



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 12:43 PM UTC

PDB ID : 2ABQ / pdb_00002abq
Title : Crystal structure of fructose-1-phosphate kinase from *Bacillus halodurans*
Authors : Eswaramoorthy, S.; Swaminathan, S.; Burley, S.K.; New York SGX Research Center for Structural Genomics (NYSGXRC)
Deposited on : 2005-07-15
Resolution : 2.10 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
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (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

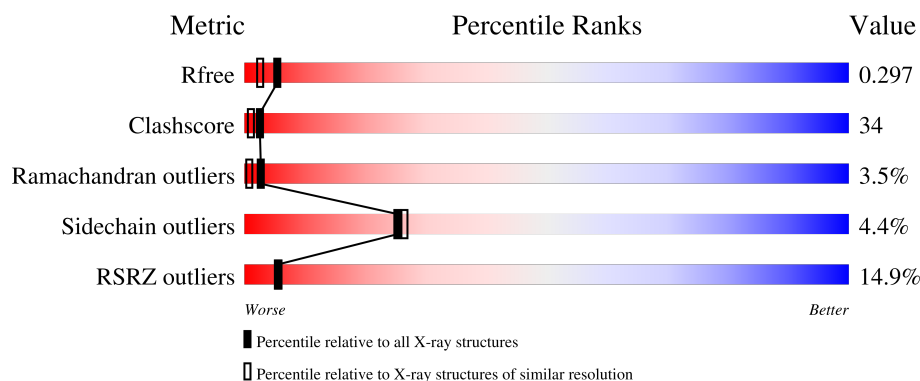
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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	6658 (2.10-2.10)
Clashscore	190562	7164 (2.10-2.10)
Ramachandran outliers	187476	7099 (2.10-2.10)
Sidechain outliers	187428	7100 (2.10-2.10)
RSRZ outliers	180081	6662 (2.10-2.10)

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	306	
1	B	306	

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 criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	PO4	A	308	-	-	X	-

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4713 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.

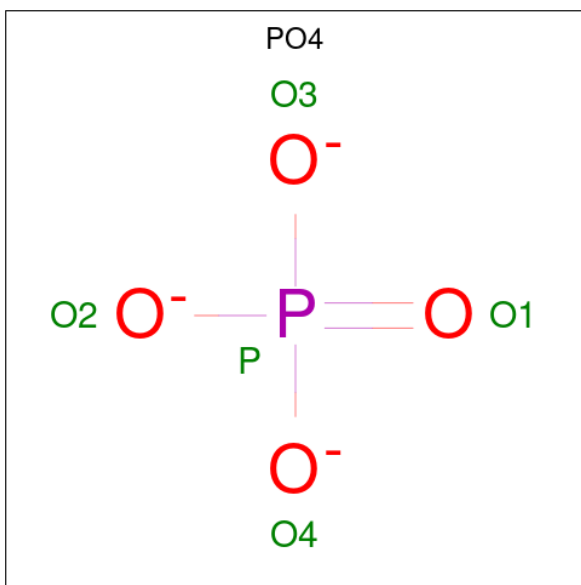
- Molecule 1 is a protein called fructose 1-phosphate kinase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	306	Total	C	N	O	S	Se	0	0	0
			2289	1441	400	443	1	4			
1	B	306	Total	C	N	O	S	Se	0	0	0
			2297	1446	403	443	1	4			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MSE	MET	modified residue	UNP Q9KEM5
A	139	MSE	MET	modified residue	UNP Q9KEM5
A	147	MSE	MET	modified residue	UNP Q9KEM5
A	231	MSE	MET	modified residue	UNP Q9KEM5
B	1	MSE	MET	modified residue	UNP Q9KEM5
B	139	MSE	MET	modified residue	UNP Q9KEM5
B	147	MSE	MET	modified residue	UNP Q9KEM5
B	231	MSE	MET	modified residue	UNP Q9KEM5

- Molecule 2 is PHOSPHATE ION (CCD ID: PO4) (formula: O₄P).



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

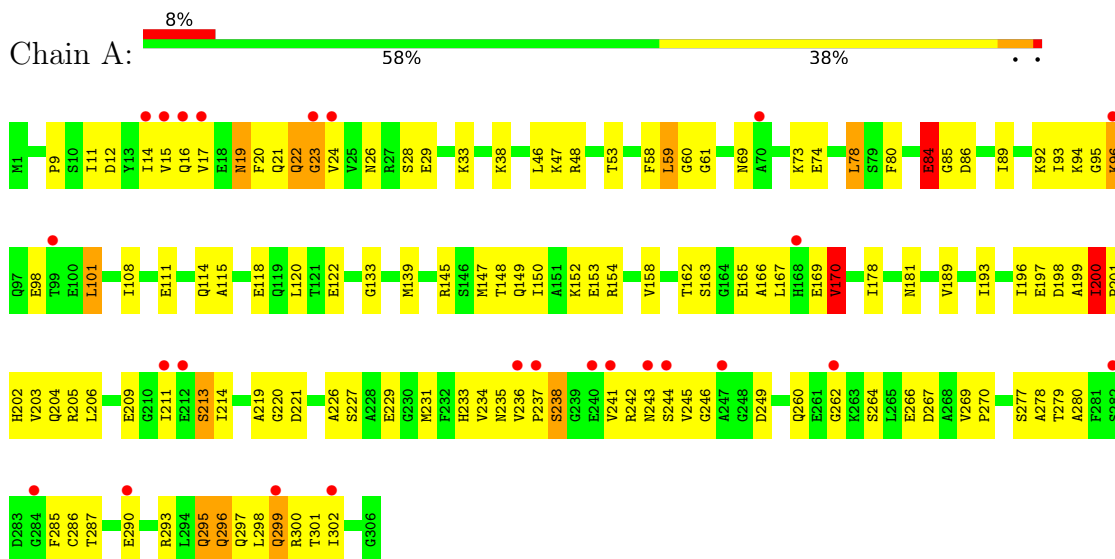
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	62	Total	O	0	0
			62	62		
3	B	45	Total	O	0	0
			45	45		

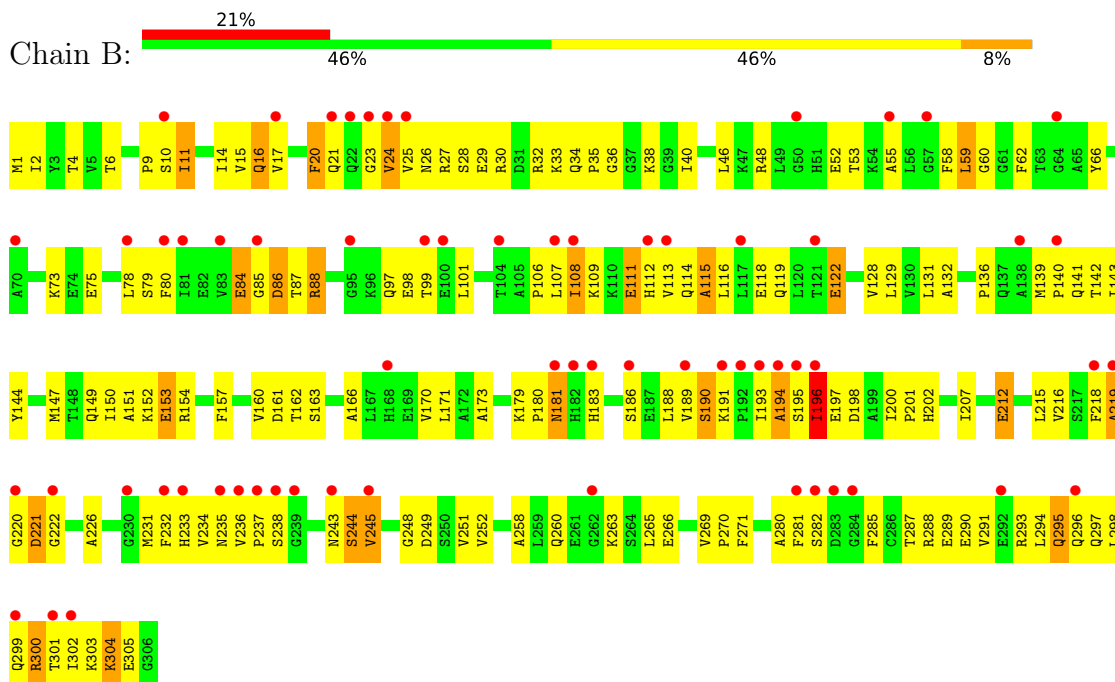
3 Residue-property plots

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: fructose 1-phosphate kinase



- Molecule 1: fructose 1-phosphate kinase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	42.62Å 48.71Å 79.05Å 82.38° 87.28° 82.14°	Depositor
Resolution (Å)	39.20 – 2.10 39.20 – 2.10	Depositor EDS
% Data completeness (in resolution range)	(Not available) (39.20-2.10) 85.7 (39.20-2.10)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.38 (at 2.10Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.255 , 0.299 0.253 , 0.297	Depositor DCC
R_{free} test set	1246 reflections (3.78%)	wwPDB-VP
Wilson B-factor (Å ²)	35.0	Xtriage
Anisotropy	0.209	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 56.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	4713	wwPDB-VP
Average B, all atoms (Å ²)	51.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.93% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: PO4

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	0.53	1/2320 (0.0%)	0.94	5/3129 (0.2%)
1	B	0.45	0/2328	0.93	8/3139 (0.3%)
All	All	0.49	1/4648 (0.0%)	0.94	13/6268 (0.2%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	200	ILE	CA-CB	5.62	1.56	1.54

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	84	GLU	N-CA-C	6.98	118.67	111.14
1	A	181	ASN	N-CA-C	-6.40	102.28	110.53
1	B	196	ILE	N-CA-C	-5.98	104.93	113.07
1	B	115	ALA	N-CA-C	-5.95	105.52	112.89
1	B	181	ASN	N-CA-C	-5.72	102.98	110.53
1	B	212	GLU	N-CA-C	5.65	117.52	111.36
1	B	29	GLU	N-CA-C	-5.47	106.97	113.97
1	B	244	SER	N-CA-C	-5.44	107.65	114.56
1	A	158	VAL	N-CA-C	5.36	115.57	107.80
1	A	170	VAL	N-CA-C	5.27	117.64	111.05
1	B	11	ILE	N-CA-C	-5.23	100.21	107.80
1	A	11	ILE	N-CA-C	-5.19	100.28	107.80
1	B	88	ARG	N-CA-C	5.02	116.58	110.41

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	2289	0	2293	147	0
1	B	2297	0	2311	175	0
2	A	15	0	0	2	0
2	B	5	0	0	0	0
3	A	62	0	0	4	0
3	B	45	0	0	5	0
All	All	4713	0	4604	317	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 34.

All (317) 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:200:ILE:HG13	1:B:201:PRO:HD3	1.38	1.04
1:B:32:ARG:HH21	1:B:34:GLN:HE22	1.05	0.98
1:B:304:LYS:H	1:B:304:LYS:HD2	1.27	0.96
1:A:16:GLN:HE21	1:A:95:GLY:HA2	1.29	0.96
1:B:46:LEU:HD13	1:B:53:THR:HG21	1.57	0.85
1:B:162:THR:HG22	1:B:163:SER:H	1.40	0.84
1:A:162:THR:HG22	1:A:163:SER:H	1.41	0.83
1:A:189:VAL:HG21	1:A:202:HIS:ND1	1.93	0.83
1:B:2:ILE:HB	1:B:53:THR:HG22	1.60	0.83
1:A:17:VAL:HG23	1:A:20:PHE:HB2	1.59	0.83
1:B:289:GLU:CD	1:B:289:GLU:H	1.88	0.81
1:A:150:ILE:HA	1:A:153:GLU:OE1	1.81	0.81
1:A:114:GLN:O	1:A:118:GLU:HG3	1.81	0.80
1:B:143:ILE:HG13	1:B:147:MSE:HE2	1.65	0.79
1:B:149:GLN:O	1:B:153:GLU:HG2	1.81	0.79
1:A:205:ARG:O	1:A:209:GLU:HG3	1.84	0.78
1:B:16:GLN:HG2	1:B:30:ARG:HB3	1.64	0.78
1:B:32:ARG:NH2	1:B:34:GLN:HE22	1.81	0.77
1:B:111:GLU:CD	1:B:111:GLU:H	1.90	0.77
1:A:204:GLN:HG2	1:A:231:MSE:HE1	1.66	0.77
1:B:243:ASN:HD21	1:B:245:VAL:HG23	1.49	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:32:ARG:HE	1:B:34:GLN:HE21	1.30	0.76
1:B:84:GLU:CD	1:B:84:GLU:H	1.94	0.76
1:A:20:PHE:HA	1:A:26:ASN:OD1	1.86	0.75
1:A:19:ASN:HB3	3:A:347:HOH:O	1.86	0.75
1:A:94:LYS:HD2	1:A:98:GLU:OE1	1.88	0.74
1:B:32:ARG:HE	1:B:34:GLN:NE2	1.84	0.74
1:B:1:MSE:HG2	1:B:260:GLN:HE22	1.51	0.74
1:B:207:ILE:HD11	1:B:226:ALA:HB1	1.70	0.74
1:B:166:ALA:O	1:B:170:VAL:HG23	1.88	0.74
1:B:196:ILE:HG23	1:B:197:GLU:OE2	1.88	0.73
1:B:109:LYS:HB3	1:B:111:GLU:OE2	1.90	0.71
1:A:293:ARG:HG2	1:A:293:ARG:HH11	1.56	0.71
1:B:1:MSE:HB3	3:B:417:HOH:O	1.90	0.71
1:A:296:GLN:O	1:A:299:GLN:HG2	1.91	0.71
1:A:17:VAL:HA	1:A:29:GLU:OE2	1.92	0.70
1:B:16:GLN:CG	1:B:30:ARG:HB3	2.21	0.69
1:B:248:GLY:O	1:B:251:VAL:HG22	1.92	0.69
1:A:178:ILE:HG12	1:A:214:ILE:HG12	1.73	0.69
1:B:180:PRO:HG2	1:B:216:VAL:HG22	1.73	0.69
1:A:16:GLN:NE2	1:A:95:GLY:HA2	2.03	0.69
1:B:36:GLY:O	1:B:40:ILE:HD12	1.93	0.68
1:B:119:GLN:HA	1:B:122:GLU:OE2	1.93	0.68
1:B:196:ILE:HA	1:B:218:PHE:CZ	2.29	0.68
1:B:112:HIS:C	1:B:114:GLN:H	2.02	0.67
1:B:108:ILE:HD12	1:B:108:ILE:N	2.09	0.66
1:A:189:VAL:HG21	1:A:202:HIS:CE1	2.29	0.66
1:B:301:THR:HG23	1:B:301:THR:O	1.94	0.66
1:A:196:ILE:O	1:A:200:ILE:HG22	1.94	0.66
1:A:84:GLU:H	1:A:84:GLU:CD	2.02	0.66
1:B:189:VAL:HG11	1:B:202:HIS:ND1	2.11	0.66
1:B:234:VAL:HG22	1:B:302:ILE:HD13	1.77	0.65
1:A:166:ALA:O	1:A:170:VAL:HG22	1.96	0.65
1:A:287:THR:OG1	1:A:290:GLU:HG3	1.96	0.65
1:B:207:ILE:HD11	1:B:226:ALA:CB	2.26	0.65
1:B:298:LEU:HA	1:B:301:THR:HG22	1.79	0.65
1:A:243:ASN:OD1	1:A:245:VAL:HG22	1.96	0.65
1:B:200:ILE:CG1	1:B:201:PRO:HD3	2.22	0.65
1:A:101:LEU:HA	1:B:26:ASN:O	1.97	0.64
1:B:128:VAL:HG22	1:B:157:PHE:HB3	1.79	0.64
1:A:46:LEU:HD12	1:A:53:THR:HG21	1.80	0.64
1:A:148:THR:O	1:A:152:LYS:HG3	1.96	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:17:VAL:HG12	1:A:28:SER:HA	1.80	0.64
1:B:235:ASN:O	1:B:298:LEU:HD22	1.98	0.63
1:A:234:VAL:HG22	1:A:302:ILE:CD1	2.29	0.63
1:B:212:GLU:OE1	1:B:265:LEU:HD11	1.99	0.63
1:A:14:ILE:HD13	1:A:92:LYS:HB2	1.82	0.61
1:A:23:GLY:N	1:B:99:THR:HG22	2.15	0.61
1:A:17:VAL:CG2	1:A:20:PHE:HB2	2.30	0.61
1:A:204:GLN:CG	1:A:231:MSE:HE1	2.30	0.61
1:A:69:ASN:HD21	1:A:73:LYS:CE	2.13	0.61
1:A:150:ILE:O	1:A:153:GLU:HG2	2.00	0.61
1:A:178:ILE:CG1	1:A:214:ILE:HG12	2.30	0.61
1:B:237:PRO:HB2	1:B:281:PHE:HE2	1.64	0.61
1:A:69:ASN:HD21	1:A:73:LYS:NZ	1.98	0.61
1:A:48:ARG:HG2	1:A:48:ARG:HH11	1.66	0.61
1:B:149:GLN:HG3	1:B:153:GLU:OE2	2.01	0.61
1:B:293:ARG:NH2	1:B:294:LEU:HD21	2.17	0.60
1:B:46:LEU:HD13	1:B:53:THR:CG2	2.31	0.60
1:B:52:GLU:O	1:B:53:THR:HG23	2.02	0.60
1:B:296:GLN:O	1:B:299:GLN:HB3	2.02	0.59
1:B:60:GLY:HA3	1:B:85:GLY:O	2.02	0.59
1:A:120:LEU:HD11	1:A:147:MSE:HE2	1.85	0.58
1:A:165:GLU:O	1:A:169:GLU:HG2	2.03	0.58
1:B:220:GLY:O	1:B:221:ASP:HB2	2.02	0.58
1:B:287:THR:OG1	1:B:290:GLU:HG3	2.02	0.58
1:B:200:ILE:HG13	1:B:201:PRO:CD	2.22	0.58
1:A:153:GLU:HG3	1:A:154:ARG:NH1	2.18	0.58
1:B:189:VAL:HG12	1:B:189:VAL:O	2.04	0.58
1:A:16:GLN:HE21	1:A:95:GLY:CA	2.11	0.58
1:A:235:ASN:ND2	1:A:301:THR:HB	2.19	0.58
1:B:243:ASN:HD21	1:B:245:VAL:CG2	2.17	0.57
1:A:279:THR:HG23	1:A:285:PHE:HA	1.86	0.57
1:A:300:ARG:C	1:A:302:ILE:H	2.12	0.57
1:B:73:LYS:C	1:B:75:GLU:H	2.12	0.57
1:A:219:ALA:C	1:A:221:ASP:H	2.13	0.57
1:A:287:THR:HG23	1:A:290:GLU:OE1	2.05	0.57
1:B:46:LEU:CD1	1:B:53:THR:HG21	2.31	0.57
1:B:195:SER:HB3	1:B:198:ASP:HB2	1.87	0.57
1:A:189:VAL:HG21	1:A:202:HIS:HD1	1.67	0.56
1:A:69:ASN:HD21	1:A:73:LYS:HE3	1.70	0.56
1:A:235:ASN:HD22	1:A:301:THR:HB	1.71	0.56
1:B:181:ASN:OD1	1:B:183:HIS:HB2	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:243:ASN:ND2	1:B:245:VAL:H	2.03	0.56
1:A:293:ARG:HG2	1:A:293:ARG:NH1	2.18	0.56
1:B:152:LYS:C	1:B:154:ARG:H	2.12	0.56
1:A:84:GLU:CD	1:A:84:GLU:N	2.62	0.56
1:B:25:VAL:HG12	1:B:26:ASN:H	1.70	0.56
1:A:234:VAL:HG22	1:A:302:ILE:HD13	1.87	0.55
1:A:69:ASN:OD1	1:A:73:LYS:HE3	2.07	0.55
1:B:226:ALA:HB1	1:B:231:MSE:HE2	1.89	0.55
1:A:46:LEU:CD1	1:A:53:THR:HG21	2.37	0.55
1:A:15:VAL:O	1:A:93:ILE:HA	2.07	0.54
1:A:17:VAL:HG23	1:A:17:VAL:O	2.06	0.54
1:B:188:LEU:C	1:B:190:SER:H	2.14	0.54
1:B:243:ASN:ND2	1:B:244:SER:H	2.05	0.54
1:A:69:ASN:ND2	1:A:73:LYS:HE3	2.21	0.54
1:A:48:ARG:HG2	1:A:48:ARG:NH1	2.21	0.54
1:B:207:ILE:CD1	1:B:226:ALA:HB1	2.36	0.54
1:B:113:VAL:HG12	1:B:113:VAL:O	2.06	0.54
1:B:11:ILE:HG12	1:B:66:TYR:CD2	2.43	0.54
1:B:258:ALA:HB1	1:B:263:LYS:HE3	1.90	0.54
1:A:16:GLN:NE2	1:A:95:GLY:CA	2.68	0.53
1:B:197:GLU:HA	1:B:200:ILE:HG12	1.90	0.53
1:B:296:GLN:O	1:B:300:ARG:NE	2.39	0.53
1:B:237:PRO:HB2	1:B:281:PHE:CE2	2.42	0.53
1:A:22:GLN:O	1:A:24:VAL:N	2.42	0.53
1:A:58:PHE:CD1	1:A:108:ILE:HD13	2.43	0.53
1:A:296:GLN:HE21	1:A:299:GLN:CD	2.16	0.53
1:A:213:SER:C	1:A:214:ILE:HG13	2.33	0.53
1:B:32:ARG:NE	1:B:34:GLN:NE2	2.56	0.53
1:A:296:GLN:NE2	1:A:299:GLN:NE2	2.57	0.52
1:A:300:ARG:HG3	1:A:301:THR:N	2.24	0.52
1:A:193:ILE:HG21	1:A:199:ALA:HB2	1.91	0.52
1:B:109:LYS:HB3	1:B:111:GLU:CD	2.34	0.52
1:B:237:PRO:O	1:B:238:SER:HB3	2.09	0.52
1:B:14:ILE:N	1:B:14:ILE:HD12	2.24	0.52
1:B:144:TYR:HD2	1:B:147:MSE:HE3	1.73	0.52
1:B:232:PHE:HE2	1:B:266:GLU:HB2	1.73	0.52
1:B:162:THR:HG22	1:B:163:SER:N	2.17	0.52
1:B:180:PRO:O	1:B:216:VAL:HG13	2.10	0.52
1:B:112:HIS:C	1:B:114:GLN:N	2.66	0.52
1:B:129:LEU:HD23	1:B:151:ALA:HB2	1.90	0.52
1:A:278:ALA:HB3	1:A:286:CYS:HB3	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:296:GLN:HA	1:A:299:GLN:CD	2.36	0.51
1:B:189:VAL:O	1:B:190:SER:C	2.54	0.51
1:B:269:VAL:HB	1:B:270:PRO:HD3	1.91	0.51
1:A:264:SER:OG	1:A:266:GLU:HG3	2.10	0.51
1:B:298:LEU:O	1:B:301:THR:HG22	2.10	0.51
1:B:27:ARG:HH11	1:B:27:ARG:HG3	1.75	0.51
1:B:179:LYS:HG2	3:B:449:HOH:O	2.10	0.51
1:B:25:VAL:HG12	1:B:26:ASN:N	2.26	0.51
1:A:16:GLN:NE2	1:A:95:GLY:N	2.58	0.51
1:A:206:LEU:HD23	1:A:209:GLU:OE1	2.11	0.51
1:A:266:GLU:HG3	1:A:267:ASP:H	1.76	0.50
1:A:162:THR:HG22	1:A:163:SER:N	2.21	0.50
1:B:48:ARG:HE	1:B:285:PHE:HB2	1.76	0.50
1:A:115:ALA:HA	1:A:118:GLU:CD	2.36	0.50
1:B:107:LEU:C	1:B:108:ILE:HD12	2.36	0.50
1:A:22:GLN:O	1:A:23:GLY:C	2.54	0.50
1:A:200:ILE:HG13	1:A:201:PRO:N	2.26	0.50
1:A:16:GLN:NE2	1:A:95:GLY:H	2.10	0.50
1:B:171:LEU:HD11	1:B:188:LEU:HD11	1.94	0.50
1:B:52:GLU:O	1:B:53:THR:CG2	2.59	0.49
1:B:196:ILE:HA	1:B:218:PHE:CE2	2.47	0.49
1:A:120:LEU:C	1:A:122:GLU:H	2.20	0.49
1:A:236:VAL:CG1	1:A:237:PRO:HD2	2.42	0.49
1:A:300:ARG:C	1:A:302:ILE:N	2.70	0.49
1:B:59:LEU:HD13	1:B:80:PHE:CD2	2.48	0.49
1:A:219:ALA:O	1:A:221:ASP:N	2.45	0.49
1:B:15:VAL:HG23	1:B:28:SER:OG	2.12	0.49
1:B:179:LYS:CD	1:B:251:VAL:HG21	2.42	0.49
1:B:33:LYS:NZ	3:B:450:HOH:O	2.46	0.49
1:A:145:ARG:HD3	3:A:353:HOH:O	2.12	0.49
1:B:6:THR:O	1:B:9:PRO:HD3	2.13	0.49
1:A:46:LEU:HD13	1:A:53:THR:CG2	2.43	0.49
1:B:111:GLU:CD	1:B:111:GLU:N	2.65	0.48
1:B:271:PHE:CZ	1:B:288:ARG:NH1	2.81	0.48
1:A:227:SER:C	1:A:229:GLU:N	2.71	0.48
1:A:287:THR:N	1:A:290:GLU:OE1	2.47	0.48
1:A:133:GLY:O	1:A:162:THR:HG23	2.13	0.48
1:B:197:GLU:HG3	1:B:200:ILE:HD11	1.96	0.48
1:B:4:THR:OG1	1:B:55:ALA:HA	2.14	0.48
1:B:32:ARG:HH21	1:B:34:GLN:NE2	1.90	0.48
1:B:136:PRO:CG	1:B:139:MSE:HE3	2.44	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:69:ASN:CG	1:A:73:LYS:HE3	2.39	0.48
1:B:236:VAL:CG1	1:B:237:PRO:HD2	2.44	0.48
1:A:267:ASP:HA	3:A:324:HOH:O	2.14	0.47
1:A:193:ILE:HA	1:A:198:ASP:HB3	1.96	0.47
1:B:116:LEU:O	1:B:119:GLN:N	2.39	0.47
1:B:179:LYS:HD2	1:B:251:VAL:HG21	1.95	0.47
1:A:46:LEU:CD1	1:A:53:THR:CG2	2.92	0.47
1:B:233:HIS:CG	1:B:234:VAL:N	2.82	0.47
1:B:233:HIS:HB3	1:B:303:LYS:CG	2.44	0.47
1:B:304:LYS:H	1:B:304:LYS:CD	2.03	0.47
1:A:15:VAL:HG23	1:A:28:SER:HG	1.80	0.47
1:A:233:HIS:CG	1:A:234:VAL:N	2.82	0.47
1:B:144:TYR:HB2	1:B:170:VAL:HG22	1.97	0.47
1:B:115:ALA:O	1:B:118:GLU:HB3	2.15	0.47
1:B:183:HIS:O	1:B:186:SER:OG	2.27	0.47
1:B:251:VAL:HG23	1:B:252:VAL:N	2.28	0.47
1:B:38:LYS:HG2	1:B:249:ASP:OD2	2.15	0.47
1:B:179:LYS:HA	1:B:215:LEU:O	2.13	0.47
1:B:243:ASN:HD22	1:B:244:SER:H	1.62	0.47
1:A:17:VAL:CG1	1:A:28:SER:HA	2.44	0.47
1:B:11:ILE:HG12	1:B:66:TYR:HD2	1.80	0.47
1:A:227:SER:C	1:A:229:GLU:H	2.23	0.47
1:A:241:VAL:HG23	1:A:280:ALA:O	2.14	0.47
1:A:297:GLN:O	1:A:300:ARG:HG2	2.14	0.47
1:B:243:ASN:ND2	1:B:245:VAL:HG23	2.23	0.47
1:A:236:VAL:HG13	1:A:277:SER:OG	2.15	0.47
1:B:132:ALA:HA	1:B:161:ASP:O	2.15	0.47
1:B:73:LYS:C	1:B:75:GLU:N	2.73	0.46
1:A:59:LEU:HD22	1:A:80:PHE:CG	2.51	0.46
1:A:189:VAL:HG22	1:A:189:VAL:O	2.15	0.46
1:B:295:GLN:HG3	1:B:296:GLN:N	2.30	0.46
1:A:150:ILE:HA	1:A:153:GLU:CD	2.41	0.46
1:A:236:VAL:HG13	1:A:237:PRO:HD2	1.96	0.46
1:B:48:ARG:HE	1:B:285:PHE:CB	2.29	0.46
1:B:222:GLY:HA2	1:B:236:VAL:HG23	1.98	0.46
1:B:280:ALA:C	1:B:282:SER:H	2.24	0.46
1:A:115:ALA:HA	1:A:118:GLU:OE2	2.16	0.46
1:B:231:MSE:HG3	1:B:305:GLU:HB3	1.97	0.46
1:B:10:SER:HA	1:B:87:THR:HG22	1.97	0.46
1:A:108:ILE:HD12	1:A:139:MSE:HE2	1.96	0.46
1:A:295:GLN:HE21	1:A:295:GLN:HB3	1.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:271:PHE:HZ	1:B:288:ARG:NH1	2.14	0.46
1:A:269:VAL:HB	1:A:270:PRO:HD3	1.96	0.46
1:A:226:ALA:HB2	1:A:231:MSE:HG3	1.98	0.46
1:B:59:LEU:HD22	1:B:80:PHE:CG	2.51	0.46
1:B:236:VAL:HG12	1:B:237:PRO:HD2	1.98	0.46
1:B:140:PRO:C	1:B:142:THR:H	2.23	0.45
1:B:196:ILE:HG12	1:B:196:ILE:O	2.15	0.45
1:B:297:GLN:O	1:B:300:ARG:HG2	2.16	0.45
1:B:10:SER:HB3	1:B:88:ARG:HG3	1.98	0.45
1:B:152:LYS:C	1:B:154:ARG:N	2.75	0.45
1:A:16:GLN:O	1:A:29:GLU:HG2	2.17	0.45
1:B:136:PRO:HG2	1:B:139:MSE:HE3	1.97	0.45
1:A:33:LYS:HD2	1:B:62:PHE:HE2	1.81	0.45
1:A:120:LEU:C	1:A:122:GLU:N	2.74	0.45
1:A:167:LEU:O	1:A:170:VAL:HG23	2.16	0.45
1:A:167:LEU:HA	1:A:170:VAL:CG2	2.47	0.45
1:B:193:ILE:HG22	1:B:194:ALA:N	2.32	0.45
1:A:95:GLY:O	1:A:96:LYS:C	2.60	0.45
1:B:129:LEU:CD2	1:B:151:ALA:HB2	2.47	0.45
1:A:241:VAL:HA	1:A:280:ALA:O	2.18	0.44
1:A:296:GLN:HE21	1:A:299:GLN:NE2	2.15	0.44
1:B:243:ASN:ND2	1:B:244:SER:N	2.64	0.44
1:A:92:LYS:HE2	3:A:366:HOH:O	2.17	0.44
1:A:242:ARG:HE	1:A:242:ARG:HA	1.83	0.44
1:B:287:THR:HG23	1:B:290:GLU:OE2	2.17	0.44
1:A:38:LYS:HG2	1:A:249:ASP:OD1	2.17	0.44
1:A:237:PRO:O	1:A:238:SER:HB3	2.18	0.44
1:A:243:ASN:OD1	1:A:244:SER:N	2.50	0.44
1:B:218:PHE:O	1:B:219:ALA:C	2.60	0.44
1:B:16:GLN:HG3	1:B:30:ARG:HB3	1.98	0.44
1:B:34:GLN:HB2	1:B:35:PRO:HD2	2.00	0.44
1:B:150:ILE:O	1:B:154:ARG:HG3	2.18	0.44
1:A:203:VAL:HG11	1:A:226:ALA:CB	2.48	0.43
1:A:38:LYS:HD2	1:A:133:GLY:HA2	1.99	0.43
1:B:9:PRO:HG3	1:B:59:LEU:CD1	2.48	0.43
1:B:183:HIS:O	1:B:186:SER:N	2.51	0.43
1:A:98:GLU:O	1:B:23:GLY:O	2.36	0.43
1:B:193:ILE:HA	1:B:198:ASP:OD1	2.18	0.43
1:B:78:LEU:N	1:B:78:LEU:HD23	2.34	0.43
1:A:197:GLU:O	1:A:200:ILE:HG23	2.19	0.43
1:B:14:ILE:HD12	1:B:14:ILE:H	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:78:LEU:HD23	1:A:78:LEU:O	2.19	0.43
1:B:196:ILE:HD11	1:B:305:GLU:OE1	2.18	0.43
1:B:301:THR:O	1:B:301:THR:CG2	2.63	0.43
1:A:211:ILE:HG21	1:A:214:ILE:HD11	2.01	0.43
1:B:287:THR:O	1:B:291:VAL:HG23	2.19	0.43
1:B:131:LEU:O	1:B:160:VAL:HA	2.19	0.43
1:B:115:ALA:O	1:B:119:GLN:HG3	2.19	0.42
1:B:298:LEU:CA	1:B:301:THR:HG22	2.48	0.42
1:A:15:VAL:HG11	1:B:101:LEU:HD21	2.00	0.42
1:A:21:GLN:O	1:A:22:GLN:O	2.37	0.42
1:A:296:GLN:HE21	1:A:296:GLN:HA	1.83	0.42
1:B:48:ARG:HG2	1:B:48:ARG:HH11	1.84	0.42
1:A:111:GLU:CD	1:A:111:GLU:H	2.28	0.42
1:A:145:ARG:HD2	2:A:308:PO4:O2	2.19	0.42
1:A:219:ALA:C	1:A:221:ASP:N	2.77	0.42
1:B:15:VAL:O	1:B:15:VAL:HG13	2.18	0.42
1:B:24:VAL:HB	1:B:25:VAL:H	1.71	0.42
1:A:237:PRO:HD3	1:A:298:LEU:HD21	2.02	0.42
1:A:267:ASP:O	1:A:270:PRO:HD2	2.19	0.42
1:A:153:GLU:HG3	1:A:154:ARG:HH11	1.84	0.42
1:A:287:THR:HG23	1:A:290:GLU:CD	2.45	0.42
1:B:162:THR:CG2	1:B:163:SER:N	2.81	0.42
1:B:52:GLU:C	1:B:53:THR:HG23	2.44	0.42
1:B:86:ASP:O	1:B:87:THR:C	2.63	0.42
1:B:170:VAL:O	1:B:173:ALA:HB3	2.20	0.42
1:B:232:PHE:CE2	1:B:266:GLU:HB2	2.53	0.42
1:A:226:ALA:HB1	1:A:231:MSE:HE2	2.03	0.41
1:B:222:GLY:HA3	1:B:233:HIS:CE1	2.56	0.41
1:A:89:ILE:HG13	3:B:450:HOH:O	2.19	0.41
1:A:234:VAL:HG22	1:A:302:ILE:HD12	2.02	0.41
1:B:109:LYS:O	1:B:112:HIS:HB2	2.20	0.41
1:B:20:PHE:CE1	1:B:26:ASN:ND2	2.89	0.41
1:A:47:LYS:HE2	1:A:74:GLU:O	2.20	0.41
1:B:2:ILE:HG13	3:B:417:HOH:O	2.19	0.41
1:B:15:VAL:HG22	1:B:17:VAL:HG23	2.02	0.41
1:A:260:GLN:C	1:A:262:GLY:H	2.29	0.41
1:B:9:PRO:CG	1:B:58:PHE:O	2.67	0.41
1:A:266:GLU:HG3	1:A:267:ASP:N	2.35	0.41
1:B:32:ARG:NH2	1:B:34:GLN:NE2	2.60	0.41
1:B:97:GLN:O	1:B:98:GLU:C	2.64	0.41
1:A:145:ARG:NH1	2:A:308:PO4:O4	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:205:ARG:HG2	1:A:205:ARG:HH11	1.86	0.41
1:A:60:GLY:HA3	1:A:85:GLY:O	2.21	0.40
1:A:61:GLY:HA3	1:A:86:ASP:OD1	2.21	0.40
1:B:10:SER:HA	1:B:87:THR:CG2	2.51	0.40
1:B:186:SER:HA	1:B:191:LYS:O	2.21	0.40
1:A:12:ASP:O	1:A:33:LYS:HA	2.21	0.40
1:A:296:GLN:NE2	1:A:299:GLN:HE22	2.18	0.40
1:A:115:ALA:O	1:A:118:GLU:HB2	2.22	0.40
1:B:234:VAL:HG22	1:B:302:ILE:CD1	2.49	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	304/306 (99%)	274 (90%)	21 (7%)	9 (3%)	3	1
1	B	304/306 (99%)	271 (89%)	21 (7%)	12 (4%)	2	0
All	All	608/612 (99%)	545 (90%)	42 (7%)	21 (4%)	3	1

All (21) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	19	ASN
1	A	22	GLN
1	A	23	GLY
1	B	221	ASP
1	A	96	LYS
1	A	220	GLY
1	B	21	GLN
1	B	106	PRO
1	B	219	ALA

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Mol	Chain	Res	Type
1	B	245	VAL
1	A	238	SER
1	A	246	GLY
1	B	79	SER
1	A	299	GLN
1	B	190	SER
1	B	20	PHE
1	B	141	GLN
1	B	153	GLU
1	B	194	ALA
1	B	24	VAL
1	A	9	PRO

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	239/243 (98%)	229 (96%)	10 (4%)	26	28
1	B	241/243 (99%)	230 (95%)	11 (5%)	24	25
All	All	480/486 (99%)	459 (96%)	21 (4%)	25	26

All (21) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	59	LEU
1	A	78	LEU
1	A	84	GLU
1	A	101	LEU
1	A	149	GLN
1	A	170	VAL
1	A	200	ILE
1	A	213	SER
1	A	295	GLN
1	A	296	GLN
1	B	16	GLN

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Mol	Chain	Res	Type
1	B	59	LEU
1	B	84	GLU
1	B	86	ASP
1	B	108	ILE
1	B	111	GLU
1	B	122	GLU
1	B	196	ILE
1	B	295	GLN
1	B	300	ARG
1	B	304	LYS

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

Mol	Chain	Res	Type
1	A	16	GLN
1	A	69	ASN
1	A	149	GLN
1	A	295	GLN
1	A	296	GLN
1	A	297	GLN
1	B	26	ASN
1	B	34	GLN
1	B	149	GLN
1	B	243	ASN
1	B	260	GLN
1	B	299	GLN

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 oligosaccharides 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	PO4	A	307	-	4,4,4	1.70	0	6,6,6	0.45	0
2	PO4	A	309	-	4,4,4	1.57	0	6,6,6	0.47	0
2	PO4	B	407	-	4,4,4	1.63	0	6,6,6	0.48	0
2	PO4	A	308	-	4,4,4	1.72	1 (25%)	6,6,6	0.48	0

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	308	PO4	P-O4	-2.01	1.48	1.54

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	308	PO4	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	302/306 (98%)	0.75	25 (8%) 17 18	22, 43, 72, 80	0
1	B	302/306 (98%)	1.35	65 (21%) 2 2	32, 58, 75, 83	0
All	All	604/612 (98%)	1.05	90 (14%) 5 5	22, 50, 74, 83	0

All (90) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	219	ALA	4.4
1	B	100	GLU	4.0
1	B	138	ALA	3.8
1	B	22	GLN	3.7
1	B	193	ILE	3.6
1	B	85	GLY	3.6
1	A	236	VAL	3.5
1	B	284	GLY	3.4
1	B	140	PRO	3.3
1	A	99	THR	3.2
1	A	284	GLY	3.2
1	B	112	HIS	3.2
1	B	83	VAL	3.1
1	B	81	ILE	3.0
1	B	194	ALA	3.0
1	B	99	THR	3.0
1	A	24	VAL	2.9
1	B	296	GLN	2.9
1	B	23	GLY	2.9
1	B	196	ILE	2.8
1	B	21	GLN	2.8
1	B	245	VAL	2.8
1	A	23	GLY	2.8
1	B	50	GLY	2.8

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Mol	Chain	Res	Type	RSRZ
1	B	117	LEU	2.8
1	B	24	VAL	2.8
1	B	232	PHE	2.7
1	A	15	VAL	2.7
1	B	220	GLY	2.7
1	A	290	GLU	2.7
1	B	182	HIS	2.7
1	B	195	SER	2.7
1	B	25	VAL	2.7
1	B	95	GLY	2.7
1	B	239	GLY	2.7
1	B	262	GLY	2.7
1	A	282	SER	2.6
1	A	302	ILE	2.6
1	B	113	VAL	2.6
1	A	262	GLY	2.6
1	B	191	LYS	2.6
1	B	236	VAL	2.5
1	A	14	ILE	2.5
1	A	241	VAL	2.5
1	B	282	SER	2.5
1	B	80	PHE	2.5
1	A	211	ILE	2.5
1	B	302	ILE	2.5
1	A	70	ALA	2.5
1	B	168	HIS	2.5
1	B	78	LEU	2.4
1	B	104	THR	2.4
1	B	108	ILE	2.4
1	B	121	THR	2.3
1	B	237	PRO	2.3
1	B	243	ASN	2.3
1	B	238	SER	2.3
1	B	189	VAL	2.3
1	A	237	PRO	2.3
1	A	244	SER	2.3
1	A	299	GLN	2.3
1	B	70	ALA	2.2
1	B	281	PHE	2.2
1	B	283	ASP	2.2
1	B	57	GLY	2.2
1	B	17	VAL	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	64	GLY	2.2
1	B	230	GLY	2.1
1	B	183	HIS	2.1
1	B	235	ASN	2.1
1	A	240	GLU	2.1
1	B	299	GLN	2.1
1	B	233	HIS	2.1
1	A	247	ALA	2.1
1	B	55	ALA	2.1
1	B	10	SER	2.1
1	B	292	GLU	2.1
1	B	181	ASN	2.1
1	A	17	VAL	2.1
1	B	218	PHE	2.1
1	A	212	GLU	2.0
1	B	186	SER	2.1
1	B	107	LEU	2.0
1	A	168	HIS	2.0
1	B	192	PRO	2.0
1	B	301	THR	2.0
1	A	96	LYS	2.0
1	A	243	ASN	2.0
1	A	16	GLN	2.0
1	B	222	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 oligosaccharides 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($\text{\AA}^2$)	Q<0.9
2	PO4	B	407	5/5	0.77	0.12	84,84,85,86	0
2	PO4	A	307	5/5	0.82	0.12	71,72,73,74	0
2	PO4	A	309	5/5	0.85	0.12	70,70,72,72	0
2	PO4	A	308	5/5	0.93	0.11	83,83,83,84	0

6.5 Other polymers [i](#)

There are no such residues in this entry.