0/0/0/0	0/0/0/0
2	SO4	B	3	-	-	0/0/0/0	0/0/0/0
2	SO4	C	5	-	-	0/0/0/0	0/0/0/0
2	SO4	D	4	-	-	0/0/0/0	0/0/0/0
2	SO4	E	6	-	-	0/0/0/0	0/0/0/0
2	SO4	F	1	-	-	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.

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, 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	360/448 (80%)	-0.23	4 (1%)	82 63	61, 83, 117, 142	1 (0%)
1	B	362/448 (80%)	-0.27	1 (0%)	94 87	59, 77, 117, 138	1 (0%)
1	C	354/448 (79%)	-0.21	4 (1%)	82 63	62, 86, 125, 150	1 (0%)
1	D	360/448 (80%)	-0.26	4 (1%)	82 63	60, 84, 127, 138	1 (0%)
1	E	360/448 (80%)	-0.17	4 (1%)	82 63	60, 82, 120, 158	1 (0%)
1	F	363/448 (81%)	-0.27	1 (0%)	94 87	58, 78, 118, 138	1 (0%)
All	All	2159/2688 (80%)	-0.23	18 (0%)	87 72	58, 82, 122, 158	6 (0%)

All (18) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	606	TRP	4.4
1	E	606	TRP	4.1
1	C	606	TRP	3.7
1	D	604	TYR	3.3
1	B	554	ASP	3.0
1	F	614	MET	2.7
1	D	566	THR	2.7
1	C	563	GLU	2.6
1	A	554	ASP	2.6
1	D	349	PHE	2.5
1	C	694	LEU	2.5
1	A	555	GLU	2.3
1	A	307	GLU	2.3
1	E	486	GLU	2.3
1	E	554	ASP	2.2
1	D	606	TRP	2.1
1	E	559	LYS	2.1
1	C	307	GLU	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 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, 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	LLDF	B-factors(\AA^2)	Q<0.9
2	SO4	B	3	5/5	0.90	0.23	0.16	125,126,126,126	0
2	SO4	C	5	5/5	0.95	0.17	-0.83	116,116,117,117	0
2	SO4	E	6	5/5	0.88	0.15	-1.06	139,139,140,140	0
2	SO4	A	2	5/5	0.92	0.17	-	112,113,113,113	0
2	SO4	D	4	5/5	0.85	0.27	-	127,128,128,128	0
2	SO4	F	1	5/5	0.93	0.14	-	120,120,120,121	0

6.5 Other polymers [i](#)

There are no such residues in this entry.