



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 06:44 AM UTC

PDB ID : 3CDI / pdb_00003cdi
Title : Crystal structure of E. coli PNPase
Authors : Shi, Z.; Yang, W.Z.; Lin-Chao, S.; Chak, K.F.; Yuan, H.S.
Deposited on : 2008-02-27
Resolution : 2.60 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 ⓘ 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 ⓘ](#)) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0
Xtrriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

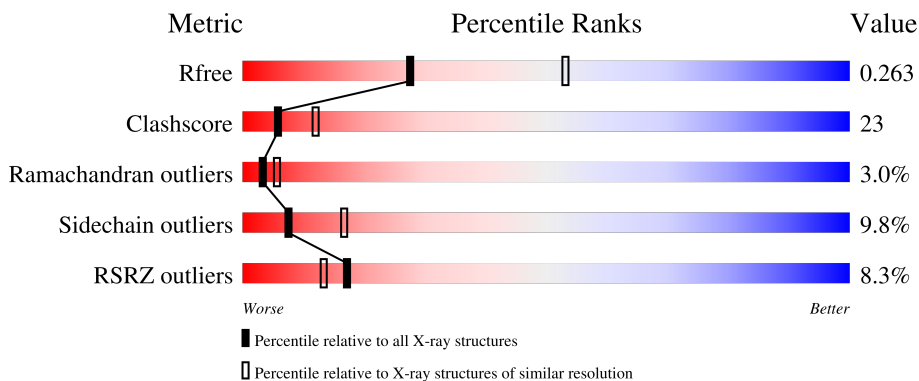
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	4008 (2.60-2.60)
Clashscore	190562	4347 (2.60-2.60)
Ramachandran outliers	187476	4277 (2.60-2.60)
Sidechain outliers	187428	4277 (2.60-2.60)
RSRZ outliers	180081	4008 (2.60-2.60)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments 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 $\leq 5\%$. 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	723	

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 4025 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 Polynucleotide phosphorylase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	516	3924	2462	684	759	19	0	0	0

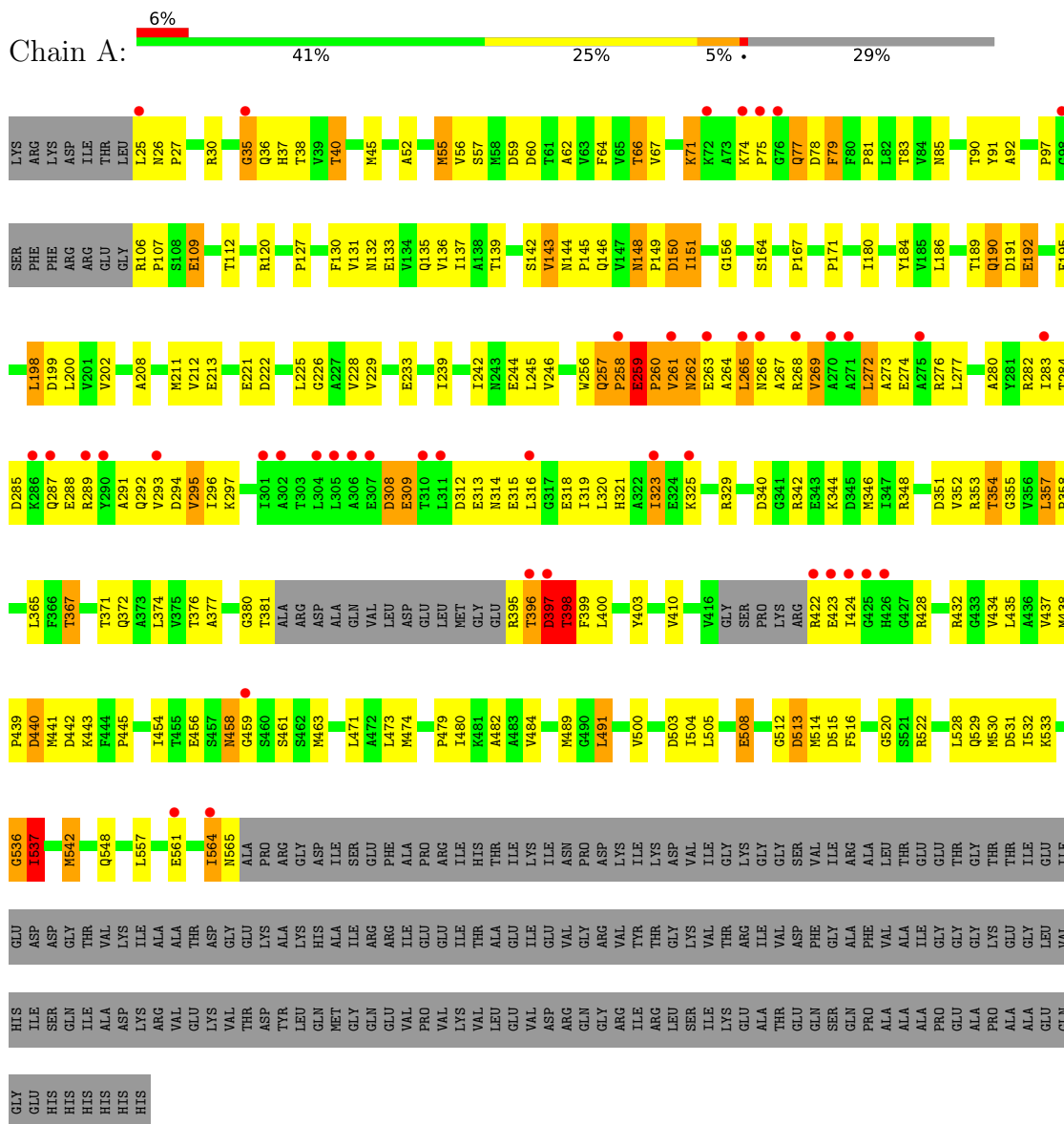
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	101	Total	O	0	0
			101	101		

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: Polynucleotide phosphorylase



4 Data and refinement statistics

Property	Value	Source
Space group	F 41 3 2	Depositor
Cell constants a, b, c, α , β , γ	270.12Å 270.12Å 270.12Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.60 50.00 – 2.60	Depositor EDS
% Data completeness (in resolution range)	93.0 (50.00-2.60) 99.3 (50.00-2.60)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.58 (at 2.61Å)	Xtrriage
Refinement program	CNS	Depositor
R, R_{free}	0.232 , 0.277 0.255 , 0.263	Depositor DCC
R_{free} test set	2644 reflections (10.06%)	wwPDB-VP
Wilson B-factor (Å ²)	60.6	Xtrriage
Anisotropy	0.000	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 38.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	4025	wwPDB-VP
Average B, all atoms (Å ²)	54.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.75% 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	0.48	0/3980	1.05	20/5393 (0.4%)

There are no bond length outliers.

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	269	VAL	N-CA-C	-13.90	99.86	111.81
1	A	398	THR	N-CA-C	-9.56	101.73	113.97
1	A	357	LEU	CA-C-N	9.50	129.12	119.24
1	A	357	LEU	C-N-CA	9.50	129.12	119.24
1	A	308	ASP	N-CA-C	-9.37	101.10	108.78
1	A	259	GLU	CA-C-N	8.33	130.25	119.84
1	A	259	GLU	C-N-CA	8.33	130.25	119.84
1	A	536	GLY	N-CA-C	-7.40	102.47	111.35
1	A	397	ASP	N-CA-C	-7.01	95.87	110.80
1	A	257	GLN	CA-C-N	6.94	128.52	119.84
1	A	257	GLN	C-N-CA	6.94	128.52	119.84
1	A	143	VAL	N-CA-C	6.30	117.09	107.77
1	A	513	ASP	N-CA-C	-6.28	104.72	112.38
1	A	150	ASP	N-CA-C	5.90	118.21	111.02
1	A	192	GLU	N-CA-C	-5.82	105.06	111.82
1	A	508	GLU	N-CA-C	-5.50	105.35	113.61
1	A	208	ALA	N-CA-C	5.31	117.15	108.76
1	A	295	VAL	N-CA-C	-5.23	105.62	110.53
1	A	515	ASP	N-CA-C	-5.22	100.52	109.24
1	A	344	LYS	N-CA-C	5.04	118.20	111.75

There are no chirality outliers.

There are no planarity outliers.

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	3924	0	3955	182	0
2	A	101	0	0	5	0
All	All	4025	0	3955	182	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 23.

All (182) 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:106:ARG:HB3	1:A:107:PRO:HA	1.25	1.09
1:A:146:GLN:HG3	1:A:189:THR:HB	1.42	1.00
1:A:171:PRO:HG2	1:A:239:ILE:HG23	1.45	0.99
1:A:396:THR:O	1:A:397:ASP:HB3	1.62	0.97
1:A:106:ARG:HB3	1:A:107:PRO:CA	1.98	0.92
1:A:437:VAL:HG12	1:A:480:ILE:HB	1.52	0.90
1:A:77:GLN:HB3	1:A:131:VAL:HG11	1.57	0.86
1:A:109:GLU:HB2	1:A:424:ILE:HD11	1.58	0.85
1:A:309:GLU:HB2	2:A:817:HOH:O	1.76	0.83
1:A:463:MET:HA	1:A:463:MET:HE2	1.60	0.82
1:A:40:THR:HG23	1:A:57:SER:HB3	1.60	0.81
1:A:557:LEU:O	1:A:561:GLU:HG3	1.80	0.79
1:A:202:VAL:HG12	1:A:212:VAL:HG22	1.64	0.79
1:A:438:MET:HE1	1:A:473:LEU:HD13	1.66	0.78
1:A:283:ILE:HD11	1:A:289:ARG:HA	1.67	0.77
1:A:66:THR:HG23	2:A:763:HOH:O	1.86	0.75
1:A:372:GLN:HB3	1:A:456:GLU:HB2	1.67	0.74
1:A:294:ASP:HB3	2:A:835:HOH:O	1.87	0.74
1:A:148:ASN:ND2	1:A:150:ASP:H	1.85	0.73
1:A:308:ASP:CG	1:A:309:GLU:H	1.95	0.73
1:A:348:ARG:HD3	1:A:503:ASP:OD1	1.89	0.72
1:A:320:LEU:O	1:A:323:ILE:HD13	1.88	0.72
1:A:148:ASN:HD22	1:A:149:PRO:N	1.88	0.72
1:A:437:VAL:CG1	1:A:480:ILE:HB	2.19	0.71
1:A:74:LYS:HB3	1:A:75:PRO:HD2	1.75	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:258:PRO:O	1:A:259:GLU:HB3	1.91	0.68
1:A:403:TYR:OH	1:A:461:SER:HB2	1.95	0.67
1:A:437:VAL:HG13	1:A:482:ALA:H	1.60	0.66
1:A:351:ASP:HB3	1:A:367:THR:HG23	1.77	0.66
1:A:513:ASP:HA	1:A:533:LYS:HE2	1.77	0.66
1:A:285:ASP:HB2	1:A:288:GLU:HB3	1.79	0.65
1:A:410:VAL:O	1:A:410:VAL:HG12	1.97	0.65
1:A:198:LEU:HD22	1:A:199:ASP:N	2.10	0.64
1:A:30:ARG:HH21	1:A:244:GLU:HG3	1.62	0.64
1:A:148:ASN:HD22	1:A:148:ASN:C	2.05	0.64
1:A:537:ILE:C	1:A:537:ILE:HD13	2.23	0.63
1:A:59:ASP:O	1:A:60:ASP:HB2	1.97	0.63
1:A:200:LEU:HD21	1:A:202:VAL:HG13	1.80	0.63
1:A:40:THR:CG2	1:A:57:SER:HB3	2.27	0.63
1:A:522:ARG:NH1	1:A:561:GLU:OE1	2.32	0.62
1:A:81:PRO:HB2	1:A:133:GLU:HG3	1.83	0.61
1:A:489:MET:HB2	1:A:516:PHE:CE2	2.36	0.61
1:A:537:ILE:HD13	1:A:537:ILE:O	2.01	0.61
1:A:131:VAL:HG12	1:A:131:VAL:O	2.01	0.60
1:A:474:MET:HE3	1:A:480:ILE:HD11	1.82	0.60
1:A:280:ALA:O	1:A:283:ILE:HG12	2.00	0.60
1:A:55:MET:HE1	1:A:62:ALA:HB1	1.84	0.60
1:A:268:ARG:O	1:A:272:LEU:HD21	2.02	0.60
1:A:37:HIS:HD2	1:A:59:ASP:OD2	1.86	0.59
1:A:530:MET:HE1	1:A:542:MET:HG2	1.84	0.59
1:A:242:ILE:O	1:A:246:VAL:HG23	2.02	0.59
1:A:92:ALA:HB1	1:A:143:VAL:HG23	1.85	0.59
1:A:35:GLY:O	1:A:36:GLN:HB3	2.03	0.59
1:A:74:LYS:HB2	1:A:77:GLN:HG2	1.83	0.59
1:A:291:ALA:O	1:A:295:VAL:HG23	2.02	0.58
1:A:308:ASP:CG	1:A:309:GLU:N	2.60	0.58
1:A:395:ARG:HG2	1:A:398:THR:CG2	2.33	0.58
1:A:55:MET:HG2	1:A:64:PHE:CD1	2.38	0.58
1:A:256:TRP:CZ2	1:A:258:PRO:HA	2.39	0.58
1:A:395:ARG:HD3	1:A:399:PHE:HB2	1.86	0.57
1:A:396:THR:C	1:A:398:THR:H	2.11	0.57
1:A:150:ASP:OD1	1:A:151:ILE:N	2.37	0.57
1:A:463:MET:HA	1:A:463:MET:CE	2.34	0.57
1:A:340:ASP:OD1	1:A:342:ARG:HD3	2.04	0.57
1:A:148:ASN:HD22	1:A:150:ASP:H	1.51	0.55
1:A:79:PHE:C	1:A:131:VAL:HG13	2.30	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:491:LEU:HB3	1:A:514:MET:HB3	1.87	0.55
1:A:537:ILE:O	1:A:537:ILE:HG23	2.07	0.55
1:A:395:ARG:NH1	1:A:439:PRO:O	2.41	0.54
1:A:463:MET:HE2	1:A:463:MET:CA	2.34	0.54
1:A:422:ARG:NE	1:A:422:ARG:HA	2.22	0.54
1:A:30:ARG:NH2	1:A:244:GLU:HG3	2.23	0.54
1:A:277:LEU:HD12	1:A:323:ILE:HD11	1.91	0.53
1:A:55:MET:HG2	1:A:64:PHE:HD1	1.74	0.53
1:A:395:ARG:O	1:A:396:THR:O	2.27	0.53
1:A:79:PHE:O	1:A:131:VAL:HG13	2.09	0.52
1:A:256:TRP:CH2	1:A:258:PRO:HA	2.45	0.52
1:A:321:HIS:NE2	1:A:325:LYS:HE2	2.25	0.52
1:A:77:GLN:O	1:A:78:ASP:HB2	2.07	0.52
1:A:308:ASP:O	1:A:309:GLU:HB3	2.09	0.52
1:A:484:VAL:HG23	1:A:520:GLY:C	2.35	0.52
1:A:536:GLY:O	1:A:537:ILE:C	2.51	0.51
1:A:292:GLN:O	1:A:296:ILE:HG13	2.10	0.51
1:A:259:GLU:O	1:A:259:GLU:HG3	2.11	0.51
1:A:397:ASP:C	1:A:397:ASP:OD2	2.54	0.51
1:A:225:LEU:HD21	1:A:542:MET:HB3	1.91	0.51
1:A:202:VAL:HG11	1:A:228:VAL:HA	1.92	0.51
1:A:229:VAL:O	1:A:233:GLU:HG3	2.11	0.51
1:A:354:THR:CG2	1:A:355:GLY:N	2.73	0.51
1:A:500:VAL:HB	1:A:548:GLN:NE2	2.26	0.51
1:A:276:ARG:HH21	1:A:296:ILE:HA	1.76	0.50
1:A:120:ARG:NH2	1:A:213:GLU:HB2	2.26	0.50
1:A:27:PRO:HB3	1:A:45:MET:HB2	1.92	0.50
1:A:329:ARG:NH2	1:A:513:ASP:OD1	2.44	0.50
1:A:352:VAL:HG13	1:A:471:LEU:HD13	1.93	0.50
1:A:376:THR:HG22	1:A:377:ALA:N	2.27	0.50
1:A:272:LEU:N	1:A:272:LEU:HD23	2.26	0.50
1:A:474:MET:SD	1:A:564:ILE:HD12	2.51	0.50
1:A:190:GLN:HG3	1:A:191:ASP:N	2.26	0.50
1:A:90:THR:OG1	1:A:97:PRO:HD3	2.12	0.49
1:A:283:ILE:CD1	1:A:289:ARG:HA	2.40	0.49
1:A:395:ARG:HG2	1:A:398:THR:HG22	1.94	0.49
1:A:30:ARG:HH21	1:A:244:GLU:CG	2.25	0.49
1:A:422:ARG:C	1:A:424:ILE:H	2.21	0.49
1:A:213:GLU:OE1	1:A:529:GLN:HG3	2.13	0.49
1:A:130:PHE:CZ	1:A:132:ASN:HB2	2.48	0.49
1:A:564:ILE:O	1:A:565:ASN:C	2.55	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:351:ASP:OD2	1:A:353:ARG:NH1	2.47	0.48
1:A:258:PRO:O	1:A:259:GLU:CB	2.59	0.47
1:A:261:VAL:O	1:A:263:GLU:N	2.46	0.47
1:A:277:LEU:CD1	1:A:323:ILE:HD11	2.45	0.47
1:A:56:VAL:HG21	1:A:156:GLY:HA2	1.97	0.47
1:A:285:ASP:CB	1:A:288:GLU:HB3	2.45	0.47
1:A:85:ASN:ND2	1:A:135:GLN:HE21	2.13	0.47
1:A:308:ASP:O	1:A:309:GLU:CB	2.63	0.46
1:A:381:THR:HG22	1:A:381:THR:O	2.15	0.46
1:A:79:PHE:O	1:A:81:PRO:HD3	2.16	0.46
1:A:432:ARG:HA	1:A:435:LEU:HD12	1.97	0.46
1:A:265:LEU:C	1:A:267:ALA:H	2.23	0.46
1:A:342:ARG:NH2	1:A:503:ASP:HB3	2.30	0.46
1:A:395:ARG:O	1:A:396:THR:C	2.59	0.46
1:A:434:VAL:HG12	1:A:438:MET:HE3	1.98	0.46
1:A:66:THR:HG22	1:A:137:ILE:HB	1.97	0.46
1:A:512:GLY:C	1:A:514:MET:N	2.73	0.46
1:A:422:ARG:O	1:A:424:ILE:N	2.49	0.45
1:A:266:ASN:HB3	1:A:319:ILE:HD13	1.99	0.45
1:A:422:ARG:NE	1:A:422:ARG:CA	2.79	0.45
1:A:395:ARG:HG2	1:A:398:THR:HG21	1.98	0.45
1:A:92:ALA:CB	1:A:143:VAL:HG23	2.47	0.45
1:A:441:MET:HE3	1:A:445:PRO:HA	1.99	0.45
1:A:120:ARG:HH22	1:A:213:GLU:HB2	1.82	0.45
1:A:297:LYS:HG2	1:A:320:LEU:HD13	1.99	0.45
1:A:315:GLU:O	1:A:318:GLU:HB3	2.18	0.44
1:A:441:MET:CE	1:A:445:PRO:HA	2.47	0.44
1:A:30:ARG:HB2	1:A:245:LEU:HD13	1.99	0.44
1:A:25:LEU:HG	1:A:45:MET:HG3	1.98	0.44
1:A:144:ASN:O	1:A:146:GLN:N	2.51	0.44
1:A:454:ILE:HG13	1:A:461:SER:HB3	1.99	0.44
1:A:180:ILE:HG12	1:A:195:GLU:O	2.18	0.44
1:A:262:ASN:CG	1:A:265:LEU:HB2	2.43	0.43
1:A:329:ARG:HH22	1:A:513:ASP:CG	2.26	0.43
1:A:342:ARG:HB3	1:A:346:MET:HB2	2.01	0.43
1:A:71:LYS:HG2	2:A:833:HOH:O	2.17	0.43
1:A:282:ARG:HH11	1:A:282:ARG:HG3	1.84	0.43
1:A:312:ASP:O	1:A:313:GLU:C	2.62	0.43
1:A:148:ASN:ND2	1:A:148:ASN:C	2.76	0.43
1:A:316:LEU:HD23	1:A:316:LEU:HA	1.85	0.43
1:A:30:ARG:HG2	2:A:830:HOH:O	2.17	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:52:ALA:HB2	1:A:164:SER:HA	2.01	0.43
1:A:200:LEU:C	1:A:200:LEU:HD23	2.44	0.43
1:A:380:GLY:O	1:A:381:THR:C	2.62	0.43
1:A:265:LEU:O	1:A:269:VAL:HG23	2.19	0.42
1:A:313:GLU:O	1:A:316:LEU:HB2	2.19	0.42
1:A:443:LYS:HE2	1:A:479:PRO:HB2	2.02	0.42
1:A:357:LEU:HA	1:A:358:PRO:HD3	1.75	0.42
1:A:67:VAL:HG22	1:A:136:VAL:HG22	2.01	0.42
1:A:148:ASN:HA	1:A:149:PRO:HD3	1.90	0.42
1:A:189:THR:HG23	1:A:192:GLU:OE1	2.20	0.42
1:A:340:ASP:OD1	1:A:342:ARG:CD	2.67	0.42
1:A:340:ASP:CG	1:A:342:ARG:HD3	2.44	0.42
1:A:428:ARG:O	1:A:432:ARG:HG3	2.20	0.42
1:A:289:ARG:O	1:A:293:VAL:HG23	2.20	0.41
1:A:458:ASN:CG	1:A:458:ASN:O	2.63	0.41
1:A:505:LEU:HB2	1:A:508:GLU:HG3	2.01	0.41
1:A:91:TYR:CD2	1:A:91:TYR:C	2.98	0.41
1:A:120:ARG:HH11	1:A:531:ASP:CG	2.28	0.41
1:A:262:ASN:C	1:A:264:ALA:H	2.28	0.41
1:A:120:ARG:NH1	1:A:531:ASP:OD2	2.51	0.41
1:A:184:TYR:OH	1:A:226:GLY:HA3	2.21	0.41
1:A:273:ALA:O	1:A:274:GLU:C	2.64	0.41
1:A:62:ALA:HB3	1:A:142:SER:OG	2.20	0.41
1:A:437:VAL:HG12	1:A:437:VAL:O	2.20	0.41
1:A:284:THR:O	1:A:285:ASP:C	2.64	0.41
1:A:127:PRO:HD2	1:A:167:PRO:O	2.21	0.40
1:A:440:ASP:C	1:A:442:ASP:H	2.29	0.40
1:A:532:ILE:HD12	1:A:532:ILE:N	2.35	0.40
1:A:106:ARG:CB	1:A:107:PRO:CA	2.83	0.40
1:A:277:LEU:HD23	1:A:296:ILE:HD12	2.03	0.40
1:A:148:ASN:HD22	1:A:149:PRO:CD	2.34	0.40
1:A:313:GLU:O	1:A:314:ASN:C	2.64	0.40
1:A:78:ASP:O	1:A:79:PHE:HB2	2.22	0.40
1:A:262:ASN:OD1	1:A:265:LEU:HB2	2.22	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	508/723 (70%)	454 (89%)	39 (8%)	15 (3%)	3 6

All (15) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	396	THR
1	A	423	GLU
1	A	537	ILE
1	A	35	GLY
1	A	260	PRO
1	A	309	GLU
1	A	458	ASN
1	A	397	ASP
1	A	257	GLN
1	A	259	GLU
1	A	262	ASN
1	A	440	ASP
1	A	145	PRO
1	A	79	PHE
1	A	459	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	420/587 (72%)	379 (90%)	41 (10%)	7 17

All (41) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	26	ASN
1	A	38	THR
1	A	40	THR
1	A	55	MET
1	A	66	THR
1	A	71	LYS
1	A	77	GLN
1	A	83	THR
1	A	109	GLU
1	A	112	THR
1	A	139	THR
1	A	148	ASN
1	A	151	ILE
1	A	186	LEU
1	A	190	GLN
1	A	198	LEU
1	A	211	MET
1	A	221	GLU
1	A	222	ASP
1	A	258	PRO
1	A	259	GLU
1	A	260	PRO
1	A	261	VAL
1	A	265	LEU
1	A	272	LEU
1	A	287	GLN
1	A	323	ILE
1	A	354	THR
1	A	365	LEU
1	A	367	THR
1	A	371	THR
1	A	374	LEU
1	A	397	ASP
1	A	398	THR
1	A	400	LEU
1	A	491	LEU
1	A	504	ILE
1	A	528	LEU
1	A	537	ILE
1	A	542	MET
1	A	564	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	33	GLN
1	A	37	HIS
1	A	135	GLN
1	A	146	GLN
1	A	148	ASN
1	A	232	HIS
1	A	234	GLN
1	A	257	GLN
1	A	287	GLN
1	A	402	HIS
1	A	426	HIS
1	A	510	HIS
1	A	529	GLN
1	A	543	GLN
1	A	548	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	516/723 (71%)	0.54	43 (8%) 17 13	27, 49, 88, 97	0

All (43) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	287	GLN	4.6
1	A	76	GLY	4.6
1	A	306	ALA	4.0
1	A	304	LEU	3.9
1	A	258	PRO	3.8
1	A	290	TYR	3.7
1	A	397	ASP	3.7
1	A	35	GLY	3.6
1	A	422	ARG	3.6
1	A	311	LEU	3.4
1	A	426	HIS	3.4
1	A	396	THR	3.3
1	A	289	ARG	3.3
1	A	265	LEU	3.2
1	A	424	ILE	3.2
1	A	564	ILE	3.1
1	A	293	VAL	3.0
1	A	75	PRO	2.9
1	A	301	ILE	2.8
1	A	25	LEU	2.8
1	A	316	LEU	2.7
1	A	270	ALA	2.7
1	A	283	ILE	2.7
1	A	275	ALA	2.7
1	A	268	ARG	2.6
1	A	263	GLU	2.6
1	A	423	GLU	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	266	ASN	2.6
1	A	561	GLU	2.5
1	A	459	GLY	2.5
1	A	323	ILE	2.5
1	A	261	VAL	2.4
1	A	98	GLY	2.4
1	A	72	LYS	2.4
1	A	286	LYS	2.3
1	A	425	GLY	2.3
1	A	325	LYS	2.2
1	A	305	LEU	2.2
1	A	74	LYS	2.2
1	A	271	ALA	2.2
1	A	310	THR	2.2
1	A	302	ALA	2.1
1	A	307	GLU	2.1

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 oligosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.