Full wwPDB X-ray Structure Validation Report (i)

Oct 18, 2023 – 11:31 PM EDT

PDB ID	:	2IP4
Title	:	Crystal Structure of Glycinamide Ribonucleotide Synthetase from Thermus thermophilus HB8
Authors	:	Sampei, G.; Baba, S.; Kanagawa, M.; Yanai, H.; Ishii, T.; Kawai, H.; Fukai, Y.; Ebihara, A.; Nakagawa, N.; Kawai, G.; RIKEN Structural Genomics/Proteomics Initiative (RSGI)
Deposited on	:	2006-10-11
Resolution	:	2.80 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

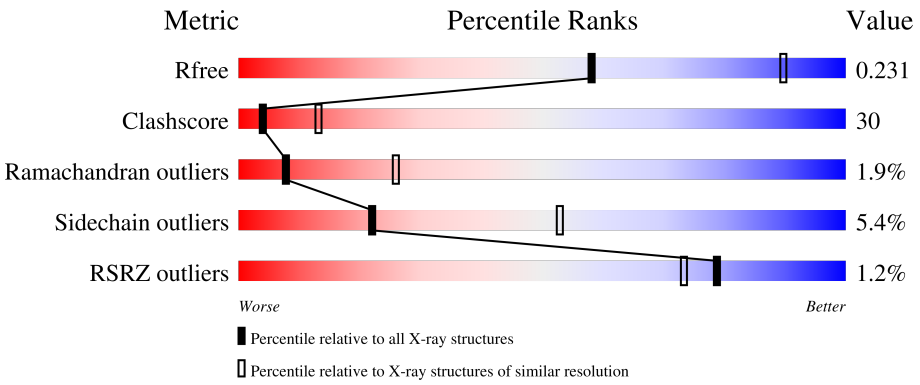
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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}	130704	3140 (2.80-2.80)
Clashscore	141614	3569 (2.80-2.80)
Ramachandran outliers	138981	3498 (2.80-2.80)
Sidechain outliers	138945	3500 (2.80-2.80)
RSRZ outliers	127900	3078 (2.80-2.80)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=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	417	2% 54% 41%
1	B	417	% 54% 42%

2 Entry composition (i)

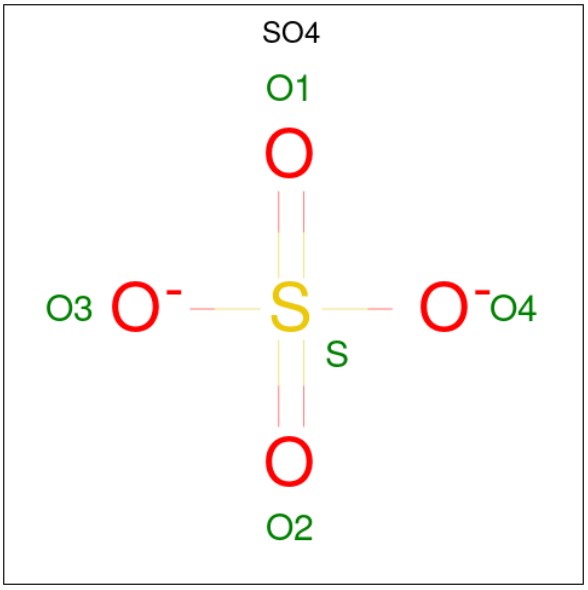
There are 3 unique types of molecules in this entry. The entry contains 6268 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Phosphoribosylamine--glycine ligase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	S	Se			
1	A	414	3112	1979	554	570	1	8	0	0	0
1	B	414	3112	1979	554	570	1	8	0	0	0

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



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

- Molecule 3 is water.

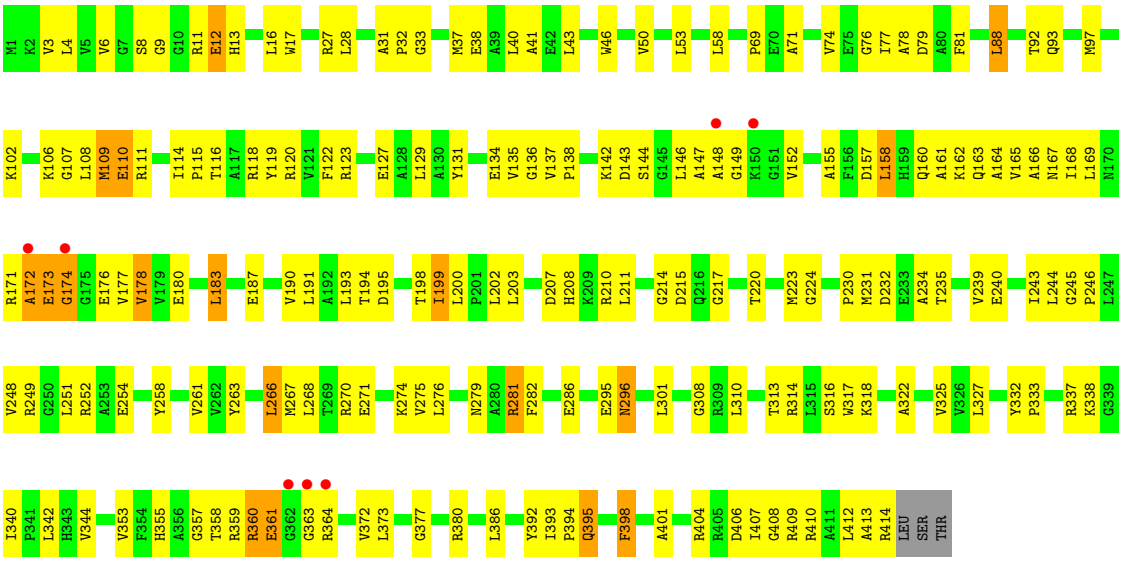
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
3	A	11	11	11	0	0
			Total	O		
3	B	13	13	13	0	0

3 Residue-property plots (i)

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

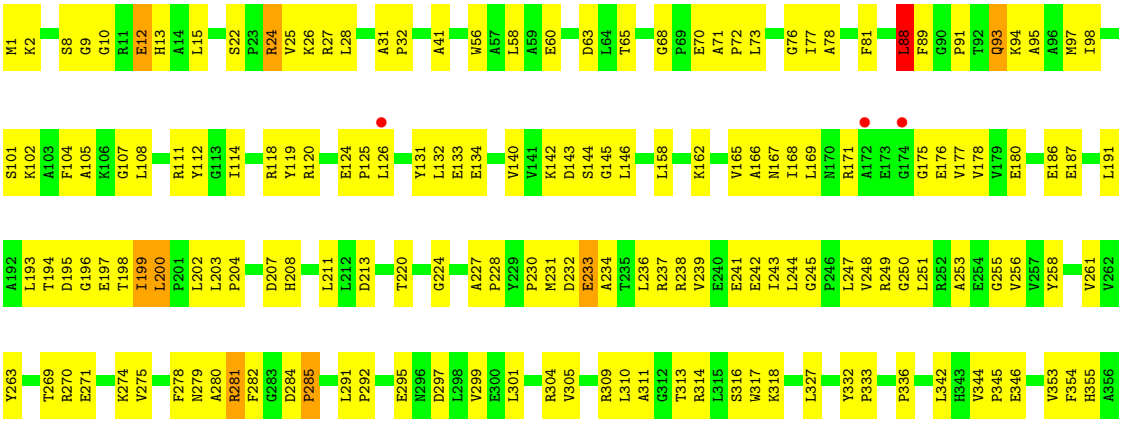
• Molecule 1: Phosphoribosylamine--glycine ligase

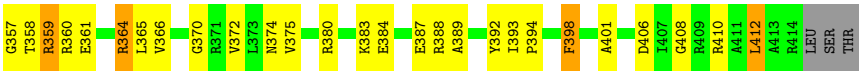
Chain A: 2% 54% 41%



• Molecule 1: Phosphoribosylamine--glycine ligase

Chain B: % 54% 42%




G357
T358
R359
R360
E361
R364
L365
V366
G370
R371
V372
L373
N374
V375
R380
K383
E384
E387
R388
A389
Y392
I393
P394
F398
A401
D406
I407
G408
R409
R410
A411
L412
A413
R414
LEU
SER
THR

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	72.31Å 98.07Å 121.14Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	60.00 – 2.80 46.43 – 2.79	Depositor EDS
% Data completeness (in resolution range)	(Not available) (60.00-2.80) 98.8 (46.43-2.79)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.14 (at 2.77Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.218 , 0.238 0.228 , 0.231	Depositor DCC
R_{free} test set	1117 reflections (5.10%)	wwPDB-VP
Wilson B-factor (Å^2)	36.4	Xtriage
Anisotropy	0.312	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.31 , 53.2	EDS
L-test for twinning[2]	$< \|L\| > = 0.47$, $< L^2 > = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.91	EDS
Total number of atoms	6268	wwPDB-VP
Average B, all atoms (Å^2)	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 41.76 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 2.2514e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: SO4

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\| >5$	RMSZ	$\#\|Z\| >5$
1	A	0.35	0/3165	0.63	1/4285 (0.0%)
1	B	0.35	0/3165	0.64	1/4285 (0.0%)
All	All	0.35	0/6330	0.63	2/8570 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	88	LEU	CA-CB-CG	5.71	128.44	115.30
1	A	158	LEU	N-CA-C	-5.21	96.92	111.00

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3112	0	3174	193	0
1	B	3112	0	3174	187	0
2	A	10	0	0	0	0
2	B	10	0	0	0	0
3	A	11	0	0	5	0
3	B	13	0	0	3	0
All	All	6268	0	6348	380	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 30.

All (380) 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:A:360:ARG:HH11	1:A:360:ARG:HB2	1.23	1.04
1:A:193:LEU:HD13	1:A:202:LEU:HD21	1.36	1.03
1:A:16:LEU:HD22	1:A:37:MSE:HE2	1.41	1.02
1:A:267:MSE:HG2	1:A:276:LEU:HD11	1.38	1.02
1:B:108:LEU:HB3	1:B:114:ILE:HD12	1.43	1.00
1:B:126:LEU:H	1:B:126:LEU:HD12	1.31	0.94
1:A:157:ASP:HB3	1:A:160:GLN:H	1.31	0.93
1:A:263:TYR:HB3	1:A:279:ASN:HB2	1.55	0.89
1:B:94:LYS:HG2	3:B:429:HOH:O	1.75	0.87
1:B:231:MSE:HE3	1:B:236:LEU:HB2	1.58	0.85
1:A:108:LEU:HB3	1:A:114:ILE:HG13	1.58	0.84
1:A:279:ASN:ND2	1:A:281:ARG:HH21	1.75	0.84
1:A:360:ARG:HB2	1:A:360:ARG:NH1	1.93	0.82
1:A:199:ILE:HG12	1:A:248:VAL:HG21	1.62	0.81
1:A:144:SER:HB3	1:A:176:GLU:HB3	1.61	0.81
1:A:296:ASN:HD22	1:A:296:ASN:H	1.25	0.81
1:A:279:ASN:HD22	1:A:281:ARG:HH21	1.28	0.81
1:A:207:ASP:HB2	1:A:286:GLU:OE1	1.82	0.80
1:B:15:LEU:HD23	1:B:291:LEU:HD11	1.64	0.79
1:A:243:ILE:HD12	1:A:275:VAL:HG23	1.64	0.78
1:B:13:HIS:HD2	1:B:355:HIS:H	1.31	0.78
1:B:104:PHE:O	1:B:108:LEU:HD22	1.84	0.77
1:B:65:THR:HB	1:B:88:LEU:HB2	1.66	0.77
1:B:1:MSE:HA	1:B:26:LYS:HE2	1.65	0.77
1:A:183:LEU:H	1:A:183:LEU:HD12	1.49	0.76
1:B:200:LEU:N	1:B:200:LEU:HD12	2.01	0.75
1:A:115:PRO:HG2	1:A:243:ILE:HD11	1.67	0.75
1:B:112:TYR:HE1	1:B:249:ARG:HD2	1.53	0.74
1:A:183:LEU:HD12	1:A:183:LEU:N	2.02	0.73
1:A:9:GLY:O	1:A:12:GLU:HG2	1.88	0.73
1:A:395:GLN:HE21	1:A:395:GLN:HA	1.53	0.73
1:A:210:ARG:NH1	1:A:217:GLY:O	2.21	0.73
1:A:224:GLY:HA3	1:A:407:ILE:HD13	1.71	0.71
1:B:126:LEU:H	1:B:126:LEU:CD1	2.04	0.71
1:B:9:GLY:H	1:B:12:GLU:CG	2.04	0.71
1:B:358:THR:HB	1:B:365:LEU:HD11	1.71	0.71
1:B:263:TYR:HB3	1:B:279:ASN:HB2	1.73	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:22:SER:HB2	1:B:297:ASP:OD1	1.91	0.70
1:B:120:ARG:HD3	1:B:131:TYR:CZ	2.27	0.69
1:B:186:GLU:OE2	1:B:410:ARG:HG3	1.92	0.69
1:B:208:HIS:HD2	1:B:224:GLY:O	1.75	0.69
1:B:28:LEU:O	1:B:41:ALA:HB1	1.93	0.69
1:B:13:HIS:CD2	1:B:355:HIS:H	2.09	0.69
1:A:135:VAL:HG23	1:A:136:GLY:N	2.08	0.69
1:B:193:LEU:CD1	1:B:202:LEU:HD21	2.24	0.68
1:A:168:ILE:HD12	1:A:177:VAL:HG22	1.74	0.68
1:B:94:LYS:HD2	1:B:256:VAL:HG12	1.73	0.68
1:A:6:VAL:O	1:A:69:PRO:HD2	1.95	0.67
1:A:93:GLN:HG2	1:A:97:MSE:HE2	1.77	0.67
1:A:296:ASN:HD21	1:A:316:SER:H	1.39	0.67
1:A:183:LEU:HD23	1:A:274:LYS:HD2	1.76	0.67
1:A:120:ARG:HB2	1:A:131:TYR:CE1	2.30	0.67
1:B:360:ARG:HH11	1:B:360:ARG:HB3	1.60	0.67
1:B:125:PRO:HD3	1:B:169:LEU:HD23	1.76	0.67
1:A:210:ARG:O	1:A:404:ARG:HD2	1.95	0.66
1:B:193:LEU:HD23	1:B:305:VAL:HG21	1.78	0.66
1:B:295:GLU:OE1	1:B:318:LYS:HE3	1.94	0.66
1:B:108:LEU:CB	1:B:114:ILE:HD12	2.21	0.66
1:A:13:HIS:HD2	1:A:355:HIS:H	1.42	0.65
1:A:187:GLU:HB2	1:A:267:MSE:HE2	1.77	0.65
1:B:108:LEU:HB3	1:B:114:ILE:CD1	2.22	0.65
1:A:106:LYS:NZ	1:A:110:GLU:HG3	2.11	0.65
1:B:107:GLY:O	1:B:111:ARG:HB2	1.97	0.65
1:B:375:VAL:HG21	1:B:393:ILE:HD13	1.77	0.65
1:A:119:TYR:O	1:A:120:ARG:HG3	1.97	0.65
1:B:56:TRP:CZ2	1:B:60:GLU:HG3	2.31	0.65
1:B:112:TYR:CE1	1:B:249:ARG:HD2	2.32	0.64
1:A:190:VAL:HG12	1:A:190:VAL:O	1.97	0.64
1:B:220:THR:HB	1:B:332:TYR:OH	1.98	0.64
1:A:50:VAL:CG1	1:A:77:ILE:HA	2.27	0.64
1:A:239:VAL:O	1:A:243:ILE:HB	1.99	0.63
1:B:88:LEU:C	1:B:88:LEU:HD12	2.19	0.63
1:B:104:PHE:CD2	1:B:108:LEU:HD21	2.32	0.63
1:A:358:THR:O	1:A:359:ARG:HD2	1.98	0.62
1:B:104:PHE:CE2	1:B:108:LEU:HD21	2.34	0.62
1:A:74:VAL:O	1:A:93:GLN:HG3	1.97	0.62
1:B:357:GLY:O	1:B:372:VAL:HG13	1.99	0.62
1:B:231:MSE:HE3	1:B:236:LEU:CB	2.29	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:364:ARG:HH11	1:B:364:ARG:HG2	1.65	0.62
1:A:231:MSE:HE2	1:A:268:LEU:HD11	1.82	0.62
1:A:122:PHE:CD1	1:A:127:GLU:HB3	2.35	0.61
1:A:165:VAL:HG13	1:A:166:ALA:H	1.65	0.61
1:A:142:LYS:HB3	1:A:178:VAL:HG13	1.81	0.61
1:A:393:ILE:N	1:A:394:PRO:HD2	2.16	0.61
1:A:249:ARG:NH1	1:A:249:ARG:HB3	2.14	0.61
1:A:332:TYR:CD1	1:A:333:PRO:HA	2.35	0.61
1:A:106:LYS:HZ1	1:A:110:GLU:HG3	1.66	0.61
1:A:168:ILE:HA	1:A:171:ARG:HH12	1.66	0.60
1:A:296:ASN:HD22	1:A:296:ASN:N	1.98	0.60
1:A:143:ASP:HA	1:A:168:ILE:HD13	1.83	0.60
1:A:327:LEU:O	1:A:398:PHE:HE1	1.85	0.60
1:B:102:LYS:O	1:B:105:ALA:HB3	2.02	0.60
1:A:114:ILE:HD11	1:A:246:PRO:HB2	1.84	0.60
1:B:126:LEU:HD12	1:B:126:LEU:N	2.11	0.59
1:B:142:LYS:O	1:B:178:VAL:HG12	2.02	0.59
1:A:198:THR:HG22	1:A:200:LEU:HD13	1.84	0.59
1:A:372:VAL:HG12	1:A:373:LEU:HG	1.82	0.59
1:B:9:GLY:H	1:B:12:GLU:HG3	1.66	0.59
1:B:398:PHE:CG	1:B:401:ALA:HB2	2.38	0.59
1:B:213:ASP:HA	1:B:406:ASP:OD1	2.03	0.59
1:A:223:MSE:O	1:A:407:ILE:HD11	2.02	0.59
1:B:389:ALA:O	1:B:393:ILE:HG12	2.02	0.59
1:A:266:LEU:HA	1:A:276:LEU:HG	1.85	0.58
1:B:71:ALA:HB3	1:B:72:PRO:HD3	1.84	0.58
1:B:203:LEU:HG	1:B:317:TRP:CD2	2.37	0.58
1:B:94:LYS:O	1:B:98:ILE:HG12	2.03	0.58
1:B:295:GLU:HB2	1:B:316:SER:HB2	1.84	0.58
1:A:261:VAL:HB	1:A:281:ARG:HA	1.85	0.58
1:A:342:LEU:HD12	1:A:373:LEU:HD11	1.86	0.58
1:A:135:VAL:HG23	1:A:136:GLY:H	1.67	0.58
1:A:144:SER:C	1:A:146:LEU:H	2.07	0.58
1:A:157:ASP:CB	1:A:160:GLN:H	2.13	0.57
1:B:142:LYS:HB3	1:B:178:VAL:CG1	2.34	0.57
1:A:171:ARG:HB2	1:A:171:ARG:NH1	2.20	0.57
1:B:193:LEU:HD23	1:B:305:VAL:CG2	2.34	0.57
1:A:50:VAL:HG13	1:A:77:ILE:HA	1.87	0.57
1:B:13:HIS:HD2	1:B:355:HIS:N	2.02	0.57
1:A:195:ASP:HB2	1:A:308:GLY:HA2	1.87	0.57
1:A:325:VAL:HG13	1:A:407:ILE:HD12	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:393:ILE:N	1:B:394:PRO:HD2	2.21	0.56
1:A:157:ASP:HB3	1:A:160:GLN:N	2.13	0.56
1:A:109:MSE:HE3	1:A:116:THR:OG1	2.05	0.56
1:A:313:THR:HG22	1:A:314:ARG:H	1.70	0.56
1:B:342:LEU:HD11	1:B:372:VAL:HG11	1.88	0.56
1:B:193:LEU:HD12	1:B:202:LEU:HD21	1.88	0.56
1:B:342:LEU:HD11	1:B:372:VAL:CG1	2.36	0.55
1:B:270:ARG:HH11	1:B:270:ARG:HG2	1.72	0.55
1:A:53:LEU:HD22	1:A:81:PHE:HZ	1.71	0.55
1:B:204:PRO:HG3	1:B:231:MSE:HE2	1.88	0.55
1:A:168:ILE:HA	1:A:171:ARG:NH1	2.22	0.55
1:A:407:ILE:HG13	3:A:420:HOH:O	2.07	0.55
1:A:11:ARG:HH12	1:A:281:ARG:HH11	1.54	0.55
1:A:38:GLU:HG2	1:A:43:LEU:HD22	1.88	0.55
1:A:171:ARG:HB2	1:A:171:ARG:HH11	1.72	0.55
1:B:332:TYR:CD1	1:B:333:PRO:HA	2.42	0.55
1:A:171:ARG:O	1:A:172:ALA:HB2	2.05	0.55
1:A:398:PHE:CG	1:A:401:ALA:HB2	2.41	0.55
1:B:65:THR:HG1	1:B:81:PHE:HE2	1.55	0.55
1:A:296:ASN:ND2	1:A:316:SER:H	2.05	0.55
1:A:161:ALA:O	1:A:164:ALA:HB3	2.07	0.55
1:A:263:TYR:HE2	1:A:286:GLU:HG3	1.73	0.55
1:B:12:GLU:OE2	1:B:68:GLY:HA3	2.07	0.54
1:A:9:GLY:H	1:A:12:GLU:CG	2.19	0.54
1:B:250:GLY:O	1:B:253:ALA:HB3	2.08	0.54
1:B:304:ARG:HD2	1:B:309:ARG:O	2.08	0.54
1:B:200:LEU:HD13	1:B:310:LEU:HD21	1.90	0.54
1:A:410:ARG:HG2	1:A:410:ARG:HH11	1.73	0.54
1:B:28:LEU:C	1:B:41:ALA:HB1	2.28	0.54
1:A:392:TYR:C	1:A:394:PRO:HD2	2.27	0.54
1:B:2:LYS:HG2	1:B:27:ARG:HB2	1.89	0.54
1:B:200:LEU:N	1:B:200:LEU:CD1	2.69	0.53
1:A:295:GLU:HB2	1:A:316:SER:HB2	1.91	0.53
1:B:344:VAL:HG21	1:B:353:VAL:HG11	1.90	0.53
1:A:165:VAL:HG13	1:A:166:ALA:N	2.23	0.53
1:B:124:GLU:OE2	1:B:125:PRO:HD2	2.07	0.53
1:A:243:ILE:HD12	1:A:275:VAL:CG2	2.37	0.53
1:A:168:ILE:CD1	1:A:177:VAL:HG22	2.36	0.53
1:B:194:THR:HA	1:B:198:THR:O	2.09	0.53
1:A:210:ARG:HB2	1:A:215:ASP:HA	1.89	0.53
1:B:24:ARG:HH11	1:B:24:ARG:CB	2.22	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:267:MSE:CG	1:A:276:LEU:HD11	2.26	0.53
1:B:309:ARG:HB2	1:B:309:ARG:NH1	2.24	0.53
1:B:9:GLY:O	1:B:12:GLU:HG2	2.09	0.52
1:B:15:LEU:CD2	1:B:291:LEU:HD11	2.36	0.52
1:A:249:ARG:HH11	1:A:249:ARG:CB	2.22	0.52
1:B:360:ARG:HB3	1:B:360:ARG:NH1	2.25	0.52
1:B:166:ALA:C	1:B:168:ILE:H	2.13	0.52
1:B:197:GLU:HG3	1:B:198:THR:N	2.24	0.52
1:B:233:GLU:HA	1:B:236:LEU:HB3	1.92	0.52
1:A:414:ARG:HA	1:A:414:ARG:NE	2.24	0.52
1:A:224:GLY:HA3	1:A:407:ILE:CD1	2.39	0.52
1:B:94:LYS:HG3	1:B:95:ALA:N	2.25	0.52
1:B:119:TYR:O	1:B:120:ARG:HG3	2.09	0.52
1:A:4:LEU:HD21	1:A:53:LEU:HD21	1.92	0.52
1:B:195:ASP:HB2	1:B:310:LEU:HB3	1.90	0.52
1:A:232:ASP:OD2	1:A:234:ALA:HB3	2.11	0.51
1:B:198:THR:HG22	1:B:199:ILE:N	2.25	0.51
1:B:359:ARG:HB3	1:B:366:VAL:HG22	1.91	0.51
1:B:1:MSE:HB3	1:B:63:ASP:OD2	2.09	0.51
1:A:118:ARG:NH2	1:A:135:VAL:HA	2.26	0.51
1:B:380:ARG:H	1:B:384:GLU:CD	2.14	0.51
1:B:93:GLN:O	1:B:97:MSE:HG3	2.11	0.51
1:B:125:PRO:CD	1:B:169:LEU:HD23	2.40	0.51
1:A:137:VAL:HA	1:A:138:PRO:C	2.30	0.51
1:A:173:GLU:O	1:A:174:GLY:O	2.28	0.51
1:B:1:MSE:HE1	1:B:299:VAL:HG11	1.91	0.51
1:A:169:LEU:HD12	1:A:169:LEU:N	2.26	0.51
1:A:270:ARG:HB2	1:A:271:GLU:OE2	2.11	0.51
1:A:361:GLU:OE2	1:A:364:ARG:HB2	2.11	0.51
1:A:407:ILE:N	3:A:420:HOH:O	2.31	0.51
1:B:70:GLU:O	1:B:73:LEU:HB2	2.11	0.51
1:B:243:ILE:HD13	1:B:275:VAL:HG23	1.93	0.50
1:A:202:LEU:HB3	1:A:317:TRP:CH2	2.46	0.50
1:A:37:MSE:SE	3:A:430:HOH:O	2.79	0.50
1:A:77:ILE:HG23	1:A:78:ALA:N	2.25	0.50
1:B:383:LYS:O	1:B:387:GLU:HG3	2.12	0.50
1:A:281:ARG:C	1:A:281:ARG:HD2	2.31	0.50
1:A:406:ASP:HB2	1:A:409:ARG:HG3	1.94	0.50
1:A:11:ARG:NH2	1:A:69:PRO:HA	2.27	0.50
1:B:13:HIS:CD2	1:B:354:PHE:HA	2.47	0.50
1:A:77:ILE:CG2	1:A:78:ALA:N	2.75	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:89:PHE:CE2	1:B:261:VAL:HG23	2.47	0.50
1:B:195:ASP:HB3	1:B:198:THR:H	1.76	0.50
1:A:169:LEU:N	1:A:169:LEU:CD1	2.74	0.50
1:A:17:TRP:HA	1:A:40:LEU:HD13	1.94	0.49
1:A:249:ARG:HB3	1:A:249:ARG:HH11	1.75	0.49
1:B:202:LEU:HB3	1:B:317:TRP:CH2	2.47	0.49
1:A:135:VAL:CG2	1:A:136:GLY:N	2.74	0.49
1:B:8:SER:N	1:B:12:GLU:HG3	2.27	0.49
1:A:16:LEU:CD2	1:A:37:MSE:HE2	2.29	0.49
1:A:395:GLN:HA	1:A:395:GLN:NE2	2.25	0.49
1:B:1:MSE:HE1	1:B:299:VAL:CG1	2.42	0.49
1:B:119:TYR:C	1:B:120:ARG:HG3	2.33	0.49
1:B:345:PRO:O	1:B:346:GLU:C	2.51	0.49
1:B:9:GLY:N	1:B:12:GLU:HG2	2.28	0.49
1:B:236:LEU:O	1:B:239:VAL:HG22	2.13	0.49
1:B:88:LEU:HD12	1:B:89:PHE:N	2.27	0.49
1:B:360:ARG:HH11	1:B:360:ARG:CB	2.26	0.49
1:A:157:ASP:HB2	1:A:160:GLN:HB3	1.94	0.49
1:B:89:PHE:CZ	1:B:261:VAL:HG23	2.47	0.49
1:B:251:LEU:HD13	1:B:258:TYR:HB3	1.95	0.49
1:B:125:PRO:HG2	1:B:126:LEU:HD12	1.94	0.48
1:A:146:LEU:O	1:A:148:ALA:N	2.46	0.48
1:A:410:ARG:HG2	1:A:410:ARG:NH1	2.28	0.48
1:B:9:GLY:N	1:B:12:GLU:CG	2.75	0.48
1:A:158:LEU:HD23	1:A:158:LEU:O	2.13	0.48
1:A:313:THR:C	1:A:314:ARG:HD2	2.34	0.48
1:B:28:LEU:HB2	1:B:41:ALA:HB2	1.95	0.48
1:B:162:LYS:O	1:B:165:VAL:HG12	2.13	0.48
1:B:220:THR:HB	1:B:332:TYR:CZ	2.49	0.48
1:B:9:GLY:H	1:B:12:GLU:HG2	1.77	0.48
1:B:237:ARG:HG3	1:B:237:ARG:HH11	1.79	0.47
1:A:171:ARG:O	1:A:172:ALA:CB	2.62	0.47
1:A:183:LEU:H	1:A:183:LEU:CD1	2.24	0.47
1:B:1:MSE:CA	1:B:26:LYS:HE2	2.40	0.47
1:A:120:ARG:HD3	1:A:131:TYR:CE2	2.49	0.47
1:B:76:GLY:HA2	3:B:428:HOH:O	2.13	0.47
1:B:199:ILE:HD11	1:B:245:GLY:HA2	1.96	0.47
1:A:194:THR:HB	1:A:199:ILE:HG23	1.96	0.47
1:A:413:ALA:O	1:A:414:ARG:HB2	2.14	0.47
1:B:25:VAL:HG11	1:B:28:LEU:HD21	1.97	0.47
1:B:208:HIS:CE1	1:B:408:GLY:H	2.33	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:50:VAL:HG11	1:A:77:ILE:HA	1.96	0.47
1:A:266:LEU:HB3	1:A:275:VAL:HA	1.97	0.47
1:A:314:ARG:HD2	1:A:314:ARG:N	2.30	0.47
1:B:98:ILE:O	1:B:101:SER:HB3	2.15	0.47
1:A:8:SER:N	1:A:12:GLU:HG3	2.30	0.47
1:B:91:PRO:HG3	1:B:280:ALA:HB1	1.97	0.47
1:A:249:ARG:O	1:A:252:ARG:HG2	2.15	0.46
1:B:24:ARG:HB2	1:B:24:ARG:NH1	2.30	0.46
1:B:144:SER:C	1:B:146:LEU:H	2.18	0.46
1:B:364:ARG:HH11	1:B:364:ARG:CG	2.28	0.46
1:A:135:VAL:CG2	1:A:136:GLY:H	2.28	0.46
1:B:251:LEU:HD13	1:B:258:TYR:CB	2.45	0.46
1:B:269:THR:HG21	1:B:274:LYS:HD2	1.97	0.46
1:B:392:TYR:C	1:B:394:PRO:HD2	2.36	0.46
1:A:211:LEU:HD13	1:A:211:LEU:O	2.16	0.46
1:B:199:ILE:C	1:B:200:LEU:HD12	2.36	0.46
1:A:106:LYS:HD3	1:A:107:GLY:N	2.31	0.46
1:B:256:VAL:HG23	1:B:256:VAL:O	2.15	0.46
1:B:327:LEU:HD21	1:B:393:ILE:HD12	1.96	0.46
1:A:119:TYR:HB2	1:A:180:GLU:HB3	1.97	0.46
1:A:296:ASN:H	1:A:296:ASN:ND2	2.02	0.46
1:A:235:THR:O	1:A:239:VAL:HG23	2.16	0.46
1:A:76:GLY:HA2	1:A:93:GLN:HB2	1.96	0.45
1:A:144:SER:CB	1:A:176:GLU:HB3	2.41	0.45
1:A:211:LEU:HD23	1:A:220:THR:HG21	1.98	0.45
1:A:142:LYS:HG3	1:A:152:VAL:HG22	1.97	0.45
1:B:238:ARG:O	1:B:242:GLU:HB2	2.16	0.45
1:A:338:LYS:HA	3:A:426:HOH:O	2.16	0.45
1:A:386:LEU:HD13	1:A:412:LEU:HD11	1.99	0.45
1:A:414:ARG:HA	1:A:414:ARG:CZ	2.45	0.45
1:B:227:ALA:HA	1:B:228:PRO:C	2.36	0.45
1:A:251:LEU:HD21	1:A:258:TYR:CD2	2.51	0.45
1:B:15:LEU:HD23	1:B:291:LEU:CD1	2.42	0.45
1:B:364:ARG:N	1:B:364:ARG:HD2	2.31	0.45
1:B:144:SER:O	1:B:146:LEU:N	2.50	0.45
1:B:244:LEU:O	1:B:247:LEU:HB3	2.17	0.45
1:A:122:PHE:HD1	1:A:127:GLU:HB3	1.82	0.45
1:A:200:LEU:HD22	1:A:310:LEU:HG	2.00	0.45
1:A:240:GLU:HA	1:A:244:LEU:HB2	1.98	0.45
1:B:133:GLU:HG2	1:B:158:LEU:HD21	1.98	0.45
1:A:79:ASP:OD1	1:A:92:THR:HB	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:108:LEU:HB3	1:A:114:ILE:CG1	2.39	0.44
1:A:149:GLY:O	1:A:152:VAL:HG23	2.17	0.44
1:A:342:LEU:CD1	1:A:373:LEU:HD11	2.47	0.44
1:B:336:PRO:HB3	1:B:370:GLY:HA2	1.99	0.44
1:A:33:GLY:HA2	1:A:37:MSE:SE	2.67	0.44
1:A:203:LEU:HG	1:A:317:TRP:CD2	2.53	0.44
1:A:313:THR:HG22	1:A:314:ARG:N	2.33	0.44
1:B:193:LEU:O	1:B:199:ILE:HA	2.17	0.44
1:A:11:ARG:NH1	1:A:281:ARG:HH11	2.16	0.44
1:B:354:PHE:HB2	1:B:374:ASN:HB2	1.99	0.44
1:A:102:LYS:HD2	1:A:119:TYR:CZ	2.53	0.44
1:A:208:HIS:CE1	1:A:408:GLY:H	2.35	0.44
1:B:31:ALA:HA	1:B:32:PRO:HA	1.89	0.44
1:B:232:ASP:O	1:B:234:ALA:N	2.51	0.44
1:B:233:GLU:CD	1:B:233:GLU:H	2.21	0.44
1:A:123:ARG:HG2	1:A:176:GLU:HG3	1.99	0.44
1:A:16:LEU:HD21	1:A:41:ALA:HB3	1.99	0.44
1:B:94:LYS:HG3	1:B:95:ALA:H	1.81	0.44
1:B:143:ASP:HB2	1:B:168:ILE:HD13	2.00	0.44
1:B:384:GLU:OE2	1:B:388:ARG:NH2	2.47	0.44
1:A:71:ALA:HA	1:A:74:VAL:HG22	2.00	0.44
1:A:187:GLU:HB2	1:A:267:MSE:CE	2.48	0.44
1:B:93:GLN:O	1:B:94:LYS:C	2.57	0.43
1:B:207:ASP:OD1	1:B:208:HIS:N	2.49	0.43
1:B:358:THR:HB	1:B:365:LEU:CD1	2.45	0.43
1:A:46:TRP:CD2	1:A:53:LEU:HD12	2.53	0.43
1:A:16:LEU:HB2	1:A:37:MSE:HE3	1.99	0.43
1:B:243:ILE:HD13	1:B:275:VAL:CG2	2.47	0.43
1:A:109:MSE:O	1:A:109:MSE:SE	2.86	0.43
1:B:120:ARG:HD3	1:B:131:TYR:CE1	2.53	0.43
1:B:275:VAL:HG11	1:B:278:PHE:CE2	2.54	0.43
1:A:281:ARG:HD2	1:A:281:ARG:O	2.18	0.43
1:B:22:SER:OG	1:B:24:ARG:HG2	2.19	0.43
1:B:234:ALA:O	1:B:237:ARG:HB3	2.18	0.43
1:A:12:GLU:CD	1:A:12:GLU:H	2.22	0.43
1:A:412:LEU:C	1:A:414:ARG:H	2.23	0.43
1:B:165:VAL:HG13	1:B:166:ALA:N	2.34	0.43
1:B:291:LEU:N	1:B:292:PRO:HD2	2.33	0.43
1:B:77:ILE:HG23	1:B:78:ALA:N	2.34	0.42
1:B:105:ALA:HA	1:B:108:LEU:HD23	2.00	0.42
1:A:183:LEU:N	1:A:183:LEU:CD1	2.74	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:199:ILE:HD13	1:B:248:VAL:CG2	2.50	0.42
1:A:78:ALA:HA	1:A:88:LEU:HG	2.01	0.42
1:A:393:ILE:N	1:A:394:PRO:CD	2.82	0.42
1:B:1:MSE:CE	1:B:299:VAL:HG11	2.50	0.42
1:A:211:LEU:HA	1:A:223:MSE:HG3	2.01	0.42
1:B:196:GLY:HA2	1:B:258:TYR:O	2.20	0.42
1:A:214:GLY:O	1:A:215:ASP:C	2.58	0.42
1:A:138:PRO:HA	1:A:155:ALA:O	2.19	0.42
1:A:144:SER:C	1:A:146:LEU:N	2.72	0.42
1:B:10:GLY:HA3	1:B:374:ASN:OD1	2.20	0.42
1:A:191:LEU:HD23	1:A:263:TYR:HA	2.00	0.42
1:B:191:LEU:HD12	3:B:421:HOH:O	2.19	0.42
1:A:360:ARG:HD2	1:A:363:GLY:C	2.41	0.41
1:B:258:TYR:CD1	1:B:258:TYR:C	2.94	0.41
1:B:131:TYR:O	1:B:134:GLU:HB3	2.20	0.41
1:B:313:THR:HG22	1:B:314:ARG:N	2.35	0.41
1:A:296:ASN:N	1:A:296:ASN:ND2	2.65	0.41
1:B:237:ARG:O	1:B:241:GLU:HG2	2.20	0.41
1:B:412:LEU:HD12	1:B:412:LEU:HA	1.87	0.41
1:B:253:ALA:C	1:B:255:GLY:H	2.24	0.41
1:A:202:LEU:HB3	1:A:317:TRP:HH2	1.85	0.41
1:B:208:HIS:CD2	1:B:224:GLY:O	2.64	0.41
1:B:271:GLU:HB2	1:B:274:LYS:NZ	2.36	0.41
1:B:281:ARG:HD3	1:B:282:PHE:O	2.20	0.41
1:A:107:GLY:HA3	1:A:111:ARG:HH21	1.85	0.41
1:A:163:GLN:O	1:A:167:ASN:HB2	2.21	0.41
1:A:261:VAL:HG11	1:A:282:PHE:N	2.35	0.41
1:A:322:ALA:HA	1:A:377:GLY:O	2.21	0.41
1:B:187:GLU:O	1:B:187:GLU:HG3	2.20	0.41
1:A:318:LYS:HB3	1:A:380:ARG:HH22	1.85	0.41
1:B:304:ARG:HA	1:B:304:ARG:HD3	1.94	0.41
1:A:3:VAL:HB	1:A:28:LEU:HD23	2.03	0.41
1:A:160:GLN:O	1:A:160:GLN:HG2	2.21	0.41
1:A:168:ILE:CA	1:A:171:ARG:HH12	2.32	0.41
1:A:344:VAL:HG21	1:A:353:VAL:HG11	2.02	0.41
1:A:386:LEU:CD1	1:A:412:LEU:HD11	2.51	0.41
1:B:88:LEU:HD12	1:B:89:PHE:C	2.42	0.41
1:B:140:VAL:HB	1:B:180:GLU:HG3	2.03	0.41
1:B:301:LEU:O	1:B:304:ARG:HB2	2.21	0.41
1:B:358:THR:CB	1:B:365:LEU:HD11	2.46	0.41
1:A:31:ALA:HA	1:A:32:PRO:HA	1.74	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:129:LEU:HD22	1:A:162:LYS:HG2	2.02	0.41
1:A:8:SER:HA	3:A:430:HOH:O	2.21	0.40
1:B:81:PHE:CG	1:B:88:LEU:HD23	2.56	0.40
1:B:132:LEU:HD12	1:B:132:LEU:HA	1.77	0.40
1:B:165:VAL:HG23	1:B:177:VAL:HG11	2.03	0.40
1:B:197:GLU:HG3	1:B:198:THR:OG1	2.21	0.40
1:B:197:GLU:CG	1:B:198:THR:N	2.83	0.40
1:A:245:GLY:O	1:A:249:ARG:HG3	2.21	0.40
1:B:144:SER:HB3	1:B:176:GLU:HB3	2.04	0.40
1:A:131:TYR:O	1:A:134:GLU:HB3	2.22	0.40
1:B:346:GLU:CD	1:B:346:GLU:H	2.24	0.40
1:A:78:ALA:HB3	1:A:92:THR:HA	2.03	0.40
1:A:243:ILE:CD1	1:A:275:VAL:HG23	2.45	0.40
1:B:284:ASP:HA	1:B:285:PRO:HA	1.69	0.40
1:B:336:PRO:CB	1:B:370:GLY:HA2	2.52	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	412/417 (99%)	365 (89%)	40 (10%)	7 (2%)	9 29
1	B	412/417 (99%)	375 (91%)	28 (7%)	9 (2%)	6 22
All	All	824/834 (99%)	740 (90%)	68 (8%)	16 (2%)	8 26

All (16) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	147	ALA
1	A	174	GLY
1	B	171	ARG

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Mol	Chain	Res	Type
1	A	172	ALA
1	A	173	GLU
1	B	167	ASN
1	B	233	GLU
1	B	311	ALA
1	A	230	PRO
1	B	93	GLN
1	B	230	PRO
1	B	361	GLU
1	A	357	GLY
1	B	145	GLY
1	A	340	ILE
1	B	175	GLY

5.3.2 Protein sidechains (i)

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	308/303 (102%)	289 (94%)	19 (6%)	18	47
1	B	308/303 (102%)	294 (96%)	14 (4%)	27	60
All	All	616/606 (102%)	583 (95%)	33 (5%)	22	53

All (33) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	12	GLU
1	A	27	ARG
1	A	58	LEU
1	A	88	LEU
1	A	109	MSE
1	A	110	GLU
1	A	178	VAL
1	A	183	LEU
1	A	199	ILE
1	A	254	GLU

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Mol	Chain	Res	Type
1	A	266	LEU
1	A	281	ARG
1	A	296	ASN
1	A	301	LEU
1	A	337	ARG
1	A	360	ARG
1	A	361	GLU
1	A	395	GLN
1	A	398	PHE
1	B	12	GLU
1	B	24	ARG
1	B	58	LEU
1	B	88	LEU
1	B	118	ARG
1	B	199	ILE
1	B	200	LEU
1	B	211	LEU
1	B	281	ARG
1	B	285	PRO
1	B	359	ARG
1	B	364	ARG
1	B	398	PHE
1	B	412	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	13	HIS
1	A	21	GLN
1	A	82	GLN
1	A	208	HIS
1	A	279	ASN
1	A	296	ASN
1	A	343	HIS
1	A	395	GLN
1	B	13	HIS
1	B	21	GLN
1	B	93	GLN
1	B	159	HIS
1	B	167	ASN
1	B	208	HIS

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 monosaccharides in this entry.

5.6 Ligand geometry (i)

4 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	B	418	-	4,4,4	0.29	0	6,6,6	0.14	0
2	SO4	B	419	-	4,4,4	0.31	0	6,6,6	0.13	0
2	SO4	A	418	-	4,4,4	0.31	0	6,6,6	0.13	0
2	SO4	A	419	-	4,4,4	0.24	0	6,6,6	0.13	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 (i)

6.1 Protein, DNA and RNA chains (i)

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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	406/417 (97%)	-0.23	7 (1%)	70	63	3, 28, 76, 147	0
1	B	406/417 (97%)	-0.34	3 (0%)	87	84	3, 24, 80, 136	0
All	All	812/834 (97%)	-0.29	10 (1%)	79	73	3, 26, 80, 147	0

All (10) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	172	ALA	3.9
1	A	363	GLY	3.2
1	B	174	GLY	2.8
1	A	150	LYS	2.6
1	A	362	GLY	2.4
1	B	126	LEU	2.1
1	A	172	ALA	2.1
1	A	364	ARG	2.1
1	A	148	ALA	2.0
1	A	174	GLY	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 monosaccharides in this entry.

6.4 Ligands (i)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	SO4	A	419	5/5	0.94	0.14	49,49,51,52	0
2	SO4	B	418	5/5	0.95	0.16	48,49,50,50	0
2	SO4	A	418	5/5	0.98	0.12	33,33,33,34	0
2	SO4	B	419	5/5	0.98	0.16	29,30,32,33	0

6.5 Other polymers (i)

There are no such residues in this entry.