



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 21, 2023 – 07:49 PM EDT

PDB ID : 2Q5R
Title : Structure of apo Staphylococcus aureus D-tagatose-6-phosphate kinase
Authors : McGrath, T.E.; Soloveychik, M.; Romanov, V.; Thambipillai, D.; Dharamsi, A.; Virag, C.; Domagala, M.; Pai, E.F.; Edwards, A.M.; Battaile, K.; Chirgadze, N.Y.
Deposited on : 2007-06-01
Resolution : 2.30 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 : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.35
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) : 2.35

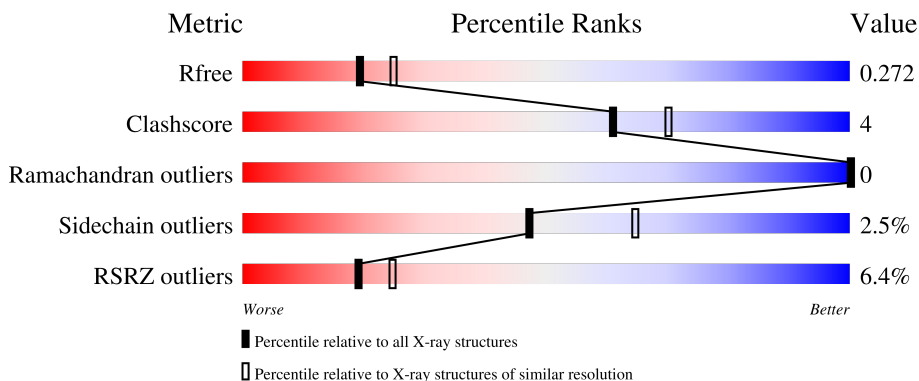
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

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	330	
1	B	330	
1	C	330	
1	D	330	

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 10117 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 Tagatose-6-phosphate kinase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	S	Se			
1	A	318	2459	1560	416	478	3	2	0	3	0
1	B	312	2413	1531	406	471	3	2	0	2	0
1	C	303	2350	1494	395	456	3	2	0	3	0
1	D	310	2396	1519	404	467	3	3	0	2	0

There are 88 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MSE	-	cloning artifact	UNP Q5HE12
A	-18	GLY	-	cloning artifact	UNP Q5HE12
A	-17	SER	-	cloning artifact	UNP Q5HE12
A	-16	SER	-	cloning artifact	UNP Q5HE12
A	-15	HIS	-	cloning artifact	UNP Q5HE12
A	-14	HIS	-	cloning artifact	UNP Q5HE12
A	-13	HIS	-	cloning artifact	UNP Q5HE12
A	-12	HIS	-	cloning artifact	UNP Q5HE12
A	-11	HIS	-	cloning artifact	UNP Q5HE12
A	-10	HIS	-	cloning artifact	UNP Q5HE12
A	-9	SER	-	cloning artifact	UNP Q5HE12
A	-8	SER	-	cloning artifact	UNP Q5HE12
A	-7	GLY	-	cloning artifact	UNP Q5HE12
A	-6	LEU	-	cloning artifact	UNP Q5HE12
A	-5	VAL	-	cloning artifact	UNP Q5HE12
A	-4	PRO	-	cloning artifact	UNP Q5HE12
A	-3	ARG	-	cloning artifact	UNP Q5HE12
A	-2	GLY	-	cloning artifact	UNP Q5HE12
A	-1	SER	-	cloning artifact	UNP Q5HE12
A	0	HIS	-	cloning artifact	UNP Q5HE12
A	1	MSE	MET	modified residue	UNP Q5HE12

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
A	282	MSE	MET	modified residue	UNP Q5HE12
B	-19	MSE	-	cloning artifact	UNP Q5HE12
B	-18	GLY	-	cloning artifact	UNP Q5HE12
B	-17	SER	-	cloning artifact	UNP Q5HE12
B	-16	SER	-	cloning artifact	UNP Q5HE12
B	-15	HIS	-	cloning artifact	UNP Q5HE12
B	-14	HIS	-	cloning artifact	UNP Q5HE12
B	-13	HIS	-	cloning artifact	UNP Q5HE12
B	-12	HIS	-	cloning artifact	UNP Q5HE12
B	-11	HIS	-	cloning artifact	UNP Q5HE12
B	-10	HIS	-	cloning artifact	UNP Q5HE12
B	-9	SER	-	cloning artifact	UNP Q5HE12
B	-8	SER	-	cloning artifact	UNP Q5HE12
B	-7	GLY	-	cloning artifact	UNP Q5HE12
B	-6	LEU	-	cloning artifact	UNP Q5HE12
B	-5	VAL	-	cloning artifact	UNP Q5HE12
B	-4	PRO	-	cloning artifact	UNP Q5HE12
B	-3	ARG	-	cloning artifact	UNP Q5HE12
B	-2	GLY	-	cloning artifact	UNP Q5HE12
B	-1	SER	-	cloning artifact	UNP Q5HE12
B	0	HIS	-	cloning artifact	UNP Q5HE12
B	1	MSE	MET	modified residue	UNP Q5HE12
B	282	MSE	MET	modified residue	UNP Q5HE12
C	-19	MSE	-	cloning artifact	UNP Q5HE12
C	-18	GLY	-	cloning artifact	UNP Q5HE12
C	-17	SER	-	cloning artifact	UNP Q5HE12
C	-16	SER	-	cloning artifact	UNP Q5HE12
C	-15	HIS	-	cloning artifact	UNP Q5HE12
C	-14	HIS	-	cloning artifact	UNP Q5HE12
C	-13	HIS	-	cloning artifact	UNP Q5HE12
C	-12	HIS	-	cloning artifact	UNP Q5HE12
C	-11	HIS	-	cloning artifact	UNP Q5HE12
C	-10	HIS	-	cloning artifact	UNP Q5HE12
C	-9	SER	-	cloning artifact	UNP Q5HE12
C	-8	SER	-	cloning artifact	UNP Q5HE12
C	-7	GLY	-	cloning artifact	UNP Q5HE12
C	-6	LEU	-	cloning artifact	UNP Q5HE12
C	-5	VAL	-	cloning artifact	UNP Q5HE12
C	-4	PRO	-	cloning artifact	UNP Q5HE12
C	-3	ARG	-	cloning artifact	UNP Q5HE12
C	-2	GLY	-	cloning artifact	UNP Q5HE12
C	-1	SER	-	cloning artifact	UNP Q5HE12

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
C	0	HIS	-	cloning artifact	UNP Q5HE12
C	1	MSE	MET	modified residue	UNP Q5HE12
C	282	MSE	MET	modified residue	UNP Q5HE12
D	-19	MSE	-	cloning artifact	UNP Q5HE12
D	-18	GLY	-	cloning artifact	UNP Q5HE12
D	-17	SER	-	cloning artifact	UNP Q5HE12
D	-16	SER	-	cloning artifact	UNP Q5HE12
D	-15	HIS	-	cloning artifact	UNP Q5HE12
D	-14	HIS	-	cloning artifact	UNP Q5HE12
D	-13	HIS	-	cloning artifact	UNP Q5HE12
D	-12	HIS	-	cloning artifact	UNP Q5HE12
D	-11	HIS	-	cloning artifact	UNP Q5HE12
D	-10	HIS	-	cloning artifact	UNP Q5HE12
D	-9	SER	-	cloning artifact	UNP Q5HE12
D	-8	SER	-	cloning artifact	UNP Q5HE12
D	-7	GLY	-	cloning artifact	UNP Q5HE12
D	-6	LEU	-	cloning artifact	UNP Q5HE12
D	-5	VAL	-	cloning artifact	UNP Q5HE12
D	-4	PRO	-	cloning artifact	UNP Q5HE12
D	-3	ARG	-	cloning artifact	UNP Q5HE12
D	-2	GLY	-	cloning artifact	UNP Q5HE12
D	-1	SER	-	cloning artifact	UNP Q5HE12
D	0	HIS	-	cloning artifact	UNP Q5HE12
D	1	MSE	MET	modified residue	UNP Q5HE12
D	282	MSE	MET	modified residue	UNP Q5HE12

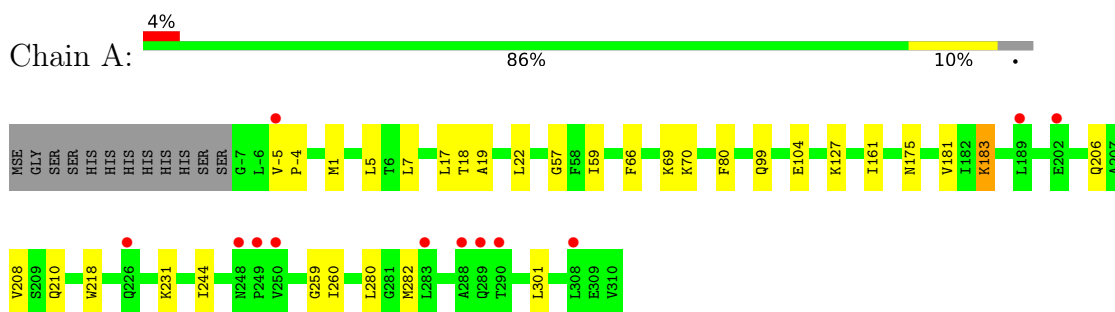
- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	122	Total O 122 122	0	0
2	B	136	Total O 136 136	0	0
2	C	99	Total O 99 99	0	0
2	D	142	Total O 142 142	0	0

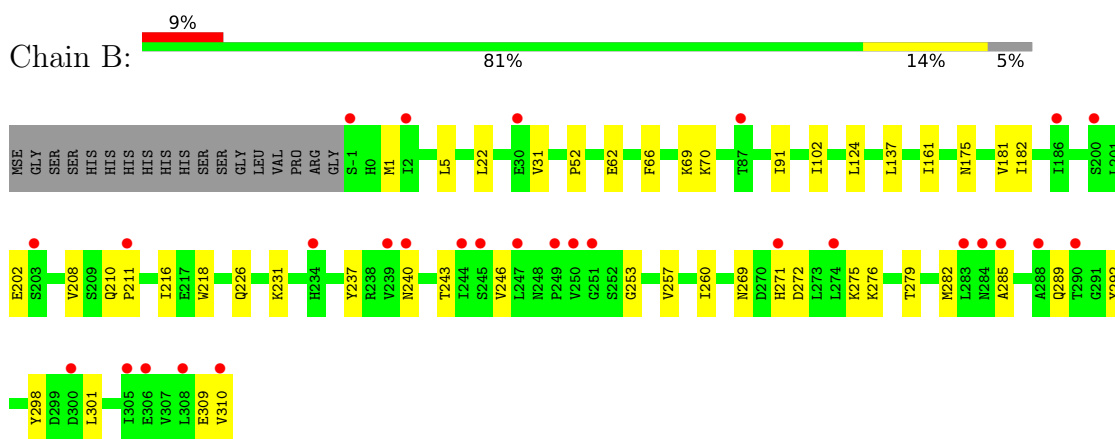
3 Residue-property plots [i](#)

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.

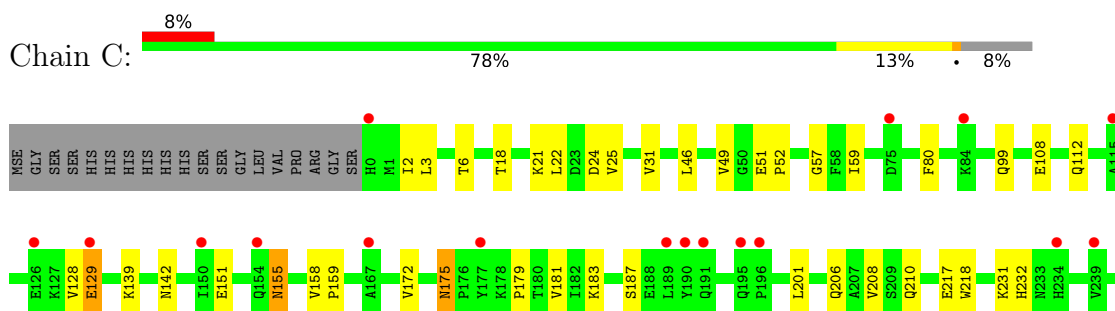
- Molecule 1: Tagatose-6-phosphate kinase

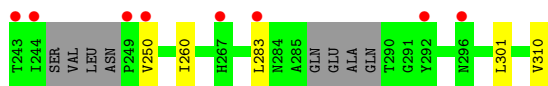


- Molecule 1: Tagatose-6-phosphate kinase

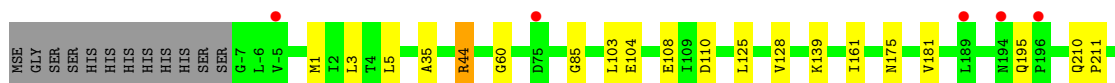
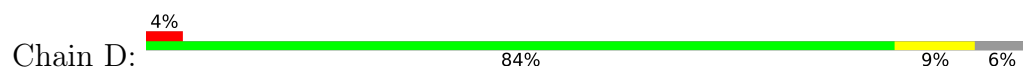


- Molecule 1: Tagatose-6-phosphate kinase





- Molecule 1: Tagatose-6-phosphate kinase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	76.95Å 96.94Å 94.48Å 90.00° 94.42° 90.00°	Depositor
Resolution (Å)	14.99 – 2.30 14.99 – 2.30	Depositor EDS
% Data completeness (in resolution range)	90.1 (14.99-2.30) 90.1 (14.99-2.30)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.85 (at 2.29Å)	Xtrriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.215 , 0.283 0.209 , 0.272	Depositor DCC
R_{free} test set	2729 reflections (4.94%)	wwPDB-VP
Wilson B-factor (Å ²)	39.9	Xtrriage
Anisotropy	0.053	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 43.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	10117	wwPDB-VP
Average B, all atoms (Å ²)	42.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.63% 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	0.44	0/2508	0.58	0/3403
1	B	0.59	3/2458 (0.1%)	0.59	0/3335
1	C	0.64	4/2397 (0.2%)	0.58	0/3250
1	D	0.48	0/2440	0.59	1/3306 (0.0%)
All	All	0.54	7/9803 (0.1%)	0.59	1/13294 (0.0%)

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	155	ASN	CG-OD1	15.47	1.57	1.24
1	C	155	ASN	CG-ND2	14.75	1.69	1.32
1	B	202	GLU	CG-CD	6.67	1.61	1.51
1	C	151	GLU	CD-OE2	5.53	1.31	1.25
1	C	151	GLU	CD-OE1	5.46	1.31	1.25
1	B	240	ASN	C-N	5.25	1.46	1.34
1	B	310	VAL	CB-CG2	5.24	1.63	1.52

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	44	ARG	NE-CZ-NH2	-5.12	117.74	120.30

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	2459	0	2482	25	0
1	B	2413	0	2430	24	0
1	C	2350	0	2365	28	0
1	D	2396	0	2404	15	0
2	A	122	0	0	1	0
2	B	136	0	0	0	0
2	C	99	0	0	3	0
2	D	142	0	0	2	0
All	All	10117	0	9681	86	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 4.

All (86) 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:C:155:ASN:ND2	1:C:155:ASN:CG	1.69	1.46
1:C:129:GLU:O	1:C:159:PRO:HD2	1.70	0.91
1:A:183:LYS:O	1:A:183:LYS:HG2	1.77	0.83
1:A:244:ILE:HD13	1:A:282:MSE:HG2	1.67	0.75
1:A:244:ILE:HG21	1:A:282:MSE:HE3	1.74	0.70
1:B:181:VAL:HG11	1:B:260:ILE:HG21	1.76	0.67
1:A:59:ILE:HG12	1:A:80:PHE:HB3	1.79	0.65
1:A:66:PHE:CZ	1:A:70:LYS:HE2	2.33	0.64
1:B:66:PHE:CZ	1:B:70[B]:LYS:HE3	2.35	0.62
1:D:35:ALA:O	1:D:44:ARG:NH2	2.29	0.61
1:D:280:LEU:HD23	1:D:283:LEU:HD12	1.84	0.60
1:C:155:ASN:ND2	1:C:155:ASN:CB	2.61	0.60
1:C:31:VAL:HG21	1:D:104:GLU:HG2	1.84	0.59
1:C:6:THR:O	1:C:57:GLY:HA3	2.02	0.59
1:A:282:MSE:HE2	1:A:301:LEU:HD13	1.87	0.57
1:C:59:ILE:HG12	1:C:80:PHE:HB3	1.86	0.56
1:B:279:THR:HG23	1:B:301:LEU:HD22	1.88	0.56
1:C:181:VAL:HG22	1:C:218:TRP:HB2	1.87	0.56
1:A:17[B]:LEU:HG	1:A:19:ALA:O	2.06	0.55
1:A:22:LEU:HD11	1:B:22:LEU:HD11	1.88	0.55
1:A:69[B]:LYS:HG3	1:B:62:GLU:OE2	2.07	0.55
1:A:244:ILE:CD1	1:A:282:MSE:HG2	2.37	0.55
1:D:211:PRO:HA	1:D:214:GLU:HG3	1.89	0.54
1:A:7:LEU:HD23	1:A:57:GLY:HA2	1.90	0.53
1:A:59:ILE:HG12	1:A:80:PHE:CB	2.39	0.52
1:B:282:MSE:SE	1:B:301:LEU:HD21	2.60	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:195:GLN:NE2	2:D:437:HOH:O	2.41	0.52
1:D:1[A]:MSE:SE	2:D:403:HOH:O	2.77	0.52
1:A:181:VAL:HG11	1:A:260:ILE:HG21	1.92	0.52
1:A:244:ILE:CG2	1:A:282:MSE:HE3	2.39	0.51
1:C:51:GLU:OE1	1:C:52:PRO:HD2	2.12	0.50
1:C:108:GLU:HG3	1:C:139:LYS:HD3	1.95	0.49
1:C:129:GLU:O	1:C:159:PRO:CD	2.53	0.49
1:A:161:ILE:HD12	1:A:161:ILE:N	2.28	0.48
1:A:104:GLU:HG2	1:B:31:VAL:HG21	1.95	0.48
1:B:181:VAL:HG22	1:B:218:TRP:HB2	1.96	0.48
1:C:99:GLN:OE1	1:C:250:VAL:HG22	2.13	0.48
1:C:181:VAL:HG11	1:C:260:ILE:HG21	1.95	0.48
1:A:69[A]:LYS:HD2	1:B:62:GLU:OE2	2.13	0.48
1:C:179:PRO:HA	2:C:400:HOH:O	2.13	0.47
1:B:276:LYS:HG3	1:B:298:TYR:OH	2.15	0.47
1:B:161:ILE:HD12	1:B:161:ILE:N	2.30	0.47
1:D:108:GLU:HG3	1:D:139:LYS:HG2	1.96	0.46
1:B:289:GLN:HB2	1:B:292:TYR:HB3	1.97	0.46
1:C:250:VAL:HG21	2:C:340:HOH:O	2.15	0.46
1:A:208:VAL:HG23	1:A:231:LYS:HD2	1.96	0.46
1:C:206:GLN:O	1:C:210:GLN:HG2	2.15	0.46
1:B:246:VAL:HG12	1:B:285:ALA:HB1	1.97	0.46
1:C:283:LEU:HD12	1:C:301:LEU:HD12	1.97	0.45
1:B:237:TYR:CE1	1:B:309:GLU:HG3	2.52	0.45
1:B:271:HIS:O	1:B:275:LYS:HG3	2.17	0.45
1:C:208:VAL:HG12	1:C:231:LYS:HD3	1.98	0.44
1:D:181:VAL:HG11	1:D:260:ILE:HG21	1.98	0.44
1:C:21:LYS:HE3	1:C:21:LYS:HB2	1.81	0.44
1:C:158:VAL:HA	1:C:159:PRO:HD3	1.85	0.44
1:A:1:MSE:HE2	1:A:127:LYS:O	2.18	0.43
1:B:253:GLY:O	1:B:257:VAL:HG23	2.17	0.43
1:D:60:GLY:HA3	1:D:85:GLY:O	2.17	0.43
1:B:91[B]:ILE:HG23	1:B:102:ILE:HB	1.99	0.43
1:B:182:ILE:HG12	1:B:216:ILE:HG21	2.00	0.43
1:D:253:GLY:O	1:D:257:VAL:HG23	2.18	0.43
1:A:181:VAL:HG22	1:A:218:TRP:HB2	2.00	0.43
1:A:259:GLY:CA	1:A:280:LEU:HD12	2.49	0.43
1:D:3:LEU:HB2	1:D:128:VAL:HG11	2.00	0.43
1:B:1:MSE:HA	1:B:52:PRO:HB2	2.01	0.43
1:C:46:LEU:HA	1:C:49:VAL:HG22	2.01	0.43
1:A:99:GLN:NE2	2:A:417:HOH:O	2.52	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:210:GLN:HG3	1:B:211:PRO:HD2	2.01	0.42
1:B:69:LYS:HB3	1:B:69:LYS:HE2	1.79	0.42
1:C:217:GLU:HG2	1:C:232:HIS:CD2	2.55	0.42
1:C:172:VAL:HA	1:C:175:ASN:HD22	1.84	0.42
1:B:62:GLU:H	1:B:62:GLU:CD	2.23	0.41
1:C:112:GLN:H	1:C:112:GLN:CD	2.23	0.41
1:B:279:THR:HA	1:B:301:LEU:HD22	2.01	0.41
1:C:25[A]:VAL:HG13	1:D:103:LEU:HG	2.01	0.41
1:C:142:ASN:HB3	2:C:394:HOH:O	2.20	0.41
1:C:201:LEU:CD1	1:C:310:VAL:HG12	2.50	0.41
1:A:206:GLN:O	1:A:210:GLN:HG2	2.20	0.41
1:C:2:ILE:HD12	1:C:51:GLU:HB3	2.03	0.41
1:D:110:ASP:OD1	1:D:110:ASP:C	2.59	0.41
1:A:-5:VAL:HA	1:A:-4:PRO:HD3	1.93	0.41
1:A:183:LYS:O	1:A:183:LYS:CG	2.58	0.41
1:B:208:VAL:HG13	1:B:231:LYS:HD2	2.02	0.41
1:D:161:ILE:HD13	1:D:261:THR:HG23	2.03	0.41
1:D:231:LYS:HE2	1:D:233:ASN:O	2.21	0.41
1:C:3:LEU:HB2	1:C:128:VAL:HG11	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	319/330 (97%)	313 (98%)	6 (2%)	0	100	100
1	B	312/330 (94%)	305 (98%)	7 (2%)	0	100	100
1	C	300/330 (91%)	293 (98%)	7 (2%)	0	100	100
1	D	306/330 (93%)	302 (99%)	4 (1%)	0	100	100
All	All	1237/1320 (94%)	1213 (98%)	24 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	272/277 (98%)	268 (98%)	4 (2%)	65	79
1	B	267/277 (96%)	259 (97%)	8 (3%)	41	57
1	C	260/277 (94%)	252 (97%)	8 (3%)	40	55
1	D	264/277 (95%)	257 (97%)	7 (3%)	44	61
All	All	1063/1108 (96%)	1036 (98%)	27 (2%)	47	65

All (27) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	5	LEU
1	A	18	THR
1	A	175	ASN
1	A	183	LYS
1	B	5	LEU
1	B	124	LEU
1	B	137	LEU
1	B	175	ASN
1	B	226	GLN
1	B	243	THR
1	B	269	ASN
1	B	272	ASP
1	C	18[A]	THR
1	C	18[B]	THR
1	C	22	LEU
1	C	24	ASP
1	C	129	GLU
1	C	175	ASN
1	C	183	LYS
1	C	187	SER
1	D	5	LEU
1	D	125	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	D	175	ASN
1	D	210	GLN
1	D	226	GLN
1	D	243	THR
1	D	252	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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](#)

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 [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	316/330 (95%)	0.34	12 (3%) 40 47	36, 42, 49, 53	0
1	B	310/330 (93%)	0.51	29 (9%) 8 11	35, 43, 51, 55	0
1	C	301/330 (91%)	0.59	25 (8%) 11 15	36, 43, 49, 55	0
1	D	308/330 (93%)	0.29	13 (4%) 36 43	35, 42, 49, 54	0
All	All	1235/1320 (93%)	0.43	79 (6%) 19 25	35, 42, 50, 55	0

All (79) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	250	VAL	6.7
1	A	250	VAL	6.6
1	B	247	LEU	6.2
1	C	243	THR	5.7
1	D	288	ALA	5.6
1	B	251	GLY	5.1
1	D	249	PRO	5.1
1	B	290	THR	5.0
1	C	292	TYR	4.6
1	A	288	ALA	4.3
1	C	126	GLU	4.2
1	B	250	VAL	4.1
1	C	250	VAL	4.0
1	D	251	GLY	4.0
1	D	194	ASN	3.9
1	B	245	SER	3.8
1	C	154	GLN	3.7
1	D	243	THR	3.7
1	A	290	THR	3.6
1	C	267	HIS	3.5
1	C	0	HIS	3.4

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	C	296	ASN	3.4
1	C	244	ILE	3.3
1	A	289	GLN	3.2
1	A	283	LEU	3.1
1	B	306	GLU	3.1
1	B	30	GLU	3.0
1	B	249	PRO	2.9
1	A	226	GLN	2.8
1	C	75	ASP	2.7
1	B	283	LEU	2.7
1	B	288	ALA	2.7
1	B	203	SER	2.7
1	C	177	TYR	2.7
1	B	211	PRO	2.6
1	B	284	ASN	2.6
1	B	308	LEU	2.6
1	B	200	SER	2.6
1	B	239	VAL	2.6
1	C	189	LEU	2.5
1	B	240	ASN	2.5
1	C	115	ALA	2.5
1	B	310	VAL	2.5
1	C	249	PRO	2.5
1	B	234	HIS	2.5
1	D	292	TYR	2.4
1	A	308	LEU	2.4
1	B	300	ASP	2.4
1	A	-5	VAL	2.4
1	B	271	HIS	2.4
1	B	285	ALA	2.4
1	B	2	ILE	2.3
1	A	189	LEU	2.3
1	B	274	LEU	2.3
1	B	-1	SER	2.3
1	D	75[A]	ASP	2.3
1	C	195	GLN	2.3
1	B	186	ILE	2.3
1	C	167	ALA	2.3
1	C	129	GLU	2.2
1	D	252	SER	2.2
1	B	244	ILE	2.2
1	D	196	PRO	2.2

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	B	305	ILE	2.2
1	C	234	HIS	2.1
1	C	84	LYS	2.1
1	C	239	VAL	2.1
1	D	-5	VAL	2.1
1	D	189	LEU	2.1
1	C	150	ILE	2.1
1	C	196	PRO	2.1
1	A	202	GLU	2.1
1	B	87	THR	2.1
1	A	249	PRO	2.0
1	D	226	GLN	2.0
1	C	190	TYR	2.0
1	A	248	ASN	2.0
1	C	283	LEU	2.0
1	C	191	GLN	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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.