



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 10:59 AM UTC

PDB ID : 7E77 / pdb_00007e77
Title : The structure of cytosolic TaPGI
Authors : Gao, F.; Liu, C.M.
Deposited on : 2021-02-25
Resolution : 2.04 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
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

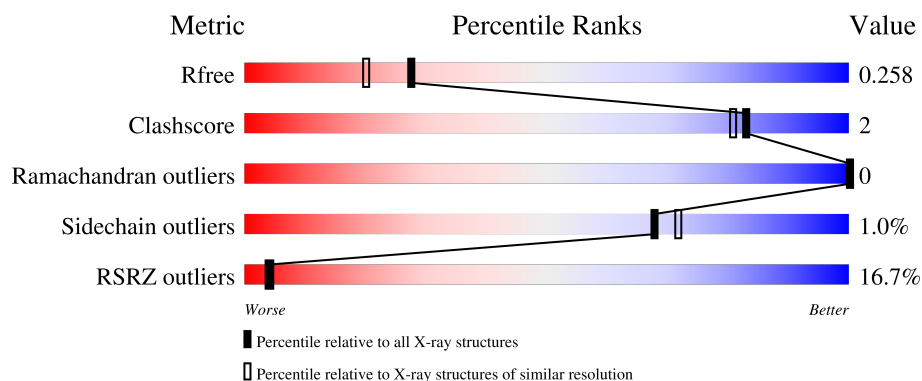
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.04 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	2260 (2.04-2.04)
Clashscore	190562	2333 (2.04-2.04)
Ramachandran outliers	187476	2318 (2.04-2.04)
Sidechain outliers	187428	2318 (2.04-2.04)
RSRZ outliers	180081	2260 (2.04-2.04)

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	567	21% 92% 7% .
1	B	567	17% 90% 6% .
1	C	567	14% 93% 7% .
1	D	567	13% 90% 7% .

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 17830 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 Glucose-6-phosphate isomerase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	562	Total	C	N	O	S	0	0	0
			4362	2791	745	815	11			
1	B	549	Total	C	N	O	S	0	0	0
			4265	2728	731	795	11			
1	C	562	Total	C	N	O	S	0	0	0
			4360	2790	744	815	11			
1	D	549	Total	C	N	O	S	0	0	0
			4265	2728	731	795	11			

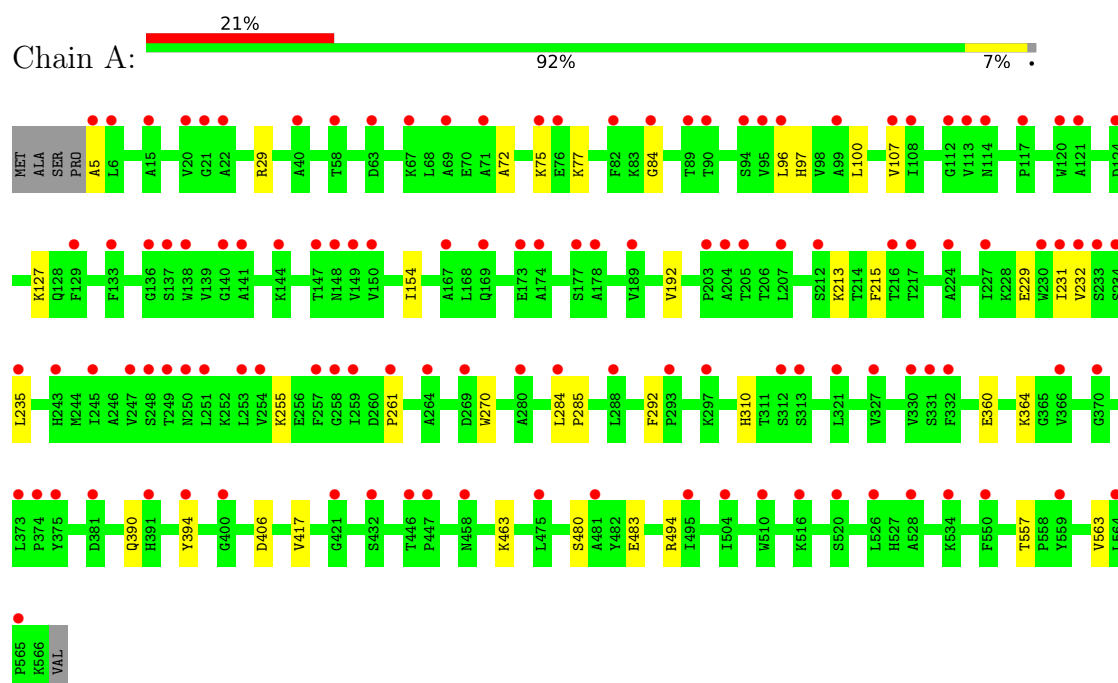
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	136	Total	O	0	0
			136	136		
2	B	127	Total	O	0	0
			127	127		
2	C	146	Total	O	0	0
			146	146		
2	D	169	Total	O	0	0
			169	169		

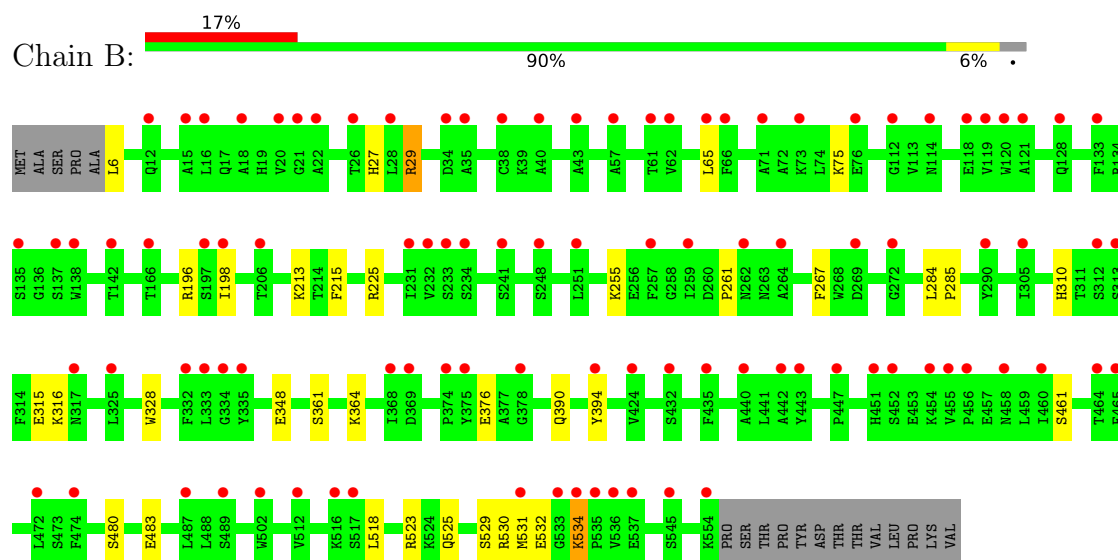
3 Residue-property plots

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.

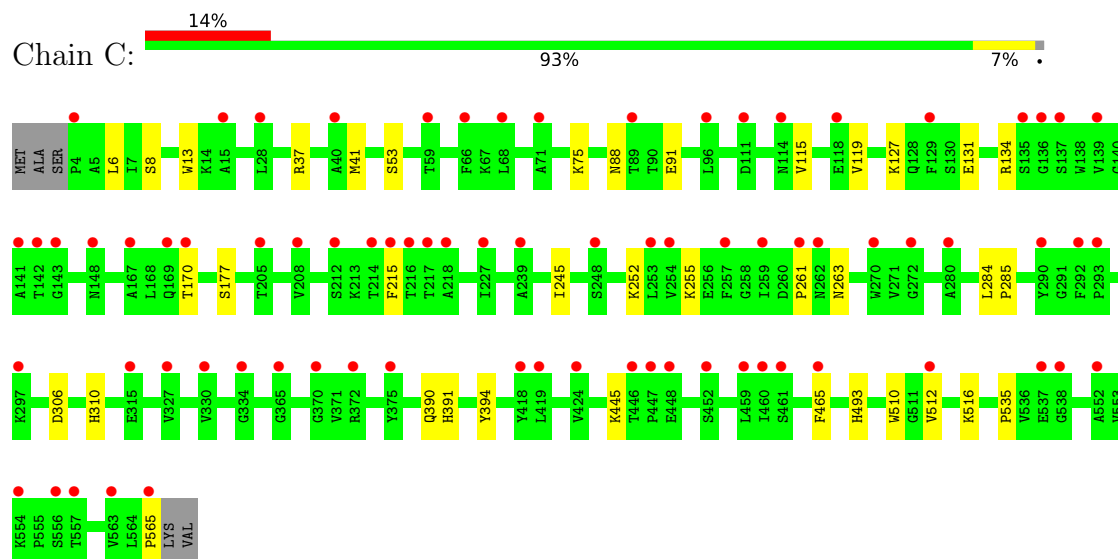
- Molecule 1: Glucose-6-phosphate isomerase



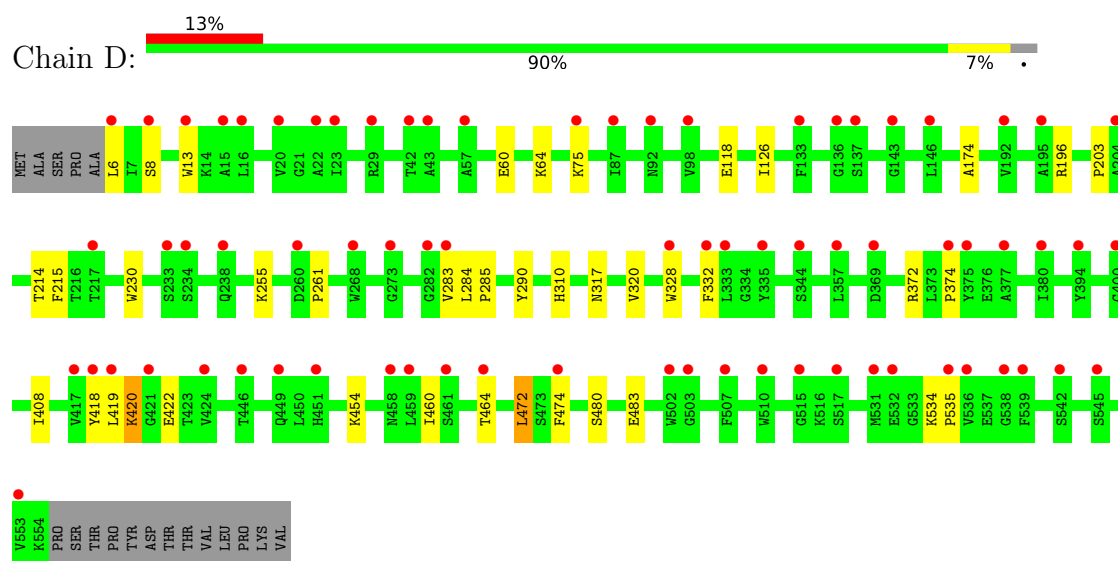
- Molecule 1: Glucose-6-phosphate isomerase



● Molecule 1: Glucose-6-phosphate isomerase



● Molecule 1: Glucose-6-phosphate isomerase



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	244.32Å 74.90Å 125.34Å 90.00° 93.80° 90.00°	Depositor
Resolution (Å)	37.91 – 2.04 37.91 – 2.04	Depositor EDS
% Data completeness (in resolution range)	91.5 (37.91-2.04) 91.4 (37.91-2.04)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.28 (at 2.05Å)	Xtriage
Refinement program	PHENIX 1.19.1_4122	Depositor
R, R_{free}	0.254 , 0.260 (Not available) , 0.258	Depositor DCC
R_{free} test set	2004 reflections (1.40%)	wwPDB-VP
Wilson B-factor (Å ²)	33.1	Xtriage
Anisotropy	0.509	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 46.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	17830	wwPDB-VP
Average B, all atoms (Å ²)	59.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.00% 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	0.12	0/4464	0.32	0/6060
1	B	0.10	0/4363	0.30	0/5918
1	C	0.10	0/4463	0.29	0/6060
1	D	0.11	0/4363	0.30	0/5918
All	All	0.11	0/17653	0.30	0/23956

There are no bond length outliers.

There are no bond angle outliers.

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	4362	0	4367	20	0
1	B	4265	0	4269	21	0
1	C	4360	0	4362	22	0
1	D	4265	0	4269	24	0
2	A	136	0	0	1	0
2	B	127	0	0	5	0
2	C	146	0	0	2	0
2	D	169	0	0	2	0
All	All	17830	0	17267	81	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 2.

All (81) 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:41:MET:HE3	1:C:53:SER:HA	1.64	0.79
1:B:529:SER:HA	1:B:534:LYS:H	1.51	0.74
1:C:134:ARG:NH2	1:C:177:SER:O	2.22	0.73
1:D:418:TYR:HE1	1:D:420:LYS:HG3	1.62	0.65
1:D:75:LYS:NZ	1:D:310:HIS:O	2.31	0.64
1:A:557:THR:HG21	1:A:563:VAL:HG11	1.81	0.62
1:D:6:LEU:N	2:D:603:HOH:O	2.33	0.61
1:A:84:GLY:HA2	1:A:96:LEU:HD21	1.83	0.61
1:B:255:LYS:HB2	1:B:261:PRO:HG3	1.82	0.61
1:A:97:HIS:HA	1:A:100:LEU:HD23	1.84	0.60
1:D:418:TYR:CE1	1:D:420:LYS:HG3	2.37	0.59
1:B:6:LEU:N	2:B:608:HOH:O	2.35	0.59
1:A:72:ALA:O	1:A:77:LYS:NZ	2.36	0.59
1:B:65:LEU:HD11	1:B:328:TRP:HB2	1.83	0.58
1:C:37:ARG:HG2	1:C:41:MET:HE2	1.87	0.57
1:C:127:LYS:NZ	1:C:131:GLU:OE2	2.32	0.56
1:D:255:LYS:HB2	1:D:261:PRO:HG3	1.86	0.56
1:C:252:LYS:NZ	2:C:603:HOH:O	2.30	0.55
1:D:472:LEU:HD11	1:D:474:PHE:CE2	2.41	0.55
1:B:361:SER:O	1:B:364:LYS:NZ	2.39	0.55
1:C:245:ILE:HG22	1:C:263:ASN:HB3	1.88	0.55
1:C:37:ARG:CZ	1:C:41:MET:HE1	2.37	0.54
1:B:348:GLU:OE1	1:D:196:ARG:NH2	2.41	0.53
1:C:75:LYS:NZ	1:C:310:HIS:O	2.42	0.52
1:A:75:LYS:NZ	1:A:310:HIS:O	2.42	0.52
1:D:408:ILE:HG12	1:D:474:PHE:CD2	2.45	0.51
1:A:480:SER:OG	1:A:483:GLU:OE1	2.29	0.49
1:B:213:LYS:HB2	1:B:267:PHE:CZ	2.47	0.49
1:A:255:LYS:HB2	1:A:261:PRO:HG3	1.94	0.48
1:D:60:GLU:HG2	1:D:64:LYS:HE2	1.96	0.48
1:D:408:ILE:HG12	1:D:474:PHE:HD2	1.77	0.48
1:D:480:SER:OG	1:D:483:GLU:OE1	2.30	0.48
1:A:154:ILE:HD12	1:C:391:HIS:CD2	2.49	0.47
1:B:376:GLU:O	2:B:601:HOH:O	2.20	0.47
1:C:8:SER:HA	1:C:13:TRP:CG	2.50	0.47
1:C:535:PRO:O	2:C:601:HOH:O	2.20	0.47
1:C:255:LYS:HB2	1:C:261:PRO:HG3	1.97	0.46
1:A:5:ALA:N	2:A:616:HOH:O	2.47	0.46
1:B:27:HIS:ND1	1:B:29:ARG:HG2	2.30	0.46
1:A:406:ASP:OD2	1:A:494:ARG:NH1	2.33	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:306:ASP:OD1	1:C:493:HIS:NE2	2.41	0.46
1:B:530:ARG:NH2	2:B:610:HOH:O	2.45	0.46
1:A:231:ILE:HG23	1:A:235:LEU:HD12	1.96	0.46
1:A:390:GLN:HA	1:A:394:TYR:CG	2.50	0.46
1:D:328:TRP:HA	1:D:332:PHE:HD2	1.80	0.46
1:B:523:ARG:NH1	2:B:605:HOH:O	2.32	0.46
1:D:419:LEU:HD23	1:D:419:LEU:HA	1.86	0.45
1:A:229:GLU:HA	1:A:232:VAL:HG22	1.98	0.45
1:A:284:LEU:HB3	1:A:285:PRO:HD3	1.98	0.45
1:A:360:GLU:O	1:A:364:LYS:NZ	2.51	0.44
1:D:126:ILE:HG21	1:D:283:VAL:HG12	1.99	0.44
1:A:417:VAL:HG22	1:C:565:PRO:HD3	1.99	0.44
1:B:480:SER:OG	1:B:483:GLU:OE1	2.25	0.44
1:D:317:ASN:HB3	1:D:320:VAL:HB	1.99	0.44
1:B:198:ILE:O	2:B:602:HOH:O	2.21	0.44
1:C:88:ASN:ND2	1:C:91:GLU:OE1	2.47	0.43
1:B:284:LEU:HB3	1:B:285:PRO:HD3	2.00	0.43
1:B:390:GLN:HA	1:B:394:TYR:CG	2.54	0.43
1:C:390:GLN:HA	1:C:394:TYR:CG	2.54	0.43
1:D:203:PRO:HG3	1:D:230:TRP:CE2	2.54	0.42
1:A:127:LYS:HD3	1:A:292:PHE:CD2	2.54	0.42
1:C:512:VAL:HG22	1:C:516:LYS:HE3	2.01	0.42
1:A:192:VAL:HG13	1:C:170:THR:HG21	2.01	0.42
1:B:525:GLN:NE2	1:B:529:SER:OG	2.50	0.42
1:C:445:LYS:H	1:C:465:PHE:HB2	1.85	0.42
1:D:460:ILE:O	1:D:464:THR:OG1	2.35	0.42
1:C:284:LEU:HB3	1:C:285:PRO:HD3	2.01	0.42
1:D:214:THR:HA	2:D:650:HOH:O	2.19	0.42
1:B:75:LYS:NZ	1:B:310:HIS:O	2.53	0.41
1:D:174:ALA:HB1	1:D:290:TYR:CD1	2.55	0.41
1:B:315:GLU:OE2	1:B:316:LYS:NZ	2.54	0.41
1:D:8:SER:HA	1:D:13:TRP:CG	2.56	0.41
1:D:534:LYS:HG2	1:D:535:PRO:HD2	2.02	0.41
1:B:532:GLU:H	1:B:532:GLU:HG3	1.69	0.41
1:B:225:ARG:NE	1:D:422:GLU:OE2	2.50	0.41
1:A:96:LEU:HB2	1:A:270:TRP:CE3	2.56	0.41
1:B:6:LEU:HD12	1:B:6:LEU:HA	1.84	0.41
1:A:463:LYS:HE2	1:C:510:TRP:CZ3	2.56	0.40
1:C:115:VAL:O	1:C:119:VAL:HG23	2.20	0.40
1:D:6:LEU:HD21	1:D:374:PRO:HD3	2.04	0.40
1:D:284:LEU:HB3	1:D:285:PRO:HD3	2.03	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	560/567 (99%)	552 (99%)	8 (1%)	0	100	100
1	B	547/567 (96%)	536 (98%)	11 (2%)	0	100	100
1	C	560/567 (99%)	549 (98%)	11 (2%)	0	100	100
1	D	547/567 (96%)	535 (98%)	12 (2%)	0	100	100
All	All	2214/2268 (98%)	2172 (98%)	42 (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	477/481 (99%)	473 (99%)	4 (1%)	73	77
1	B	465/481 (97%)	458 (98%)	7 (2%)	57	58
1	C	477/481 (99%)	475 (100%)	2 (0%)	84	88
1	D	465/481 (97%)	459 (99%)	6 (1%)	61	63
All	All	1884/1924 (98%)	1865 (99%)	19 (1%)	68	72

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	29	ARG
1	A	107	VAL
1	A	213	LYS
1	A	215	PHE
1	B	29	ARG
1	B	196	ARG
1	B	215	PHE
1	B	461	SER
1	B	518	LEU
1	B	531	MET
1	B	534	LYS
1	C	6	LEU
1	C	215	PHE
1	D	118	GLU
1	D	215	PHE
1	D	372	ARG
1	D	420	LYS
1	D	454	LYS
1	D	472	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	353	HIS
1	B	148	ASN
1	B	388	ASN
1	B	466	GLN
1	C	148	ASN
1	C	353	HIS
1	C	388	ASN
1	C	486	GLN
1	D	289	GLN
1	D	353	HIS

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 [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 [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	562/567 (99%)	1.36	120 (21%) 2 1	38, 59, 88, 114	0
1	B	549/567 (96%)	1.28	99 (18%) 3 3	41, 59, 82, 177	0
1	C	562/567 (99%)	1.24	77 (13%) 6 6	39, 59, 90, 113	0
1	D	549/567 (96%)	1.21	74 (13%) 7 6	35, 53, 83, 125	0
All	All	2222/2268 (97%)	1.27	370 (16%) 4 4	35, 57, 87, 177	0

All (370) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	248	SER	6.6
1	A	5	ALA	6.2
1	B	536	VAL	5.1
1	A	258	GLY	4.9
1	C	253	LEU	4.7
1	B	464	THR	4.5
1	D	15	ALA	4.5
1	A	136	GLY	4.4
1	C	15	ALA	4.3
1	B	535	PRO	4.3
1	C	254	VAL	4.2
1	D	233	SER	4.2
1	A	15	ALA	4.1
1	D	503	GLY	4.1
1	C	4	PRO	4.1
1	B	76	GLU	4.0
1	A	233	SER	4.0
1	A	248	SER	4.0
1	C	257	PHE	4.0
1	B	272	GLY	3.9
1	D	535	PRO	3.9

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Mol	Chain	Res	Type	RSRZ
1	A	564	LEU	3.8
1	C	217	THR	3.8
1	C	565	PRO	3.8
1	C	556	SER	3.7
1	C	280	ALA	3.7
1	A	261	PRO	3.7
1	B	533	GLY	3.6
1	D	421	GLY	3.6
1	B	43	ALA	3.6
1	A	254	VAL	3.6
1	C	40	ALA	3.6
1	B	65	LEU	3.6
1	A	269	ASP	3.5
1	B	452	SER	3.5
1	A	216	THR	3.5
1	A	141	ALA	3.5
1	C	214	THR	3.4
1	B	135	SER	3.4
1	A	89	THR	3.4
1	A	373	LEU	3.4
1	B	332	PHE	3.4
1	C	292	PHE	3.4
1	B	26	THR	3.3
1	B	472	LEU	3.3
1	D	510	TRP	3.3
1	C	143	GLY	3.3
1	B	62	VAL	3.3
1	C	96	LEU	3.3
1	B	516	LYS	3.2
1	A	177	SER	3.2
1	B	112	GLY	3.2
1	D	192	VAL	3.2
1	D	418	TYR	3.2
1	D	6	LEU	3.2
1	C	137	SER	3.2
1	D	449	GLN	3.2
1	A	245	ILE	3.2
1	B	21	GLY	3.2
1	D	531	MET	3.2
1	A	113	VAL	3.1
1	D	43	ALA	3.1
1	C	259	ILE	3.1

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Mol	Chain	Res	Type	RSRZ
1	A	432	SER	3.1
1	D	234	SER	3.1
1	C	512	VAL	3.1
1	B	531	MET	3.1
1	C	89	THR	3.0
1	B	38	CYS	3.0
1	C	419	LEU	3.0
1	C	216	THR	3.0
1	D	375	TYR	3.0
1	D	57	ALA	3.0
1	B	66	PHE	3.0
1	D	29	ARG	2.9
1	B	374	PRO	2.9
1	A	510	TRP	2.9
1	D	13	TRP	2.9
1	B	118	GLU	2.9
1	A	71	ALA	2.9
1	A	446	THR	2.9
1	C	557	THR	2.9
1	A	458	ASN	2.9
1	B	465	PHE	2.9
1	C	135	SER	2.9
1	A	178	ALA	2.9
1	C	261	PRO	2.8
1	B	489	SER	2.8
1	C	375	TYR	2.8
1	C	538	GLY	2.8
1	D	204	ALA	2.8
1	D	553	VAL	2.8
1	D	458	ASN	2.8
1	C	169	GLN	2.8
1	A	264	ALA	2.8
1	B	440	ALA	2.8
1	D	532	GLU	2.8
1	B	325	LEU	2.8
1	D	419	LEU	2.8
1	A	212	SER	2.8
1	C	66	PHE	2.8
1	A	189	VAL	2.8
1	B	233	SER	2.7
1	C	215	PHE	2.7
1	D	332	PHE	2.7

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Mol	Chain	Res	Type	RSRZ
1	A	6	LEU	2.7
1	A	375	TYR	2.7
1	B	251	LEU	2.7
1	C	447	PRO	2.7
1	A	231	ILE	2.7
1	D	8	SER	2.7
1	B	120	TRP	2.7
1	A	21	GLY	2.7
1	A	140	GLY	2.7
1	A	297	LYS	2.7
1	D	507	PHE	2.7
1	A	293	PRO	2.7
1	B	451	HIS	2.7
1	A	331	SER	2.7
1	A	22	ALA	2.7
1	A	249	THR	2.7
1	A	253	LEU	2.7
1	A	120	TRP	2.7
1	A	40	ALA	2.6
1	A	117	PRO	2.6
1	A	108	ILE	2.6
1	B	455	VAL	2.6
1	A	84	GLY	2.6
1	B	12	GLN	2.6
1	A	69	ALA	2.6
1	B	142	THR	2.6
1	B	454	LYS	2.6
1	C	227	ILE	2.6
1	C	460	ILE	2.6
1	D	20	VAL	2.6
1	A	205	THR	2.6
1	B	18	ALA	2.6
1	B	35	ALA	2.6
1	A	257	PHE	2.6
1	A	381	ASP	2.6
1	B	313	SER	2.6
1	A	259	ILE	2.6
1	C	330	VAL	2.6
1	B	534	LYS	2.6
1	B	15	ALA	2.6
1	A	526	LEU	2.6
1	C	459	LEU	2.6

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Mol	Chain	Res	Type	RSRZ
1	C	461	SER	2.6
1	D	333	LEU	2.6
1	B	231	ILE	2.5
1	D	87	ILE	2.5
1	B	375	TYR	2.5
1	C	148	ASN	2.5
1	D	75	LYS	2.5
1	A	167	ALA	2.5
1	D	377	ALA	2.5
1	D	446	THR	2.5
1	A	374	PRO	2.5
1	D	545	SER	2.5
1	A	138	TRP	2.5
1	D	539	PHE	2.5
1	B	119	VAL	2.5
1	B	334	GLY	2.5
1	C	139	VAL	2.5
1	C	418	TYR	2.5
1	A	124	ASP	2.5
1	A	137	SER	2.5
1	B	432	SER	2.5
1	D	374	PRO	2.5
1	D	459	LEU	2.5
1	D	328	TRP	2.5
1	A	370	GLY	2.5
1	A	391	HIS	2.5
1	B	198	ILE	2.5
1	B	460	ILE	2.5
1	D	536	VAL	2.5
1	C	71	ALA	2.5
1	A	82	PHE	2.5
1	A	144	LYS	2.5
1	D	538	GLY	2.5
1	C	111	ASP	2.4
1	A	94	SER	2.4
1	A	217	THR	2.4
1	B	545	SER	2.4
1	C	205	THR	2.4
1	B	28	LEU	2.4
1	A	227	ILE	2.4
1	C	327	VAL	2.4
1	D	137	SER	2.4

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Mol	Chain	Res	Type	RSRZ
1	D	542	SER	2.4
1	C	446	THR	2.4
1	D	464	THR	2.4
1	A	447	PRO	2.4
1	A	565	PRO	2.4
1	A	75	LYS	2.4
1	B	121	ALA	2.4
1	C	167	ALA	2.4
1	A	207	LEU	2.4
1	A	63	ASP	2.4
1	A	20	VAL	2.4
1	D	283	VAL	2.4
1	D	344	SER	2.4
1	C	170	THR	2.4
1	C	293	PRO	2.4
1	A	174	ALA	2.4
1	A	224	ALA	2.4
1	B	264	ALA	2.4
1	B	114	ASN	2.4
1	C	370	GLY	2.4
1	A	247	VAL	2.4
1	A	504	ILE	2.4
1	C	424	VAL	2.4
1	D	461	SER	2.4
1	C	142	THR	2.4
1	C	141	ALA	2.3
1	B	458	ASN	2.3
1	C	28	LEU	2.3
1	B	269	ASP	2.3
1	B	257	PHE	2.3
1	C	129	PHE	2.3
1	A	520	SER	2.3
1	D	517	SER	2.3
1	A	243	HIS	2.3
1	A	76	GLU	2.3
1	D	502	TRP	2.3
1	B	335	TYR	2.3
1	C	218	ALA	2.3
1	A	67	LYS	2.3
1	A	313	SER	2.3
1	C	452	SER	2.3
1	A	495	ILE	2.3

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Mol	Chain	Res	Type	RSRZ
1	D	451	HIS	2.3
1	A	149	VAL	2.3
1	C	114	ASN	2.3
1	A	99	ALA	2.3
1	A	204	ALA	2.3
1	B	57	ALA	2.3
1	B	333	LEU	2.3
1	B	378	GLY	2.3
1	C	272	GLY	2.3
1	D	335	TYR	2.3
1	C	297	LYS	2.3
1	A	332	PHE	2.3
1	B	133	PHE	2.3
1	B	435	PHE	2.3
1	D	474	PHE	2.3
1	A	366	VAL	2.3
1	B	20	VAL	2.3
1	D	417	VAL	2.3
1	B	206	THR	2.3
1	B	22	ALA	2.3
1	B	34	ASP	2.3
1	C	136	GLY	2.3
1	B	16	LEU	2.3
1	B	502	TRP	2.3
1	D	268	TRP	2.3
1	A	173	GLU	2.2
1	C	118	GLU	2.2
1	A	234	SER	2.2
1	B	241	SER	2.2
1	B	474	PHE	2.2
1	D	92	ASN	2.2
1	A	528	ALA	2.2
1	B	40	ALA	2.2
1	B	71	ALA	2.2
1	B	442	ALA	2.2
1	C	239	ALA	2.2
1	A	235	LEU	2.2
1	A	475	LEU	2.2
1	D	146	LEU	2.2
1	D	357	LEU	2.2
1	B	290	TYR	2.2
1	C	448	GLU	2.2

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Mol	Chain	Res	Type	RSRZ
1	C	537	GLU	2.2
1	A	230	TRP	2.2
1	B	137	SER	2.2
1	B	166	THR	2.2
1	B	259	ILE	2.2
1	B	456	PRO	2.2
1	D	380	ILE	2.2
1	B	424	VAL	2.2
1	D	22	ALA	2.2
1	B	394	TYR	2.2
1	C	270	TRP	2.2
1	B	554	LYS	2.2
1	C	554	LYS	2.2
1	A	148	ASN	2.2
1	A	147	THR	2.2
1	B	305	ILE	2.2
1	B	447	PRO	2.2
1	D	133	PHE	2.2
1	A	107	VAL	2.2
1	A	327	VAL	2.2
1	B	232	VAL	2.2
1	D	282	GLY	2.2
1	B	128	GLN	2.2
1	D	195	ALA	2.2
1	A	96	LEU	2.2
1	A	251	LEU	2.2
1	D	16	LEU	2.2
1	C	290	TYR	2.2
1	D	42	THR	2.2
1	A	133	PHE	2.1
1	B	368	ILE	2.1
1	D	23	ILE	2.1
1	A	232	VAL	2.1
1	D	98	VAL	2.1
1	D	400	GLY	2.1
1	A	280	ALA	2.1
1	A	481	ALA	2.1
1	C	552	ALA	2.1
1	B	487	LEU	2.1
1	B	234	SER	2.1
1	B	248	SER	2.1
1	A	534	LYS	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	250	ASN	2.1
1	D	394	TYR	2.1
1	B	369	ASP	2.1
1	C	315	GLU	2.1
1	B	138	TRP	2.1
1	A	150	VAL	2.1
1	A	400	GLY	2.1
1	A	421	GLY	2.1
1	C	334	GLY	2.1
1	A	284	LEU	2.1
1	B	197	SER	2.1
1	D	260	ASP	2.1
1	D	369	ASP	2.1
1	A	58	THR	2.1
1	A	203	PRO	2.1
1	C	365	GLY	2.1
1	C	372	ARG	2.1
1	A	129	PHE	2.1
1	A	330	VAL	2.1
1	C	208	VAL	2.1
1	D	424	VAL	2.1
1	A	516	LYS	2.1
1	A	312	SER	2.1
1	B	312	SER	2.1
1	B	537	GLU	2.1
1	B	262	ASN	2.1
1	A	169	GLN	2.1
1	A	559	TYR	2.1
1	B	443	TYR	2.1
1	C	59	THR	2.1
1	D	217	THR	2.1
1	D	136	GLY	2.1
1	D	143	GLY	2.1
1	D	273	GLY	2.1
1	C	465	PHE	2.1
1	C	563	VAL	2.1
1	B	517	SER	2.1
1	C	212	SER	2.1
1	C	68	LEU	2.0
1	A	90	THR	2.0
1	A	394	TYR	2.0
1	A	95	VAL	2.0

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Mol	Chain	Res	Type	RSRZ
1	A	550	PHE	2.0
1	B	512	VAL	2.0
1	A	121	ALA	2.0
1	A	114	ASN	2.0
1	B	317	ASN	2.0
1	C	262	ASN	2.0
1	A	288	LEU	2.0
1	A	321	LEU	2.0
1	D	238	GLN	2.0
1	B	73	LYS	2.0
1	B	61	THR	2.0
1	A	112	GLY	2.0
1	D	515	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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.