



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 16, 2017 – 12:04 PM EDT

PDB ID : 3C1N
Title : Crystal Structure of Allosteric Inhibition Threonine-sensitive Aspartokinase from *Methanococcus jannaschii* with L-threonine
Authors : Liu, X.; Pavlovshy, A.G.; Viola, R.E.
Deposited on : unknown
Resolution : 2.72 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 : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20030345
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) : rb-20030345

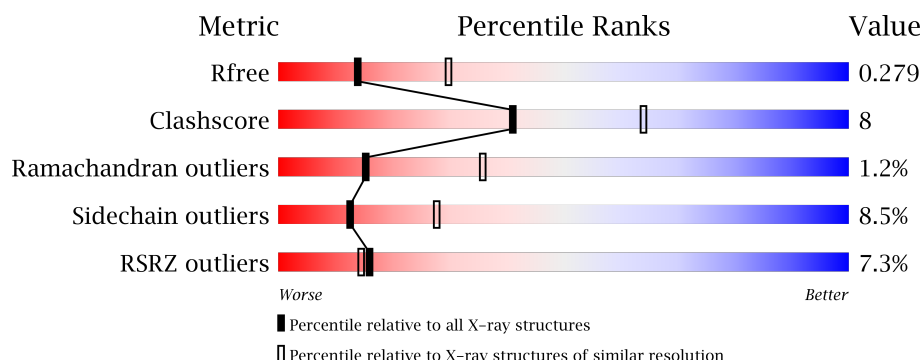
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.72 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	2649 (2.74-2.70)
Clashscore	112137	2993 (2.74-2.70)
Ramachandran outliers	110173	2946 (2.74-2.70)
Sidechain outliers	110143	2947 (2.74-2.70)
RSRZ outliers	101464	2665 (2.74-2.70)

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 ≥ 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	473	<div> <div>5%</div> <div> <div></div> <div>75%</div> <div>19%</div> <div>• •</div> </div> </div>
1	B	473	<div> <div>4%</div> <div> <div></div> <div>74%</div> <div>19%</div> <div>• •</div> </div> </div>
1	C	473	<div> <div>8%</div> <div> <div></div> <div>77%</div> <div>16%</div> <div>• •</div> </div> </div>
1	D	473	<div> <div>12%</div> <div> <div></div> <div>72%</div> <div>20%</div> <div>• •</div> </div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	THR	A	471	-	-	X	-
2	THR	A	473	-	-	X	X
2	THR	B	470	-	-	X	X
2	THR	B	474	-	-	X	-
2	THR	C	475	-	-	-	X
2	THR	D	472	-	-	X	X
2	THR	D	476	-	-	-	X

2 Entry composition [i](#)

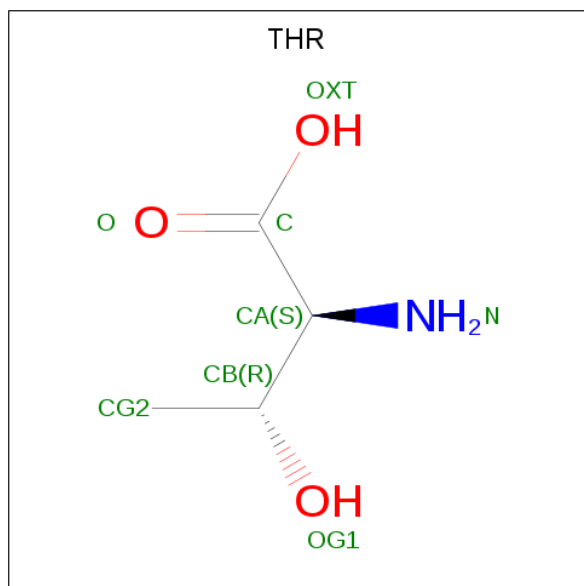
There are 3 unique types of molecules in this entry. The entry contains 13893 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Probable aspartokinase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	458	Total	C	N	O	S	0	0	0
			3456	2193	573	680	10			
1	B	459	Total	C	N	O	S	0	0	0
			3459	2194	574	682	9			
1	C	456	Total	C	N	O	S	0	0	0
			3441	2186	571	674	10			
1	D	452	Total	C	N	O	S	0	0	0
			3410	2167	567	667	9			

- Molecule 2 is THREONINE (three-letter code: THR) (formula: $C_4H_9NO_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			8	4	1	3		
2	A	1	Total	C	N	O	0	0
			8	4	1	3		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	B	1	Total 8	C 4	N 1	O 3	0	0
2	B	1	Total 8	C 4	N 1	O 3	0	0
2	C	1	Total 8	C 4	N 1	O 3	0	0
2	D	1	Total 8	C 4	N 1	O 3	0	0
2	D	1	Total 8	C 4	N 1	O 3	0	0

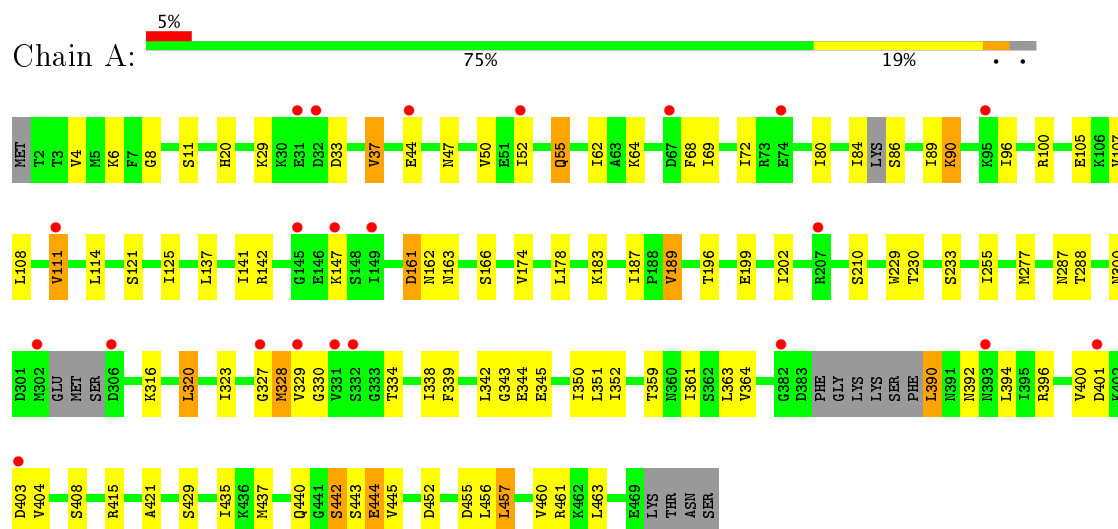
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	18	Total 18	O 18	0	0
3	B	20	Total 20	O 20	0	0
3	C	19	Total 19	O 19	0	0
3	D	14	Total 14	O 14	0	0

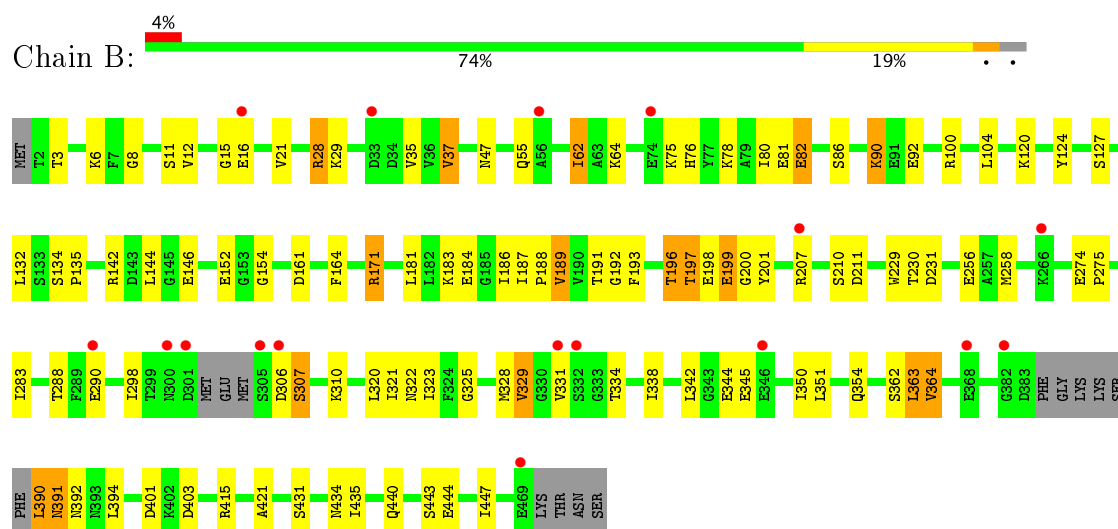
3 Residue-property plots [i](#)

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.

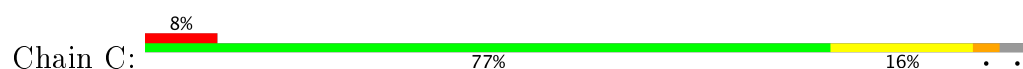
- Molecule 1: Probable aspartokinase

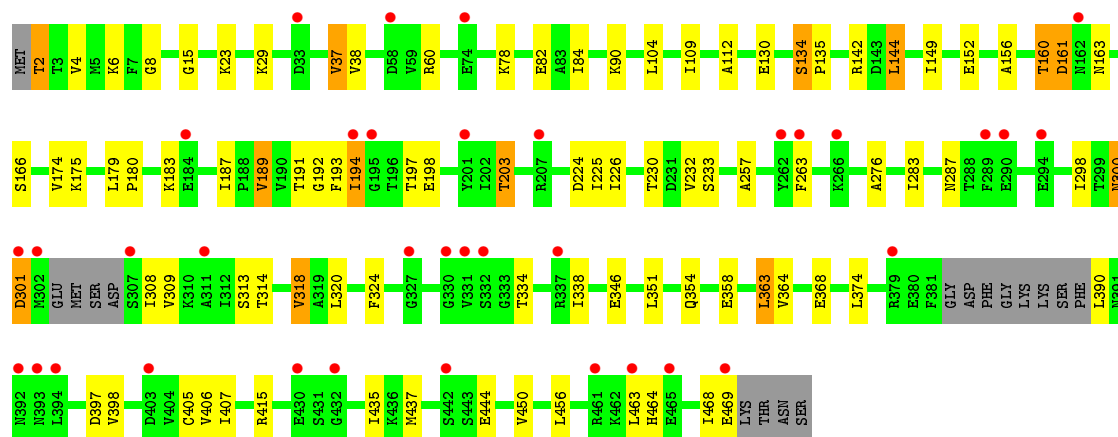


- Molecule 1: Probable aspartokinase

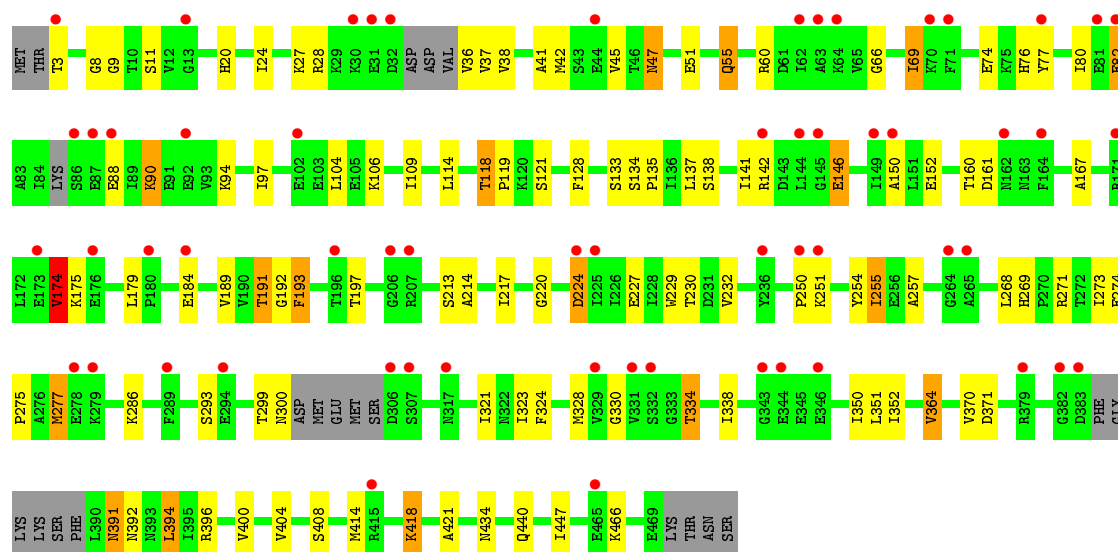
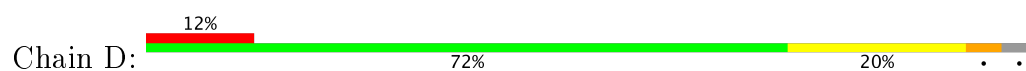


- Molecule 1: Probable aspartokinase





• Molecule 1: Probable aspartokinase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	110.04Å 144.32Å 155.36Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.72 14.98 – 2.72	Depositor EDS
% Data completeness (in resolution range)	84.4 (50.00-2.72) 84.4 (14.98-2.72)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.81 (at 2.73Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.236 , 0.290 0.226 , 0.279	Depositor DCC
R_{free} test set	2872 reflections (5.39%)	DCC
Wilson B-factor (Å ²)	75.3	Xtriage
Anisotropy	0.213	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 73.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	13893	wwPDB-VP
Average B, all atoms (Å ²)	63.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 13.27% 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, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	0.42	1/3492 (0.0%)	0.59	1/4708 (0.0%)
1	B	0.42	0/3496	0.57	1/4716 (0.0%)
1	C	0.36	0/3478	0.53	0/4691
1	D	0.44	2/3445 (0.1%)	0.53	0/4642
All	All	0.41	3/13911 (0.0%)	0.56	2/18757 (0.0%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	82	GLU	CD-OE2	10.28	1.36	1.25
1	D	82	GLU	CD-OE1	10.13	1.36	1.25
1	A	86	SER	CA-CB	5.58	1.61	1.52

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	390	LEU	CA-CB-CG	7.29	132.07	115.30
1	B	390	LEU	CA-CB-CG	5.48	127.91	115.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3456	0	3549	63	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	3459	0	3548	68	0
1	C	3441	0	3541	41	0
1	D	3410	0	3511	61	0
2	A	16	0	12	12	0
2	B	16	0	12	10	0
2	C	8	0	6	1	0
2	D	16	0	12	7	0
3	A	18	0	0	1	0
3	B	20	0	0	0	0
3	C	19	0	0	0	0
3	D	14	0	0	0	0
All	All	13893	0	14191	228	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 8.

All (228) 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:440:GLN:HE22	2:A:471:THR:HG21	1.15	1.08
1:B:8:GLY:HA3	2:B:474:THR:HA	1.30	1.07
1:B:11:SER:HG	2:B:474:THR:N	1.56	1.03
1:D:351:LEU:HB2	1:D:364:VAL:HG13	1.47	0.95
1:A:328:MET:HG2	1:A:334:THR:HG21	1.49	0.93
1:B:8:GLY:CA	2:B:474:THR:HA	2.06	0.83
1:A:68:PHE:CZ	1:A:72:ILE:HD11	2.13	0.83
1:A:440:GLN:NE2	2:A:471:THR:HG21	1.95	0.79
1:C:435:ILE:HB	2:D:472:THR:HB	1.67	0.77
1:A:344:GLU:O	1:A:345:GLU:HB2	1.85	0.77
1:D:334:THR:O	1:D:338:ILE:HG12	1.84	0.76
1:A:229:TRP:HB3	1:A:288:THR:HG22	1.67	0.76
1:A:29:LYS:HG3	1:A:187:ILE:HD11	1.68	0.75
1:A:11:SER:HG	2:A:473:THR:N	1.84	0.75
1:B:37:VAL:HG22	1:B:189:VAL:HB	1.67	0.74
1:A:421:ALA:HB2	2:A:471:THR:HG23	1.71	0.73
1:B:29:LYS:HE3	1:B:187:ILE:HD11	1.71	0.72
1:D:328:MET:HG2	1:D:334:THR:HG21	1.73	0.71
1:B:344:GLU:O	1:B:345:GLU:HB2	1.91	0.70
1:D:192:GLY:O	1:D:193:PHE:HB3	1.93	0.68
1:D:323:ILE:HD13	1:D:338:ILE:HD12	1.75	0.67
1:A:350:ILE:HB	1:A:364:VAL:HG22	1.76	0.67

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:80:ILE:HG22	1:A:90:LYS:HG2	1.76	0.67
1:A:255:ILE:HD12	1:A:255:ILE:H	1.59	0.67
1:C:324:PHE:HB3	1:C:397:ASP:HB2	1.76	0.67
1:D:351:LEU:HB2	1:D:364:VAL:CG1	2.23	0.66
1:A:8:GLY:HA3	2:A:473:THR:HA	1.78	0.66
1:D:174:VAL:HG21	1:D:220:GLY:HA3	1.77	0.66
1:A:351:LEU:HB2	1:A:364:VAL:HG13	1.77	0.66
1:A:6:LYS:HE3	1:A:210:SER:HB3	1.78	0.65
1:B:421:ALA:H	2:B:470:THR:N	1.95	0.65
1:C:29:LYS:HE3	1:C:187:ILE:HD11	1.78	0.65
1:B:325:GLY:HA3	1:B:328:MET:HG3	1.78	0.65
1:C:161:ASP:HB3	1:C:163:ASN:H	1.61	0.65
1:A:114:LEU:HD12	1:D:114:LEU:HD12	1.79	0.64
1:B:229:TRP:HB3	1:B:288:THR:CG2	2.27	0.64
1:B:322:ASN:ND2	1:B:362:SER:OG	2.29	0.64
1:D:11:SER:HG	2:D:476:THR:N	1.95	0.64
1:A:456:LEU:O	1:A:460:VAL:HG23	1.98	0.63
1:B:192:GLY:O	1:B:193:PHE:HB3	1.98	0.63
1:B:6:LYS:HE3	1:B:210:SER:HB3	1.80	0.63
1:B:338:ILE:O	1:B:342:LEU:HD12	1.98	0.62
1:B:306:ASP:OD1	1:B:307:SER:N	2.32	0.62
1:A:320:LEU:CD1	1:A:437:MET:CE	2.77	0.62
1:B:230:THR:CB	2:B:474:THR:HB	2.30	0.62
1:C:60:ARG:HD2	1:C:112:ALA:O	2.01	0.61
1:D:255:ILE:H	1:D:255:ILE:HD13	1.65	0.61
1:A:230:THR:HA	2:A:473:THR:N	2.15	0.61
1:B:29:LYS:CE	1:B:187:ILE:HD11	2.30	0.60
1:C:320:LEU:HB3	1:C:364:VAL:HG22	1.82	0.60
1:A:8:GLY:CA	2:A:473:THR:HA	2.30	0.60
1:D:350:ILE:HG22	1:D:351:LEU:HD13	1.82	0.60
1:D:8:GLY:HA3	2:D:476:THR:HA	1.83	0.60
1:B:229:TRP:HB3	1:B:288:THR:HG22	1.83	0.59
1:A:328:MET:HG2	1:A:334:THR:CG2	2.28	0.58
1:A:174:VAL:HG13	1:A:178:LEU:HD12	1.85	0.58
1:B:154:GLY:HA3	1:B:196:THR:HB	1.86	0.58
1:D:37:VAL:HG13	1:D:189:VAL:HA	1.84	0.58
1:B:334:THR:O	1:B:338:ILE:HG12	2.03	0.57
1:D:175:LYS:HG2	1:D:179:LEU:HB2	1.86	0.57
1:A:229:TRP:HB3	1:A:288:THR:CG2	2.33	0.57
1:A:320:LEU:HD11	1:A:437:MET:CE	2.34	0.57
1:B:62:ILE:H	1:B:62:ILE:HD13	1.69	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:76:HIS:O	1:B:80:ILE:HG13	2.05	0.57
1:A:443:SER:O	1:A:445:VAL:N	2.34	0.57
1:A:359:THR:HG21	1:B:258:MET:HG3	1.87	0.57
1:D:137:LEU:O	1:D:141:ILE:HG12	2.05	0.57
1:D:213:SER:O	1:D:217:ILE:HG12	2.05	0.56
1:D:118:THR:HG22	1:D:119:PRO:HD2	1.86	0.56
1:D:254:TYR:HB3	1:D:277:MET:HG3	1.87	0.56
1:B:230:THR:HB	2:B:474:THR:HB	1.86	0.56
1:D:286:LYS:HE3	1:D:293:SER:O	2.06	0.56
1:A:161:ASP:HB3	1:A:163:ASN:H	1.70	0.56
1:A:320:LEU:HD13	1:A:437:MET:CE	2.35	0.56
1:A:47:ASN:O	1:A:50:VAL:HG12	2.06	0.55
1:D:134:SER:HB3	1:D:135:PRO:HD3	1.88	0.55
1:A:52:ILE:HA	1:A:55:GLN:HB2	1.89	0.55
1:A:52:ILE:HD13	1:A:108:LEU:HD11	1.89	0.54
1:B:440:GLN:HE21	1:B:447:ILE:HG12	1.72	0.54
1:C:15:GLY:HA3	1:C:82:GLU:HB2	1.89	0.54
1:B:86:SER:O	1:B:90:LYS:HB2	2.07	0.54
1:D:42:MET:HB2	1:D:45:VAL:HG21	1.89	0.54
2:A:471:THR:HG22	1:B:435:ILE:HB	1.90	0.53
1:C:23:LYS:HG2	1:C:144:LEU:HD21	1.91	0.53
1:B:350:ILE:HB	1:B:364:VAL:HG22	1.91	0.53
1:D:269:HIS:O	1:D:273:ILE:HG12	2.09	0.52
1:C:308:ILE:HG23	1:C:309:VAL:H	1.75	0.52
1:A:327:GLY:C	1:A:329:VAL:H	2.12	0.51
1:D:47:ASN:OD1	1:D:47:ASN:N	2.41	0.51
1:A:137:LEU:O	1:A:141:ILE:HG12	2.09	0.51
1:B:328:MET:HG2	1:B:334:THR:HG21	1.92	0.51
1:B:351:LEU:HB2	1:B:364:VAL:HG13	1.92	0.51
1:A:320:LEU:HD11	1:A:437:MET:HE2	1.92	0.51
1:C:415:ARG:HA	1:C:444:GLU:HB2	1.93	0.51
1:D:3:THR:HG21	1:D:28:ARG:HD3	1.91	0.51
1:D:51:GLU:O	1:D:55:GLN:HB2	2.11	0.51
1:D:152:GLU:HA	1:D:191:THR:HG23	1.92	0.51
1:D:418:LYS:HA	2:D:472:THR:HG23	1.93	0.51
1:A:121:SER:O	1:A:125:ILE:HG12	2.11	0.51
1:D:76:HIS:O	1:D:80:ILE:HG13	2.10	0.51
1:D:9:GLY:HA2	1:D:41:ALA:O	2.11	0.51
1:C:152:GLU:HA	1:C:191:THR:OG1	2.10	0.50
1:A:415:ARG:HA	1:A:444:GLU:HB2	1.93	0.50
1:D:350:ILE:HB	1:D:364:VAL:HG22	1.91	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:421:ALA:HB2	2:A:471:THR:CG2	2.40	0.50
1:A:107:VAL:O	1:A:111:VAL:HG12	2.12	0.50
1:B:171:ARG:HH11	1:B:171:ARG:HB3	1.77	0.50
1:C:2:THR:N	1:C:224:ASP:OD2	2.45	0.50
1:A:442:SER:HB3	1:B:322:ASN:HD22	1.76	0.50
2:A:471:THR:N	1:B:434:ASN:OD1	2.44	0.50
1:B:256:GLU:OE2	1:B:310:LYS:HD2	2.12	0.50
1:C:318:VAL:HG23	1:C:405:CYS:HA	1.94	0.49
1:C:464:HIS:CD2	1:C:468:ILE:HG13	2.47	0.49
1:A:327:GLY:C	1:A:329:VAL:N	2.66	0.49
1:C:134:SER:HB3	1:C:135:PRO:HD3	1.92	0.49
1:A:320:LEU:HB3	1:A:401:ASP:HB2	1.94	0.49
2:B:470:THR:HG22	2:B:470:THR:O	2.12	0.49
1:A:255:ILE:CD1	1:A:255:ILE:H	2.25	0.49
1:D:230:THR:HG23	1:D:232:VAL:H	1.78	0.49
1:D:66:GLY:HA2	1:D:69:ILE:HD11	1.95	0.49
1:A:52:ILE:HG21	1:A:68:PHE:CG	2.48	0.49
1:C:179:LEU:N	1:C:180:PRO:HD2	2.28	0.49
1:A:435:ILE:HB	2:B:470:THR:HA	1.96	0.48
1:C:437:MET:HG3	1:D:440:GLN:O	2.14	0.48
1:C:334:THR:O	1:C:338:ILE:HG12	2.13	0.48
1:D:418:LYS:HA	2:D:472:THR:CG2	2.43	0.48
1:B:230:THR:HA	2:B:474:THR:N	2.28	0.48
1:D:174:VAL:HG23	1:D:175:LYS:H	1.78	0.48
1:D:20:HIS:O	1:D:24:ILE:HG12	2.14	0.48
1:B:124:TYR:O	1:B:127:SER:HB3	2.14	0.48
1:D:106:LYS:HA	1:D:109:ILE:HG22	1.96	0.47
1:D:74:GLU:HA	1:D:77:TYR:HB2	1.95	0.47
1:C:406:VAL:HG22	1:C:450:VAL:HG12	1.97	0.47
1:B:440:GLN:NE2	2:B:470:THR:OG1	2.40	0.47
1:C:156:ALA:O	1:C:174:VAL:HA	2.14	0.47
1:A:37:VAL:HG13	1:A:189:VAL:HB	1.96	0.47
1:B:100:ARG:HB2	1:B:132:LEU:HD21	1.97	0.47
1:A:442:SER:HB3	1:B:322:ASN:ND2	2.28	0.47
1:C:197:THR:HG22	1:C:198:GLU:N	2.30	0.47
1:C:308:ILE:HG23	1:C:309:VAL:N	2.29	0.47
1:B:3:THR:HG21	1:B:28:ARG:HD3	1.97	0.47
1:B:415:ARG:HA	1:B:444:GLU:HB2	1.96	0.47
1:C:226:ILE:HB	1:C:283:ILE:HD13	1.96	0.46
1:C:405:CYS:SG	1:C:456:LEU:HD12	2.55	0.46
1:B:37:VAL:CG2	1:B:189:VAL:HB	2.43	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:344:GLU:O	1:A:345:GLU:CB	2.60	0.46
1:A:68:PHE:CE2	1:A:72:ILE:HD11	2.49	0.46
1:C:230:THR:HG23	1:C:232:VAL:H	1.81	0.46
1:B:8:GLY:O	1:B:12:VAL:HG22	2.16	0.45
1:B:274:GLU:HB3	1:B:275:PRO:HD3	1.97	0.45
1:C:37:VAL:HG13	1:C:189:VAL:HA	1.97	0.45
1:D:351:LEU:CB	1:D:364:VAL:HG13	2.34	0.45
1:B:152:GLU:HA	1:B:191:THR:OG1	2.17	0.45
1:B:35:VAL:HB	1:B:187:ILE:HD12	1.99	0.45
1:B:328:MET:HA	1:B:334:THR:HG21	1.98	0.45
1:C:130:GLU:O	1:C:134:SER:HB2	2.16	0.45
1:A:96:ILE:O	1:A:100:ARG:HG2	2.17	0.45
1:B:47:ASN:H	1:B:47:ASN:HD22	1.64	0.45
1:B:391:ASN:ND2	1:B:391:ASN:N	2.65	0.45
2:D:472:THR:HG22	2:D:472:THR:O	2.16	0.44
1:B:16:GLU:CD	1:B:82:GLU:HG2	2.37	0.44
1:D:227:GLU:HB3	1:D:229:TRP:NE1	2.31	0.44
1:A:84:ILE:HG21	1:A:89:ILE:HB	2.00	0.44
1:D:192:GLY:O	1:D:193:PHE:CB	2.62	0.44
1:A:339:PHE:O	1:A:343:GLY:N	2.48	0.44
1:D:391:ASN:N	1:D:391:ASN:HD22	2.16	0.44
1:C:257:ALA:HB2	1:C:298:ILE:HD12	2.00	0.44
1:C:314:THR:HG22	1:C:407:ILE:HG13	1.99	0.44
1:A:20:HIS:HD2	3:A:486:HOH:O	2.01	0.44
1:D:421:ALA:HB2	2:D:472:THR:N	2.33	0.44
1:B:197:THR:O	1:B:198:GLU:C	2.56	0.43
1:C:191:THR:OG1	1:C:194:ILE:HD11	2.18	0.43
1:C:160:THR:OG1	1:C:203:THR:HG21	2.17	0.43
1:B:320:LEU:HB3	1:B:401:ASP:HB2	2.00	0.43
1:A:457:LEU:O	1:A:461:ARG:HG2	2.18	0.43
1:A:230:THR:OG1	2:A:473:THR:HB	2.18	0.43
1:B:306:ASP:O	1:B:307:SER:HB3	2.19	0.43
1:C:175:LYS:O	1:C:179:LEU:HB2	2.18	0.43
1:D:224:ASP:OD1	1:D:224:ASP:N	2.51	0.43
1:B:142:ARG:HA	1:B:146:GLU:O	2.18	0.43
1:C:354:GLN:HB3	1:D:352:ILE:HG12	2.00	0.43
1:D:271:ARG:O	1:D:275:PRO:HD3	2.19	0.43
1:A:352:ILE:HG12	1:B:354:GLN:HB3	2.00	0.43
1:C:192:GLY:O	1:C:193:PHE:HB3	2.19	0.43
1:C:437:MET:HB3	1:C:450:VAL:HG22	1.99	0.42
1:C:8:GLY:HA3	2:C:475:THR:HG23	2.01	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:324:PHE:HE1	1:D:396:ARG:HD3	1.84	0.42
1:B:283:ILE:HB	1:B:298:ILE:HB	2.00	0.42
1:B:92:GLU:OE1	1:B:142:ARG:NH1	2.48	0.42
1:D:138:SER:HB2	1:D:150:ALA:HB2	2.01	0.42
1:D:257:ALA:HB1	1:D:268:LEU:HD22	2.01	0.42
1:D:408:SER:HA	1:D:447:ILE:O	2.19	0.42
1:D:90:LYS:NZ	1:D:94:LYS:HE3	2.34	0.42
1:B:197:THR:O	1:B:200:GLY:N	2.43	0.42
1:D:299:THR:OG1	1:D:300:ASN:N	2.48	0.42
1:B:230:THR:OG1	1:B:231:ASP:N	2.49	0.42
1:D:321:ILE:HG13	1:D:400:VAL:HG12	2.01	0.42
1:A:320:LEU:O	1:A:400:VAL:HA	2.20	0.42
1:D:38:VAL:HG21	1:D:214:ALA:HA	2.00	0.42
1:D:414:MET:CE	1:D:447:ILE:HD13	2.50	0.42
1:B:6:LYS:HD2	1:B:211:ASP:OD2	2.20	0.42
1:C:233:SER:HA	1:C:287:ASN:HB2	2.02	0.42
1:B:120:LYS:HG3	1:B:164:PHE:CZ	2.55	0.42
1:B:391:ASN:H	1:B:391:ASN:HD22	1.68	0.42
1:A:323:ILE:HG22	1:A:328:MET:HE1	2.01	0.41
1:B:134:SER:OG	1:B:135:PRO:HD3	2.20	0.41
1:C:6:LYS:HA	1:C:38:VAL:O	2.20	0.41
1:A:334:THR:O	1:A:338:ILE:HG12	2.19	0.41
1:C:276:ALA:HB2	1:C:283:ILE:HD11	2.02	0.41
1:D:104:LEU:HG	1:D:128:PHE:CD2	2.55	0.41
1:A:452:ASP:HB2	1:A:455:ASP:OD1	2.21	0.41
1:B:199:GLU:HG3	1:B:201:TYR:CE2	2.55	0.41
1:B:329:VAL:HG23	1:B:331:VAL:HG12	2.03	0.41
1:B:321:ILE:HB	1:B:363:LEU:HD12	2.03	0.41
1:C:37:VAL:HG13	1:C:189:VAL:HB	2.02	0.41
1:A:69:ILE:HG13	1:A:105:GLU:HG3	2.02	0.41
1:A:233:SER:HA	1:A:287:ASN:HB2	2.02	0.41
1:A:230:THR:CB	2:A:473:THR:HB	2.50	0.41
1:C:351:LEU:O	1:C:363:LEU:HA	2.21	0.41
1:B:186:ILE:O	1:B:188:PRO:HD3	2.20	0.40
1:B:323:ILE:HD13	1:B:338:ILE:HD12	2.02	0.40
1:D:36:VAL:HG11	1:D:217:ILE:HG21	2.02	0.40
1:D:394:LEU:HD13	1:D:394:LEU:H	1.85	0.40
1:B:15:GLY:HA3	1:B:82:GLU:HB3	2.03	0.40
1:D:274:GLU:HB3	1:D:275:PRO:HD3	2.04	0.40
1:A:44:GLU:HA	1:A:47:ASN:HD22	1.87	0.40
1:D:142:ARG:HA	1:D:146:GLU:O	2.22	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:160:THR:HB	1:D:167:ALA:HB1	2.04	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	450/473 (95%)	421 (94%)	24 (5%)	5 (1%)	17	38
1	B	453/473 (96%)	423 (93%)	26 (6%)	4 (1%)	20	45
1	C	450/473 (95%)	412 (92%)	31 (7%)	7 (2%)	11	27
1	D	442/473 (93%)	409 (92%)	28 (6%)	5 (1%)	17	38
All	All	1795/1892 (95%)	1665 (93%)	109 (6%)	21 (1%)	15	36

All (21) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	307	SER
1	C	161	ASP
1	C	300	ASN
1	A	161	ASP
1	A	328	MET
1	A	330	GLY
1	A	392	ASN
1	B	161	ASP
1	D	174	VAL
1	D	330	GLY
1	D	392	ASN
1	B	392	ASN
1	C	166	SER
1	C	301	ASP

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	C	358	GLU
1	C	263	PHE
1	C	346	GLU
1	A	444	GLU
1	D	193	PHE
1	D	250	PRO
1	B	329	VAL

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	375/397 (94%)	341 (91%)	34 (9%)	11	24
1	B	375/397 (94%)	344 (92%)	31 (8%)	13	29
1	C	373/397 (94%)	344 (92%)	29 (8%)	15	33
1	D	369/397 (93%)	337 (91%)	32 (9%)	12	27
All	All	1492/1588 (94%)	1366 (92%)	126 (8%)	12	28

All (126) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	4	VAL
1	A	33	ASP
1	A	37	VAL
1	A	55	GLN
1	A	62	ILE
1	A	64	LYS
1	A	90	LYS
1	A	111	VAL
1	A	142	ARG
1	A	147	LYS
1	A	162	ASN
1	A	166	SER
1	A	183	LYS
1	A	189	VAL

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	196	THR
1	A	199	GLU
1	A	202	ILE
1	A	277	MET
1	A	300	ASN
1	A	316	LYS
1	A	320	LEU
1	A	342	LEU
1	A	361	ILE
1	A	363	LEU
1	A	390	LEU
1	A	394	LEU
1	A	396	ARG
1	A	403	ASP
1	A	404	VAL
1	A	408	SER
1	A	429	SER
1	A	442	SER
1	A	457	LEU
1	A	463	LEU
1	B	21	VAL
1	B	28	ARG
1	B	37	VAL
1	B	55	GLN
1	B	62	ILE
1	B	64	LYS
1	B	75	LYS
1	B	78	LYS
1	B	81	GLU
1	B	82	GLU
1	B	90	LYS
1	B	104	LEU
1	B	144	LEU
1	B	171	ARG
1	B	181	LEU
1	B	183	LYS
1	B	184	GLU
1	B	189	VAL
1	B	196	THR
1	B	197	THR
1	B	199	GLU
1	B	207	ARG

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	290	GLU
1	B	363	LEU
1	B	364	VAL
1	B	390	LEU
1	B	391	ASN
1	B	394	LEU
1	B	403	ASP
1	B	431	SER
1	B	443	SER
1	C	2	THR
1	C	4	VAL
1	C	37	VAL
1	C	78	LYS
1	C	84	ILE
1	C	90	LYS
1	C	104	LEU
1	C	109	ILE
1	C	134	SER
1	C	142	ARG
1	C	144	LEU
1	C	149	ILE
1	C	160	THR
1	C	183	LYS
1	C	189	VAL
1	C	194	ILE
1	C	203	THR
1	C	225	ILE
1	C	300	ASN
1	C	301	ASP
1	C	313	SER
1	C	318	VAL
1	C	363	LEU
1	C	368	GLU
1	C	374	LEU
1	C	390	LEU
1	C	398	VAL
1	C	463	LEU
1	C	469	GLU
1	D	27	LYS
1	D	47	ASN
1	D	55	GLN
1	D	60	ARG

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	D	69	ILE
1	D	82	GLU
1	D	88	GLU
1	D	90	LYS
1	D	97	ILE
1	D	118	THR
1	D	121	SER
1	D	133	SER
1	D	146	GLU
1	D	161	ASP
1	D	174	VAL
1	D	184	GLU
1	D	191	THR
1	D	197	THR
1	D	224	ASP
1	D	251	LYS
1	D	255	ILE
1	D	277	MET
1	D	334	THR
1	D	364	VAL
1	D	370	VAL
1	D	371	ASP
1	D	391	ASN
1	D	394	LEU
1	D	404	VAL
1	D	418	LYS
1	D	434	ASN
1	D	466	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	20	HIS
1	A	47	ASN
1	A	162	ASN
1	A	300	ASN
1	A	440	GLN
1	B	47	ASN
1	B	322	ASN
1	B	391	ASN
1	B	440	GLN
1	C	54	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	C	300	ASN
1	D	391	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

7 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	THR	A	471	-	4,7,7	0.42	0	3,9,9	0.22	0
2	THR	A	473	-	4,7,7	0.66	0	3,9,9	0.39	0
2	THR	B	470	-	4,7,7	0.74	0	3,9,9	0.46	0
2	THR	B	474	-	4,7,7	0.51	0	3,9,9	0.44	0
2	THR	C	475	-	4,7,7	0.30	0	3,9,9	0.39	0
2	THR	D	472	-	4,7,7	0.54	0	3,9,9	0.31	0
2	THR	D	476	-	4,7,7	0.41	0	3,9,9	0.31	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	THR	A	471	-	-	0/4/8/8	0/0/0/0
2	THR	A	473	-	-	0/4/8/8	0/0/0/0
2	THR	B	470	-	-	0/4/8/8	0/0/0/0
2	THR	B	474	-	-	0/4/8/8	0/0/0/0
2	THR	C	475	-	-	0/4/8/8	0/0/0/0
2	THR	D	472	-	-	0/4/8/8	0/0/0/0
2	THR	D	476	-	-	0/4/8/8	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.

7 monomers are involved in 30 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	471	THR	6	0
2	A	473	THR	6	0
2	B	470	THR	4	0
2	B	474	THR	6	0
2	C	475	THR	1	0
2	D	472	THR	5	0
2	D	476	THR	2	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

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	458/473 (96%)	0.21	22 (4%) 31 30	50, 61, 72, 76	0
1	B	459/473 (97%)	0.22	17 (3%) 42 41	49, 61, 72, 79	0
1	C	456/473 (96%)	0.38	36 (7%) 13 12	49, 63, 73, 78	0
1	D	452/473 (95%)	0.50	59 (13%) 4 3	61, 69, 76, 80	0
All	All	1825/1892 (96%)	0.33	134 (7%) 16 14	49, 64, 74, 80	0

All (134) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	382	GLY	8.7
1	B	331	VAL	7.5
1	C	331	VAL	7.4
1	A	302	MET	5.2
1	C	469	GLU	5.0
1	A	331	VAL	4.8
1	D	32	ASP	4.8
1	D	62	ILE	4.7
1	D	331	VAL	4.7
1	D	86	SER	4.7
1	D	88	GLU	4.5
1	D	149	ILE	4.4
1	B	300	ASN	4.3
1	D	343	GLY	4.3
1	D	150	ALA	4.0
1	C	330	GLY	3.9
1	D	206	GLY	3.9
1	D	415	ARG	3.8
1	B	301	ASP	3.8
1	C	302	MET	3.8
1	C	262	TYR	3.7

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	D	332	SER	3.7
1	D	171	ARG	3.7
1	D	30	LYS	3.6
1	A	31	GLU	3.6
1	D	70	LYS	3.6
1	A	329	VAL	3.6
1	B	305	SER	3.5
1	D	44	GLU	3.5
1	C	432	GLY	3.5
1	D	82	GLU	3.5
1	C	263	PHE	3.5
1	D	278	GLU	3.4
1	C	290	GLU	3.4
1	D	184	GLU	3.4
1	C	403	ASP	3.3
1	C	294	GLU	3.2
1	B	469	GLU	3.2
1	A	44	GLU	3.1
1	D	207	ARG	3.1
1	C	301	ASP	3.1
1	D	317	ASN	3.0
1	A	149	ILE	3.0
1	D	294	GLU	3.0
1	A	67	ASP	3.0
1	B	306	ASP	3.0
1	A	306	ASP	3.0
1	B	332	SER	3.0
1	D	142	ARG	3.0
1	D	306	ASP	2.9
1	D	81	GLU	2.9
1	D	307	SER	2.9
1	D	71	PHE	2.8
1	D	63	ALA	2.8
1	D	3	THR	2.8
1	C	442	SER	2.7
1	C	58	ASP	2.7
1	C	162	ASN	2.7
1	D	383	ASP	2.7
1	C	33	ASP	2.7
1	C	195	GLY	2.6
1	C	307	SER	2.6
1	C	327	GLY	2.6

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	B	346	GLU	2.6
1	D	225	ILE	2.6
1	A	207	ARG	2.6
1	A	145	GLY	2.6
1	D	251	LYS	2.6
1	D	250	PRO	2.6
1	D	279	LYS	2.6
1	D	31	GLU	2.6
1	D	176	GLU	2.6
1	A	401	ASP	2.5
1	B	382	GLY	2.5
1	A	382	GLY	2.5
1	D	173	GLU	2.5
1	D	77	TYR	2.5
1	D	164	PHE	2.4
1	D	87	GLU	2.4
1	B	290	GLU	2.4
1	A	111	VAL	2.4
1	D	92	GLU	2.4
1	C	394	LEU	2.4
1	C	194	ILE	2.4
1	D	236	TYR	2.3
1	A	147	LYS	2.3
1	D	180	PRO	2.3
1	D	144	LEU	2.3
1	A	403	ASP	2.3
1	D	465	GLU	2.3
1	C	379	ARG	2.3
1	C	337	ARG	2.3
1	D	329	VAL	2.3
1	C	207	ARG	2.3
1	C	463	LEU	2.3
1	C	201	TYR	2.3
1	B	368	GLU	2.3
1	D	289	PHE	2.3
1	D	224	ASP	2.3
1	D	145	GLY	2.3
1	C	393	ASN	2.3
1	D	264	GLY	2.3
1	D	102	GLU	2.2
1	D	379	ARG	2.2
1	A	32	ASP	2.2

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	74	GLU	2.2
1	D	162	ASN	2.2
1	B	56	ALA	2.2
1	D	346	GLU	2.2
1	C	332	SER	2.2
1	C	311	ALA	2.2
1	C	266	LYS	2.2
1	C	461	ARG	2.2
1	C	465	GLU	2.2
1	A	52	ILE	2.2
1	B	207	ARG	2.2
1	A	327	GLY	2.2
1	C	430	GLU	2.1
1	B	33	ASP	2.1
1	D	265	ALA	2.1
1	D	196	THR	2.1
1	D	64	LYS	2.1
1	A	95	LYS	2.1
1	C	289	PHE	2.1
1	A	393	ASN	2.1
1	A	332	SER	2.1
1	C	392	ASN	2.1
1	B	74	GLU	2.0
1	D	344	GLU	2.0
1	B	266	LYS	2.0
1	C	184	GLU	2.0
1	B	16	GLU	2.0
1	D	13	GLY	2.0
1	C	74	GLU	2.0

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

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

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands [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(Å ²)	Q<0.9
2	THR	D	472	8/8	0.70	0.67	5.47	71,71,71,71	8
2	THR	C	475	8/8	0.33	0.51	3.61	51,53,53,53	8
2	THR	D	476	8/8	0.77	0.35	3.03	62,62,62,62	8
2	THR	A	473	8/8	0.87	0.26	2.48	66,67,67,67	0
2	THR	B	470	8/8	0.87	0.25	2.22	68,69,70,70	0
2	THR	B	474	8/8	0.90	0.21	1.00	60,60,60,61	0
2	THR	A	471	8/8	0.93	0.18	0.35	57,58,58,58	0

6.5 Other polymers [i](#)

There are no such residues in this entry.