



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 15, 2017 – 02:10 am GMT

PDB ID : 2P2G  
Title : Crystal Structure of Ornithine Carbamoyltransferase from Mycobacterium Tuberculosis (Rv1656): Orthorhombic Form  
Authors : Sankaranarayanan, R.; Cherney, M.M.; Cherney, L.T.; Garen, C.; Moradian, F.; James, M.N.G.; TB Structural Genomics Consortium (TBSGC)  
Deposited on : 2007-03-07  
Resolution : 2.70 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	:	1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix)	:	1.9-1692
EDS	:	trunk28620
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
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)	:	recalc28949

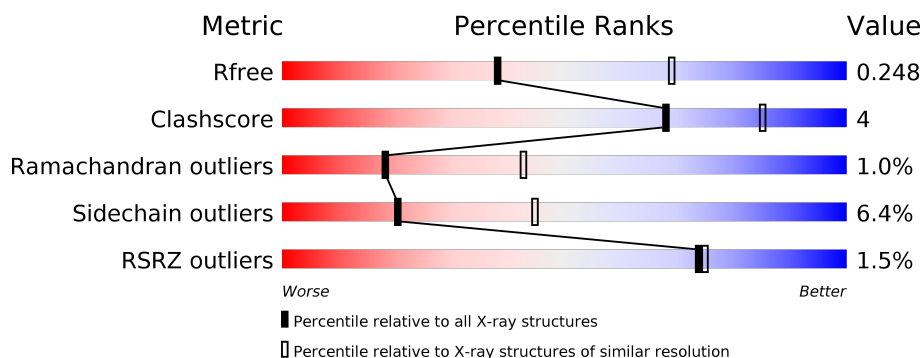
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.70 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))
$R_{free}$	100719	2259 (2.70-2.70)
Clashscore	112137	2590 (2.70-2.70)
Ramachandran outliers	110173	2550 (2.70-2.70)
Sidechain outliers	110143	2550 (2.70-2.70)
RSRZ outliers	101464	2275 (2.70-2.70)

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	307	<div> <div>2%</div> <div>81% 13% . .</div> </div>
1	B	307	<div> <div>2%</div> <div>81% 14% .</div> </div>
1	C	307	<div> <div>2%</div> <div>81% 15% . .</div> </div>
1	D	307	<div> <div>2%</div> <div>83% 11% . .</div> </div>
1	E	307	<div> <div>2%</div> <div>82% 13% . .</div> </div>
1	F	307	<div> <div>2%</div> <div>84% 11% . .</div> </div>

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 13707 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 Ornithine carbamoyltransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	295	Total	C	N	O	S	0	0	0
			2236	1398	407	426	5			
1	B	295	Total	C	N	O	S	0	0	0
			2236	1398	407	426	5			
1	C	298	Total	C	N	O	S	0	0	0
			2260	1411	413	431	5			
1	D	295	Total	C	N	O	S	0	0	0
			2236	1398	407	426	5			
1	E	301	Total	C	N	O	S	0	0	0
			2283	1424	417	437	5			
1	F	295	Total	C	N	O	S	0	0	0
			2236	1398	407	426	5			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	VAL	-	CLONING ARTIFACT	UNP P0A5M8
B	1	VAL	-	CLONING ARTIFACT	UNP P0A5M8
C	1	VAL	-	CLONING ARTIFACT	UNP P0A5M8
D	1	VAL	-	CLONING ARTIFACT	UNP P0A5M8
E	1	VAL	-	CLONING ARTIFACT	UNP P0A5M8
F	1	VAL	-	CLONING ARTIFACT	UNP P0A5M8

- 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	A	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	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	C	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	D	1	Total	O	S	0	0
			5	4	1		
2	E	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		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	F	1	Total	O	S	0	0
			5	4	1		
2	F	1	Total	O	S	0	0
			5	4	1		

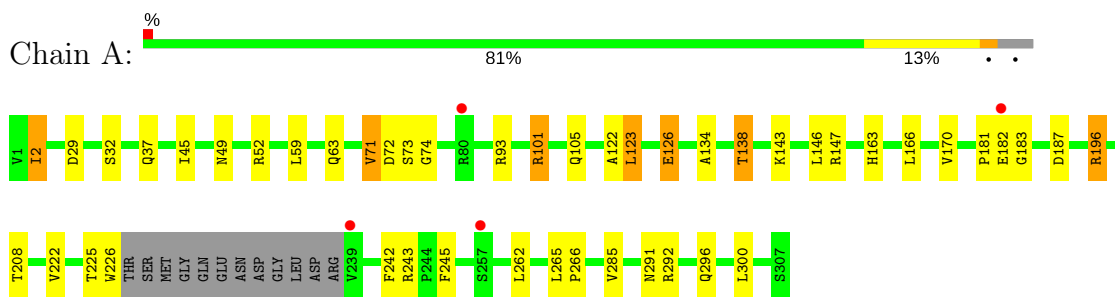
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	24	Total	O	0	0
			24	24		
3	B	21	Total	O	0	0
			21	21		
3	C	29	Total	O	0	0
			29	29		
3	D	17	Total	O	0	0
			17	17		
3	E	25	Total	O	0	0
			25	25		
3	F	24	Total	O	0	0
			24	24		

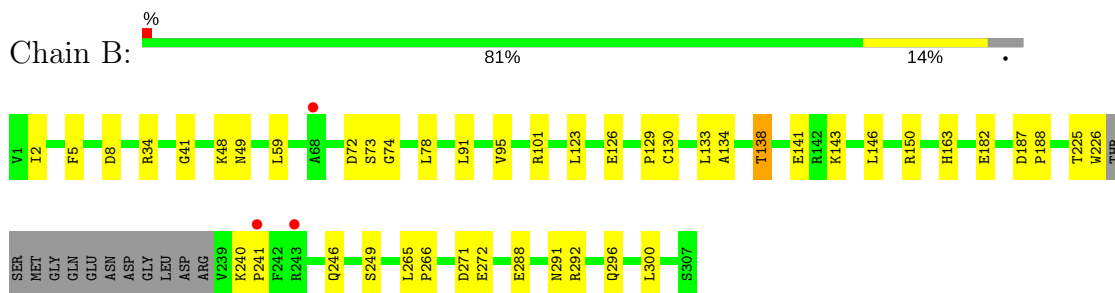
### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ( $RSRZ > 2$ ). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

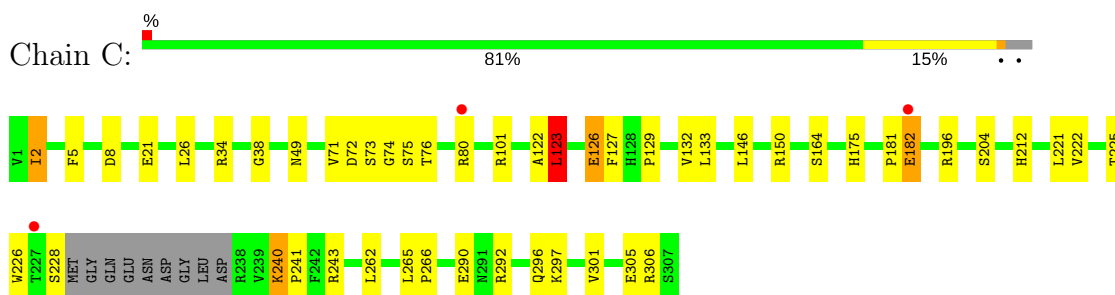
- Molecule 1: Ornithine carbamoyltransferase



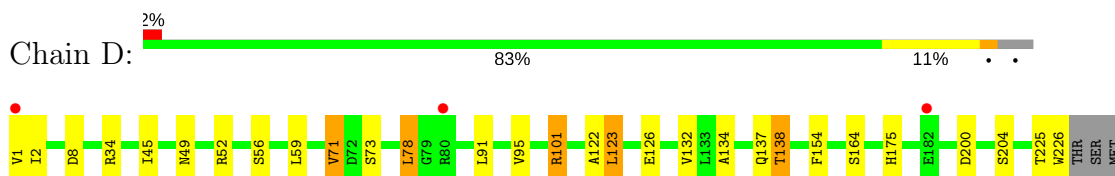
- Molecule 1: Ornithine carbamoyltransferase



- Molecule 1: Ornithine carbamoyltransferase

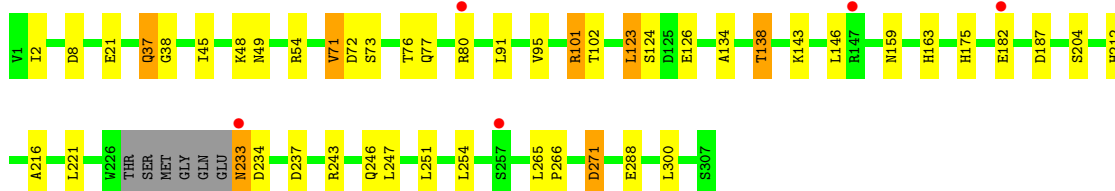
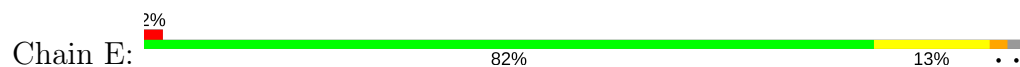


- Molecule 1: Ornithine carbamoyltransferase

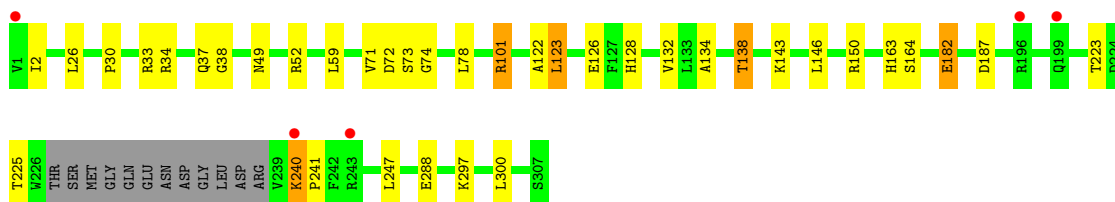
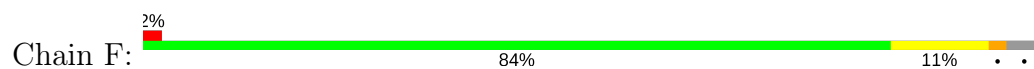




● Molecule 1: Ornithine carbamoyltransferase



● Molecule 1: Ornithine carbamoyltransferase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	79.17Å 144.65Å 187.77Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	38.18 – 2.70 38.18 – 2.70	Depositor EDS
% Data completeness (in resolution range)	96.7 (38.18-2.70) 96.7 (38.18-2.70)	Depositor EDS
$R_{merge}$	0.16	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.97 (at 2.69Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, $R_{free}$	0.202 , 0.259 0.195 , 0.248	Depositor DCC
$R_{free}$ test set	2948 reflections (5.33%)	DCC
Wilson B-factor (Å <sup>2</sup> )	51.5	Xtriage
Anisotropy	0.110	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 31.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	13707	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	43.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.52% 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, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.



## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 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	0.51	0/2276	0.68	0/3096
1	B	0.54	0/2276	0.67	0/3096
1	C	0.55	0/2300	0.70	2/3128 (0.1%)
1	D	0.53	0/2276	0.67	0/3096
1	E	0.52	0/2323	0.68	0/3159
1	F	0.55	0/2276	0.70	1/3096 (0.0%)
All	All	0.53	0/13727	0.68	3/18671 (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	C	0	1

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	123	LEU	CA-CB-CG	5.98	129.05	115.30
1	F	182	GLU	N-CA-C	5.19	125.01	111.00
1	C	2	ILE	N-CA-C	5.07	124.68	111.00

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	226	TRP	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	2236	0	2224	22	0
1	B	2236	0	2224	23	0
1	C	2260	0	2249	18	0
1	D	2236	0	2224	21	0
1	E	2283	0	2265	22	0
1	F	2236	0	2224	18	0
2	A	10	0	0	0	0
2	B	20	0	0	0	0
2	C	15	0	0	0	0
2	D	10	0	0	0	0
2	E	10	0	0	0	0
2	F	15	0	0	0	0
3	A	24	0	0	0	0
3	B	21	0	0	0	0
3	C	29	0	0	0	0
3	D	17	0	0	0	0
3	E	25	0	0	1	0
3	F	24	0	0	1	0
All	All	13707	0	13410	119	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 4.

All (119) 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:138:THR:HG22	1:B:291:ASN:HD22	1.42	0.82
1:D:45:ILE:HG12	1:D:71:VAL:HG13	1.66	0.77
1:A:134:ALA:O	1:A:138:THR:HG22	1.87	0.75
1:A:59:LEU:O	1:A:63:GLN:HG3	1.89	0.72
1:B:138:THR:HG22	1:B:291:ASN:ND2	2.04	0.70
1:B:34:ARG:NH2	1:C:38:GLY:O	2.24	0.70
1:B:134:ALA:O	1:B:138:THR:HG23	1.91	0.70
1:B:138:THR:HG21	1:B:288:GLU:HA	1.74	0.69
1:E:134:ALA:O	1:E:138:THR:HG22	1.92	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:49:ASN:HD21	1:F:73:SER:H	1.41	0.68
1:F:72:ASP:HB3	1:F:74:GLY:H	1.59	0.68
1:D:101:ARG:HG2	1:D:123:LEU:HB3	1.75	0.67
1:B:72:ASP:HB3	1:B:74:GLY:H	1.61	0.66
1:D:49:ASN:HD21	1:D:73:SER:H	1.43	0.65
1:D:292:ARG:HE	1:D:296:GLN:NE2	1.94	0.64
1:D:138:THR:HG21	1:D:288:GLU:HA	1.78	0.64
1:E:102:THR:O	1:E:124:SER:HA	1.98	0.64
1:A:59:LEU:HD11	1:B:41:GLY:HA3	1.80	0.62
1:E:247:LEU:HD12	1:E:251:LEU:HD23	1.80	0.61
1:A:72:ASP:HB3	1:A:74:GLY:H	1.64	0.61
1:E:138:THR:HG21	1:E:288:GLU:HA	1.82	0.61
1:A:101:ARG:HG2	1:A:123:LEU:HB3	1.84	0.59
1:C:122:ALA:O	1:C:123:LEU:HB2	2.02	0.59
1:A:222:VAL:HG13	1:A:262:LEU:HB2	1.83	0.58
1:B:292:ARG:HE	1:B:296:GLN:NE2	2.00	0.58
1:E:38:GLY:O	1:F:34:ARG:NH2	2.36	0.58
1:E:49:ASN:HD21	1:E:73:SER:H	1.51	0.58
1:B:292:ARG:HE	1:B:296:GLN:HE22	1.51	0.57
1:D:134:ALA:O	1:D:138:THR:HG22	2.06	0.56
1:A:138:THR:HB	1:A:291:ASN:HD22	1.71	0.56
1:E:134:ALA:O	1:E:138:THR:CG2	2.54	0.56
1:F:163:HIS:HE1	1:F:187:ASP:H	1.52	0.56
1:E:175:HIS:HD2	1:E:204:SER:OG	1.88	0.55
1:C:181:PRO:HB2	1:C:182:GLU:HG2	1.88	0.55
1:E:237:ASP:OD1	1:E:243:ARG:NH2	2.40	0.55
1:B:240:LYS:N	1:B:241:PRO:HD2	2.22	0.54
1:F:138:THR:HG21	1:F:288:GLU:HA	1.88	0.54
1:A:122:ALA:O	1:A:123:LEU:HB2	2.08	0.53
1:B:265:LEU:HB3	1:B:266:PRO:HA	1.90	0.53
1:C:222:VAL:HG22	1:C:262:LEU:HB2	1.90	0.53
1:E:163:HIS:HE1	1:E:187:ASP:H	1.54	0.53
1:D:56:SER:O	1:D:293:LEU:HD12	2.09	0.52
1:C:126:GLU:HB2	1:C:127:PHE:CD2	2.46	0.51
1:B:126:GLU:O	1:B:163:HIS:HD2	1.95	0.50
1:F:134:ALA:O	1:F:138:THR:HG22	2.10	0.50
1:C:265:LEU:HB3	1:C:266:PRO:HA	1.94	0.50
1:C:292:ARG:HE	1:C:296:GLN:NE2	2.10	0.49
1:B:246:GLN:HG3	1:B:271:ASP:O	2.13	0.49
1:F:101:ARG:HG2	1:F:123:LEU:HB3	1.94	0.49
1:B:49:ASN:HD21	1:B:73:SER:H	1.59	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:132:VAL:HG21	1:C:164:SER:HB3	1.94	0.49
1:C:175:HIS:HD2	1:C:204:SER:OG	1.96	0.49
1:A:163:HIS:HE1	1:A:187:ASP:H	1.59	0.49
1:D:292:ARG:HE	1:D:296:GLN:HE22	1.59	0.48
1:A:196:ARG:HA	1:A:196:ARG:HD2	1.74	0.48
1:C:49:ASN:HD21	1:C:73:SER:H	1.60	0.48
1:D:122:ALA:O	1:D:123:LEU:HB2	2.14	0.47
1:E:221:LEU:HB3	1:E:247:LEU:HD11	1.96	0.47
1:F:26:LEU:HD21	1:F:33:ARG:HG3	1.95	0.47
1:A:29:ASP:HB3	1:A:32:SER:HB3	1.95	0.47
1:D:56:SER:OG	1:D:296:GLN:OE1	2.28	0.47
1:D:45:ILE:HG12	1:D:71:VAL:CG1	2.42	0.47
1:E:45:ILE:HG12	1:E:71:VAL:HG13	1.97	0.47
1:E:216:ALA:HA	1:E:254:LEU:O	2.15	0.46
1:A:49:ASN:HD21	1:A:73:SER:H	1.62	0.46
1:E:265:LEU:HB3	1:E:266:PRO:HA	1.97	0.46
1:A:93:ARG:HB3	1:C:290:GLU:HB2	1.98	0.46
1:E:175:HIS:CD2	1:E:204:SER:OG	2.67	0.46
1:F:132:VAL:HG21	1:F:164:SER:HB3	1.97	0.46
1:D:175:HIS:HD2	1:D:204:SER:OG	1.99	0.46
1:B:5:PHE:CE2	1:B:129:PRO:HB2	2.50	0.45
1:B:59:LEU:HD23	1:B:59:LEU:HA	1.62	0.45
1:B:91:LEU:O	1:B:95:VAL:HG22	2.16	0.45
1:E:91:LEU:O	1:E:95:VAL:HG22	2.16	0.45
1:E:101:ARG:HG2	1:E:123:LEU:HB3	1.98	0.45
1:E:54:ARG:NH2	3:E:807:HOH:O	2.49	0.45
1:A:181:PRO:HB3	1:A:245:PHE:HE2	1.83	0.44
1:D:134:ALA:O	1:D:138:THR:CG2	2.65	0.44
1:A:292:ARG:HE	1:A:296:GLN:NE2	2.16	0.44
1:F:34:ARG:HH11	1:F:37:GLN:HE22	1.66	0.44
1:A:163:HIS:CE1	1:A:187:ASP:H	2.34	0.44
1:C:5:PHE:CE2	1:C:129:PRO:HB2	2.53	0.44
1:B:187:ASP:HA	1:B:188:PRO:HD3	1.87	0.43
1:D:137:GLN:OE1	1:D:295:ALA:HB2	2.18	0.43
1:C:26:LEU:HD13	1:C:297:LYS:HB3	2.01	0.43
1:E:233:ASN:N	1:E:233:ASN:HD22	2.16	0.43
1:F:223:THR:HB	1:F:247:LEU:HD13	2.00	0.43
1:B:130:CYS:HB3	1:B:296:GLN:HE21	1.84	0.43
1:F:163:HIS:CE1	1:F:187:ASP:H	2.35	0.43
1:D:34:ARG:NH2	1:F:38:GLY:O	2.51	0.42
1:E:300:LEU:HD12	1:E:300:LEU:HA	1.69	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:37:GLN:HE21	1:E:37:GLN:HB3	1.68	0.42
1:F:30:PRO:O	1:F:297:LYS:NZ	2.50	0.42
1:A:265:LEU:HB3	1:A:266:PRO:HA	2.02	0.42
1:F:122:ALA:O	1:F:123:LEU:HB2	2.20	0.42
1:C:72:ASP:HB3	1:C:74:GLY:H	1.85	0.41
1:A:182:GLU:HB3	1:A:183:GLY:H	1.47	0.41
1:C:292:ARG:HE	1:C:296:GLN:HE21	1.68	0.41
1:D:269:ARG:HD3	1:D:275:ASP:OD1	2.21	0.41
1:A:226:TRP:CE2	1:A:242:PHE:HB3	2.56	0.41
1:C:133:LEU:HD23	1:C:133:LEU:HA	1.80	0.41
1:D:78:LEU:HD12	1:D:78:LEU:HA	1.91	0.41
1:E:246:GLN:HG3	1:E:271:ASP:O	2.21	0.41
1:A:166:LEU:O	1:A:170:VAL:HG22	2.20	0.41
1:C:240:LYS:N	1:C:241:PRO:HD2	2.35	0.41
1:D:154:PHE:CD1	1:D:247:LEU:HD11	2.56	0.41
1:F:240:LYS:N	1:F:241:PRO:HD2	2.34	0.41
1:B:138:THR:HA	1:B:141:GLU:HG2	2.03	0.41
1:A:105:GLN:HB2	1:A:126:GLU:HG3	2.02	0.41
1:F:33:ARG:HD3	3:F:814:HOH:O	2.21	0.41
1:B:226:TRP:CZ2	1:B:272:GLU:HA	2.56	0.41
1:D:132:VAL:HG21	1:D:164:SER:HB3	2.01	0.40
1:F:134:ALA:O	1:F:138:THR:CG2	2.69	0.40
1:B:78:LEU:HD12	1:B:78:LEU:HA	1.83	0.40
1:A:45:ILE:HG12	1:A:71:VAL:HG13	2.03	0.40
1:B:133:LEU:HA	1:B:133:LEU:HD23	1.98	0.40
1:C:301:VAL:O	1:C:305:GLU:HG2	2.22	0.40
1:D:91:LEU:O	1:D:95:VAL:HG22	2.22	0.40
1:D:226:TRP:CE2	1:D:242:PHE:HB3	2.56	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	291/307 (95%)	272 (94%)	17 (6%)	2 (1%)	25	53
1	B	291/307 (95%)	282 (97%)	7 (2%)	2 (1%)	25	53
1	C	294/307 (96%)	281 (96%)	10 (3%)	3 (1%)	18	43
1	D	291/307 (95%)	275 (94%)	14 (5%)	2 (1%)	25	53
1	E	297/307 (97%)	286 (96%)	6 (2%)	5 (2%)	11	27
1	F	291/307 (95%)	279 (96%)	9 (3%)	3 (1%)	18	43
All	All	1755/1842 (95%)	1675 (95%)	63 (4%)	17 (1%)	18	43

All (17) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	123	LEU
1	C	123	LEU
1	E	234	ASP
1	F	2	ILE
1	D	2	ILE
1	E	182	GLU
1	E	271	ASP
1	F	123	LEU
1	F	182	GLU
1	B	123	LEU
1	C	2	ILE
1	D	123	LEU
1	E	123	LEU
1	A	2	ILE
1	B	2	ILE
1	C	182	GLU
1	E	2	ILE

### 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	232/242 (96%)	216 (93%)	16 (7%)	18	41

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	232/242 (96%)	221 (95%)	11 (5%)	30	60
1	C	235/242 (97%)	216 (92%)	19 (8%)	14	31
1	D	232/242 (96%)	220 (95%)	12 (5%)	27	55
1	E	237/242 (98%)	220 (93%)	17 (7%)	17	39
1	F	232/242 (96%)	218 (94%)	14 (6%)	22	48
All	All	1400/1452 (96%)	1311 (94%)	89 (6%)	20	45

All (89) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	ILE
1	A	37	GLN
1	A	52	ARG
1	A	71	VAL
1	A	101	ARG
1	A	126	GLU
1	A	138	THR
1	A	143	LYS
1	A	146	LEU
1	A	147	ARG
1	A	196	ARG
1	A	208	THR
1	A	225	THR
1	A	243	ARG
1	A	285	VAL
1	A	300	LEU
1	B	8	ASP
1	B	48	LYS
1	B	101	ARG
1	B	138	THR
1	B	143	LYS
1	B	146	LEU
1	B	150	ARG
1	B	182	GLU
1	B	225	THR
1	B	249	SER
1	B	300	LEU
1	C	8	ASP
1	C	21	GLU
1	C	34	ARG

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Mol	Chain	Res	Type
1	C	71	VAL
1	C	75	SER
1	C	76	THR
1	C	80	ARG
1	C	101	ARG
1	C	126	GLU
1	C	146	LEU
1	C	150	ARG
1	C	196	ARG
1	C	212	HIS
1	C	221	LEU
1	C	225	THR
1	C	228	SER
1	C	240	LYS
1	C	243	ARG
1	C	306	ARG
1	D	1	VAL
1	D	8	ASP
1	D	52	ARG
1	D	59	LEU
1	D	71	VAL
1	D	78	LEU
1	D	101	ARG
1	D	126	GLU
1	D	138	THR
1	D	200	ASP
1	D	225	THR
1	D	240	LYS
1	E	8	ASP
1	E	21	GLU
1	E	37	GLN
1	E	48	LYS
1	E	71	VAL
1	E	72	ASP
1	E	76	THR
1	E	77	GLN
1	E	80	ARG
1	E	101	ARG
1	E	126	GLU
1	E	138	THR
1	E	143	LYS
1	E	146	LEU

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Mol	Chain	Res	Type
1	E	159	ASN
1	E	212	HIS
1	E	233	ASN
1	F	52	ARG
1	F	59	LEU
1	F	71	VAL
1	F	78	LEU
1	F	101	ARG
1	F	126	GLU
1	F	128	HIS
1	F	138	THR
1	F	143	LYS
1	F	146	LEU
1	F	150	ARG
1	F	225	THR
1	F	240	LYS
1	F	300	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (27) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	49	ASN
1	A	77	GLN
1	A	163	HIS
1	A	175	HIS
1	A	296	GLN
1	B	49	ASN
1	B	163	HIS
1	B	175	HIS
1	B	199	GLN
1	B	296	GLN
1	C	49	ASN
1	C	175	HIS
1	C	296	GLN
1	D	37	GLN
1	D	49	ASN
1	D	163	HIS
1	D	175	HIS
1	E	49	ASN
1	E	77	GLN
1	E	163	HIS
1	E	175	HIS

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Mol	Chain	Res	Type
1	F	37	GLN
1	F	49	ASN
1	F	163	HIS
1	F	175	HIS
1	F	199	GLN
1	F	296	GLN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

### 5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

### 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

### 5.6 Ligand geometry [i](#)

16 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	800	-	4,4,4	0.14	0	6,6,6	0.22	0
2	SO4	A	801	-	4,4,4	0.17	0	6,6,6	0.23	0
2	SO4	B	800	-	4,4,4	0.14	0	6,6,6	0.25	0
2	SO4	B	801	-	4,4,4	0.11	0	6,6,6	0.26	0
2	SO4	B	802	-	4,4,4	0.18	0	6,6,6	0.12	0
2	SO4	B	803	-	4,4,4	0.25	0	6,6,6	0.16	0
2	SO4	C	800	-	4,4,4	1.31	0	6,6,6	0.21	0
2	SO4	C	801	-	4,4,4	0.12	0	6,6,6	0.19	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	SO4	C	805	-	4,4,4	0.15	0	6,6,6	0.21	0
2	SO4	D	800	-	4,4,4	0.18	0	6,6,6	0.17	0
2	SO4	D	801	-	4,4,4	0.14	0	6,6,6	0.25	0
2	SO4	E	800	-	4,4,4	0.14	0	6,6,6	0.21	0
2	SO4	E	801	-	4,4,4	0.25	0	6,6,6	0.37	0
2	SO4	F	800	-	4,4,4	0.19	0	6,6,6	0.13	0
2	SO4	F	801	-	4,4,4	0.22	0	6,6,6	0.43	0
2	SO4	F	804	-	4,4,4	0.18	0	6,6,6	0.16	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	800	-	-	0/0/0/0	0/0/0/0
2	SO4	A	801	-	-	0/0/0/0	0/0/0/0
2	SO4	B	800	-	-	0/0/0/0	0/0/0/0
2	SO4	B	801	-	-	0/0/0/0	0/0/0/0
2	SO4	B	802	-	-	0/0/0/0	0/0/0/0
2	SO4	B	803	-	-	0/0/0/0	0/0/0/0
2	SO4	C	800	-	-	0/0/0/0	0/0/0/0
2	SO4	C	801	-	-	0/0/0/0	0/0/0/0
2	SO4	C	805	-	-	0/0/0/0	0/0/0/0
2	SO4	D	800	-	-	0/0/0/0	0/0/0/0
2	SO4	D	801	-	-	0/0/0/0	0/0/0/0
2	SO4	E	800	-	-	0/0/0/0	0/0/0/0
2	SO4	E	801	-	-	0/0/0/0	0/0/0/0
2	SO4	F	800	-	-	0/0/0/0	0/0/0/0
2	SO4	F	801	-	-	0/0/0/0	0/0/0/0
2	SO4	F	804	-	-	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, 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	295/307 (96%)	-0.24	4 (1%) 75 76	31, 44, 63, 75	0
1	B	295/307 (96%)	-0.10	3 (1%) 82 82	30, 44, 58, 67	0
1	C	298/307 (97%)	-0.20	3 (1%) 82 82	29, 39, 55, 73	0
1	D	295/307 (96%)	-0.19	7 (2%) 59 60	30, 42, 56, 63	0
1	E	301/307 (98%)	-0.21	5 (1%) 70 72	28, 44, 57, 63	0
1	F	295/307 (96%)	-0.22	5 (1%) 70 72	30, 41, 55, 66	0
All	All	1779/1842 (96%)	-0.20	27 (1%) 74 75	28, 42, 57, 75	0

All (27) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	80	ARG	3.1
1	D	1	VAL	3.1
1	C	182	GLU	3.1
1	A	239	VAL	2.9
1	A	257	SER	2.8
1	E	233	ASN	2.8
1	F	240	LYS	2.7
1	B	68	ALA	2.6
1	E	182	GLU	2.6
1	A	182	GLU	2.6
1	D	270	GLY	2.6
1	E	147	ARG	2.5
1	F	196	ARG	2.5
1	E	257	SER	2.5
1	C	227	THR	2.4
1	D	239	VAL	2.4
1	B	241	PRO	2.4
1	B	243	ARG	2.4
1	D	281	PRO	2.3

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Mol	Chain	Res	Type	RSRZ
1	F	199	GLN	2.3
1	D	80	ARG	2.3
1	F	1	VAL	2.2
1	C	80	ARG	2.2
1	D	250	ARG	2.2
1	F	243	ARG	2.1
1	A	80	ARG	2.1
1	D	182	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, 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(Å <sup>2</sup> )	Q<0.9
2	SO4	A	800	5/5	0.93	0.21	1.52	86,86,88,88	0
2	SO4	C	805	5/5	0.91	0.17	0.82	109,110,110,110	0
2	SO4	E	800	5/5	0.91	0.16	0.35	103,104,104,104	0
2	SO4	F	800	5/5	0.94	0.16	-0.14	88,89,89,89	0
2	SO4	D	800	5/5	0.94	0.17	-0.16	81,81,82,82	0
2	SO4	B	803	5/5	0.96	0.18	-0.48	70,70,70,71	0
2	SO4	B	800	5/5	0.94	0.17	-0.54	80,80,80,81	0
2	SO4	F	804	5/5	0.96	0.18	-0.63	68,68,69,69	0
2	SO4	A	801	5/5	0.97	0.14	-0.66	67,67,68,69	0
2	SO4	F	801	5/5	0.98	0.14	-0.80	53,54,55,56	0
2	SO4	E	801	5/5	0.97	0.10	-1.41	43,46,48,48	0
2	SO4	B	802	5/5	0.96	0.10	-1.72	98,98,99,99	0
2	SO4	D	801	5/5	0.99	0.13	-1.74	56,57,57,59	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
2	SO4	B	801	5/5	0.98	0.08	-1.75	52,53,54,54	0
2	SO4	C	801	5/5	0.99	0.07	-1.81	44,46,46,47	0
2	SO4	C	800	5/5	0.85	0.21	-	114,114,114,114	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.