



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 13, 2017 – 02:30 pm GMT

PDB ID : 1QQR
Title : CRYSTAL STRUCTURE OF STREPTOKINASE DOMAIN B
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Deposited on : 1999-06-07
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

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.9-1692
EDS	:	trunk28620
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	recalc28949

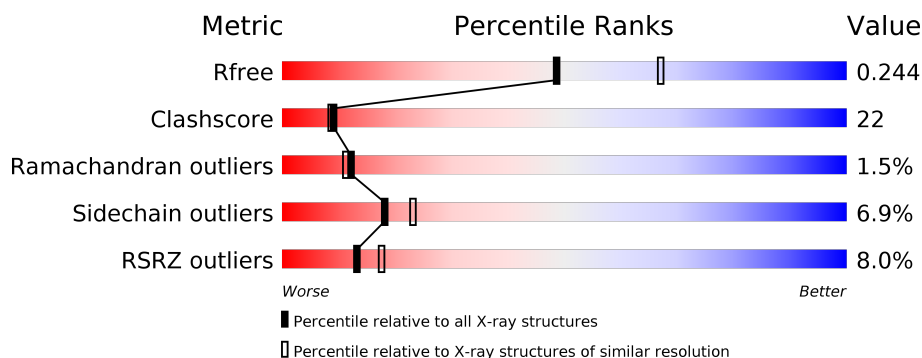
1 Overall quality at a glance

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}	100719	4130 (2.30-2.30)
Clashscore	112137	4751 (2.30-2.30)
Ramachandran outliers	110173	4705 (2.30-2.30)
Sidechain outliers	110143	4704 (2.30-2.30)
RSRZ outliers	101464	4156 (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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	138	<div> <div>9%</div> <div> <div></div> <div>67%</div> <div>25%</div> <div>8%</div> </div> </div>
1	B	138	<div> <div>4%</div> <div> <div></div> <div>72%</div> <div>20%</div> <div>• • •</div> </div> </div>
1	C	138	<div> <div>6%</div> <div> <div></div> <div>69%</div> <div>27%</div> <div>•</div> </div> </div>
1	D	138	<div> <div>12%</div> <div> <div></div> <div>63%</div> <div>29%</div> <div>6% •</div> </div> </div>

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 4794 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 STREPTOKINASE DOMAIN B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	138	Total	C	N	O	S	0	0	0
			1121	707	190	223	1			
1	B	133	Total	C	N	O	S	0	0	0
			1083	683	185	214	1			
1	C	138	Total	C	N	O	S	0	0	0
			1130	714	190	225	1			
1	D	138	Total	C	N	O	S	0	0	0
			1123	708	190	224	1			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	181	LEU	ASP	CONFLICT	UNP P00779
B	181	LEU	ASP	CONFLICT	UNP P00779
C	181	LEU	ASP	CONFLICT	UNP P00779
D	181	LEU	ASP	CONFLICT	UNP P00779

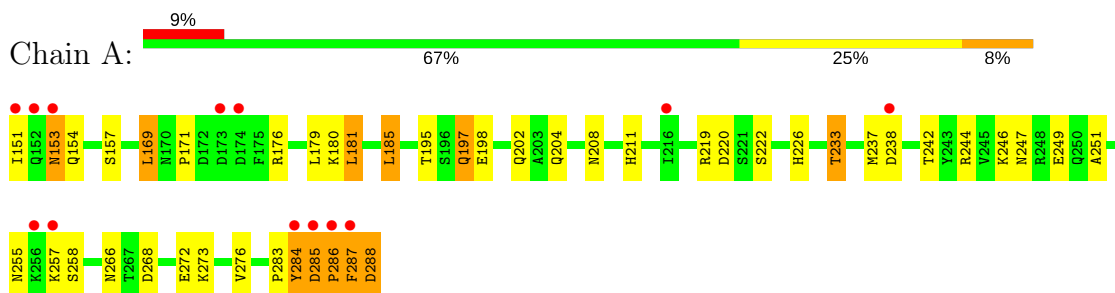
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	80	Total	O	0	0
			80	80		
2	B	82	Total	O	0	0
			82	82		
2	C	79	Total	O	0	0
			79	79		
2	D	96	Total	O	0	0
			96	96		

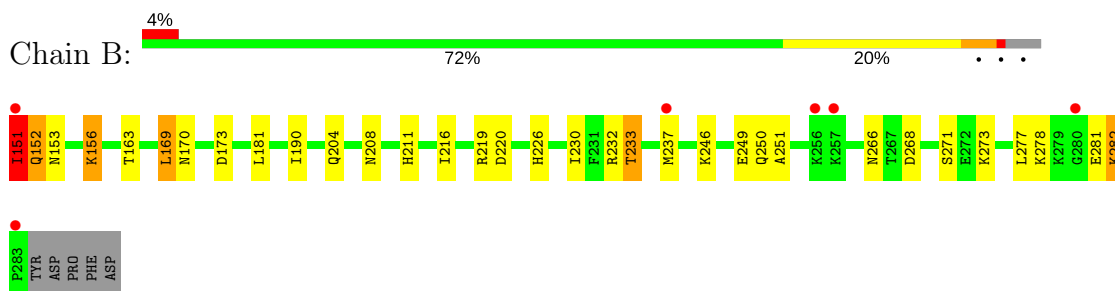
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

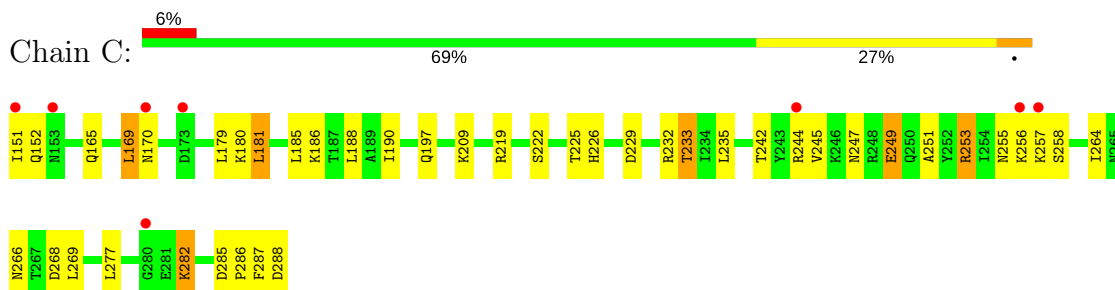
• Molecule 1: STREPTOKINASE DOMAIN B



• Molecule 1: STREPTOKINASE DOMAIN B



• Molecule 1: STREPTOKINASE DOMAIN B



• Molecule 1: STREPTOKINASE DOMAIN B





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	50.87Å 93.78Å 156.05Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.30 29.02 – 2.34	Depositor EDS
% Data completeness (in resolution range)	91.8 (50.00-2.30) 96.8 (29.02-2.34)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.00 (at 2.34Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.197 , 0.242 0.199 , 0.244	Depositor DCC
R_{free} test set	1564 reflections (5.01%)	DCC
Wilson B-factor (Å ²)	44.8	Xtriage
Anisotropy	0.028	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 65.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	4794	wwPDB-VP
Average B, all atoms (Å ²)	47.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.02% 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

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	0/1141	0.76	0/1544
1	B	0.60	1/1101 (0.1%)	0.92	5/1489 (0.3%)
1	C	0.51	0/1151	0.73	0/1557
1	D	0.71	3/1143 (0.3%)	1.10	8/1546 (0.5%)
All	All	0.58	4/4536 (0.1%)	0.89	13/6136 (0.2%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	B	0	1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	287	PHE	CB-CG	8.19	1.65	1.51
1	B	151	ILE	CB-CG2	5.27	1.69	1.52
1	D	285	ASP	CB-CG	5.19	1.62	1.51
1	D	286	PRO	CB-CG	-5.11	1.24	1.50

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	282	LYS	C-N-CD	-18.93	78.94	120.60
1	D	282	LYS	C-N-CA	13.74	179.70	122.00
1	B	151	ILE	CA-C-N	-10.98	93.05	117.20
1	B	151	ILE	C-N-CA	8.85	143.82	121.70
1	D	287	PHE	CB-CG-CD2	7.70	126.19	120.80
1	D	285	ASP	CB-CA-C	-7.64	95.11	110.40
1	D	283	PRO	CA-N-CD	-7.62	100.83	111.50
1	B	151	ILE	N-CA-C	-7.57	90.56	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	152	GLN	N-CA-CB	-6.35	99.17	110.60
1	B	151	ILE	O-C-N	6.21	132.64	122.70
1	D	285	ASP	CB-CG-OD1	6.11	123.80	118.30
1	D	283	PRO	CA-CB-CG	-5.85	92.89	104.00
1	D	285	ASP	N-CA-CB	5.10	119.78	110.60

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	151	ILE	Mainchain

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	1121	0	1109	49	0
1	B	1083	0	1084	42	0
1	C	1130	0	1118	45	1
1	D	1123	0	1111	71	1
2	A	80	0	0	11	0
2	B	82	0	0	18	0
2	C	79	0	0	12	0
2	D	96	0	0	11	0
All	All	4794	0	4422	197	1

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 22.

All (197) 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:151:ILE:CG1	2:B:340:HOH:O	2.05	1.04
1:B:151:ILE:CG2	2:B:340:HOH:O	2.07	1.03
1:B:226:HIS:HE1	1:B:233:THR:CG2	1.73	1.00

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:151:ILE:HG23	2:B:340:HOH:O	1.63	0.98
1:D:285:ASP:N	1:D:286:PRO:HD2	1.80	0.95
1:B:151:ILE:CB	2:B:340:HOH:O	2.13	0.94
1:D:226:HIS:HE1	1:D:233:THR:CG2	1.82	0.92
1:B:282:LYS:HE3	1:B:282:LYS:H	1.34	0.91
1:B:226:HIS:CE1	1:B:233:THR:HG23	2.07	0.90
1:B:226:HIS:CE1	1:B:233:THR:CG2	2.55	0.89
1:C:226:HIS:HE1	1:C:233:THR:CG2	1.84	0.89
1:A:255:ASN:ND2	1:A:258:SER:H	1.70	0.87
1:D:151:ILE:HD12	1:D:247:ASN:ND2	1.88	0.87
1:D:226:HIS:HE1	1:D:233:THR:HG22	1.39	0.87
1:C:169:LEU:HD23	1:C:277:LEU:HD13	1.58	0.85
1:D:255:ASN:HD22	1:D:258:SER:H	1.23	0.84
1:D:226:HIS:CE1	1:D:233:THR:CG2	2.61	0.83
1:C:255:ASN:HD21	1:C:257:LYS:HG3	1.43	0.82
1:B:226:HIS:HE1	1:B:233:THR:HG23	1.43	0.80
1:A:255:ASN:HD22	1:A:258:SER:H	1.28	0.80
1:A:246:LYS:HE2	2:A:303:HOH:O	1.82	0.79
1:D:170:ASN:H	1:D:170:ASN:ND2	1.81	0.79
1:D:255:ASN:ND2	1:D:258:SER:H	1.80	0.78
1:A:226:HIS:HE1	1:A:233:THR:CG2	1.97	0.78
1:D:249:GLU:HG2	2:D:350:HOH:O	1.82	0.78
1:D:285:ASP:O	1:D:285:ASP:OD2	2.02	0.77
1:B:152:GLN:HG2	2:B:340:HOH:O	1.82	0.77
1:D:285:ASP:CG	1:D:286:PRO:N	2.33	0.77
1:C:251:ALA:H	1:C:266:ASN:HD21	1.32	0.77
1:A:226:HIS:CE1	1:A:233:THR:CG2	2.68	0.77
1:D:225:THR:HG22	2:D:292:HOH:O	1.86	0.76
1:D:225:THR:HG23	1:D:269:LEU:HB3	1.67	0.76
1:D:251:ALA:H	1:D:266:ASN:HD21	1.33	0.76
1:C:255:ASN:HD22	1:C:258:SER:H	1.32	0.75
1:A:195:THR:HG22	1:A:242:THR:HG22	1.69	0.75
1:A:226:HIS:CE1	1:A:233:THR:HG23	2.21	0.75
1:D:281:GLU:O	1:D:282:LYS:HG3	1.87	0.74
1:C:244:ARG:HD2	2:C:319:HOH:O	1.88	0.74
1:C:226:HIS:CE1	1:C:233:THR:CG2	2.71	0.73
1:A:251:ALA:H	1:A:266:ASN:HD21	1.34	0.72
1:A:285:ASP:CB	1:A:286:PRO:CD	2.67	0.72
1:A:220:ASP:OD2	1:A:273:LYS:HE3	1.89	0.72
1:A:151:ILE:HG23	1:A:151:ILE:O	1.90	0.70
1:B:156:LYS:HD3	1:B:250:GLN:OE1	1.90	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:283:PRO:O	1:D:286:PRO:CD	2.39	0.70
1:D:211:HIS:HE1	2:D:295:HOH:O	1.75	0.69
1:B:251:ALA:H	1:B:266:ASN:HD21	1.38	0.68
1:B:151:ILE:HG12	2:B:340:HOH:O	1.81	0.68
1:A:176:ARG:NH2	1:D:153:ASN:HD22	1.92	0.67
1:D:283:PRO:O	1:D:286:PRO:HD2	1.95	0.67
1:C:225:THR:HG23	1:C:269:LEU:HB3	1.76	0.67
1:D:284:TYR:C	1:D:286:PRO:HD2	2.14	0.67
1:B:219:ARG:HD2	2:B:330:HOH:O	1.95	0.67
2:C:348:HOH:O	1:D:234:ILE:HG13	1.95	0.66
1:A:202:GLN:HG2	2:A:347:HOH:O	1.96	0.65
1:C:225:THR:CG2	1:C:269:LEU:HB3	2.26	0.65
1:C:225:THR:HG22	2:C:292:HOH:O	1.96	0.65
1:C:226:HIS:CE1	1:C:233:THR:HG23	2.32	0.65
1:D:195:THR:HG22	1:D:242:THR:HG22	1.79	0.65
1:D:214:TYR:CZ	1:D:278:LYS:CE	2.79	0.65
1:A:153:ASN:HB3	2:A:340:HOH:O	1.95	0.65
1:A:233:THR:HG22	2:A:310:HOH:O	1.97	0.65
1:C:255:ASN:ND2	1:C:258:SER:H	1.93	0.65
1:D:285:ASP:N	1:D:286:PRO:CD	2.58	0.64
1:B:226:HIS:HE1	1:B:233:THR:HG22	1.57	0.64
1:A:226:HIS:HE1	1:A:233:THR:HG22	1.63	0.64
1:C:229:ASP:HB2	2:C:317:HOH:O	1.98	0.64
1:D:255:ASN:HD22	1:D:258:SER:N	1.94	0.64
1:A:255:ASN:HD22	1:A:258:SER:N	1.96	0.64
1:C:226:HIS:HE1	1:C:233:THR:HG23	1.62	0.63
1:A:176:ARG:HH21	1:D:153:ASN:HD22	1.47	0.63
1:D:226:HIS:CE1	1:D:233:THR:HG23	2.34	0.63
1:D:214:TYR:CE1	1:D:278:LYS:HE2	2.34	0.63
1:D:225:THR:CG2	1:D:269:LEU:HB3	2.29	0.63
1:C:285:ASP:HB2	1:C:286:PRO:CD	2.28	0.63
1:D:285:ASP:C	1:D:285:ASP:OD2	2.32	0.62
1:C:255:ASN:ND2	1:C:257:LYS:HG3	2.12	0.62
1:B:237:MET:HA	2:B:322:HOH:O	2.00	0.62
1:D:170:ASN:HD22	1:D:170:ASN:H	1.47	0.61
1:A:197:GLN:H	1:A:197:GLN:NE2	1.99	0.61
1:C:181:LEU:HD11	2:C:350:HOH:O	2.01	0.61
1:D:170:ASN:HD22	1:D:170:ASN:N	1.98	0.61
1:A:197:GLN:H	1:A:197:GLN:HE21	1.49	0.61
1:C:253:ARG:HE	1:C:264:ILE:HG21	1.64	0.61
1:B:152:GLN:HA	1:B:249:GLU:OE2	2.00	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:219:ARG:HD2	2:C:328:HOH:O	2.01	0.60
1:C:226:HIS:HE1	1:C:233:THR:HG22	1.64	0.60
1:D:283:PRO:O	1:D:286:PRO:CG	2.50	0.60
1:B:226:HIS:HD2	1:B:268:ASP:OD1	1.84	0.60
1:D:214:TYR:CZ	1:D:278:LYS:HE3	2.37	0.60
1:C:285:ASP:HB2	1:C:286:PRO:HD2	1.84	0.60
1:B:153:ASN:N	1:B:249:GLU:OE2	2.33	0.58
1:C:242:THR:HG21	2:C:340:HOH:O	2.03	0.58
1:D:217:TYR:HB2	1:D:277:LEU:HD23	1.85	0.58
1:A:249:GLU:HG2	1:D:177:PRO:HG2	1.84	0.58
1:C:180:LYS:HA	2:C:320:HOH:O	2.03	0.58
1:A:219:ARG:HD3	2:A:314:HOH:O	2.03	0.57
1:D:209:LYS:HA	1:D:209:LYS:HE2	1.85	0.57
1:C:152:GLN:N	1:C:249:GLU:OE2	2.34	0.57
1:D:214:TYR:CZ	1:D:278:LYS:HE2	2.40	0.57
1:A:251:ALA:H	1:A:266:ASN:ND2	2.03	0.56
1:B:170:ASN:HB2	2:B:318:HOH:O	2.04	0.56
1:D:202:GLN:HG2	2:D:320:HOH:O	2.05	0.56
1:D:193:THR:HG22	1:D:244:ARG:HG2	1.87	0.55
1:D:251:ALA:H	1:D:266:ASN:ND2	2.02	0.55
1:A:255:ASN:HD21	1:A:257:LYS:HB2	1.70	0.55
1:B:220:ASP:OD2	1:B:273:LYS:HE3	2.06	0.55
1:B:151:ILE:N	2:B:340:HOH:O	2.40	0.55
1:D:283:PRO:O	1:D:286:PRO:HG3	2.06	0.55
1:C:186:LYS:HE3	1:C:188:LEU:HD11	1.88	0.55
1:D:226:HIS:HD2	1:D:268:ASP:OD1	1.89	0.54
1:A:181:LEU:HG	1:D:253:ARG:HB2	1.89	0.54
1:B:251:ALA:H	1:B:266:ASN:ND2	2.04	0.54
1:D:152:GLN:HG2	2:D:349:HOH:O	2.08	0.54
1:C:251:ALA:H	1:C:266:ASN:ND2	2.01	0.54
1:A:285:ASP:CB	1:A:286:PRO:HD2	2.37	0.54
1:D:169:LEU:HD23	1:D:277:LEU:HD22	1.89	0.53
1:B:282:LYS:CE	1:B:282:LYS:H	2.14	0.53
1:C:165:GLN:HG3	2:C:327:HOH:O	2.07	0.53
1:A:151:ILE:CG2	1:A:151:ILE:O	2.57	0.53
1:B:151:ILE:CD1	2:B:340:HOH:O	2.50	0.53
1:A:226:HIS:HD2	1:A:268:ASP:OD1	1.92	0.53
1:B:230:ILE:HD11	2:B:310:HOH:O	2.09	0.53
1:C:226:HIS:HD2	1:C:268:ASP:OD1	1.90	0.52
1:B:232:ARG:HH11	1:D:286:PRO:HA	1.74	0.52
1:C:256:LYS:NZ	1:C:256:LYS:HB3	2.24	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:190:ILE:HG12	2:B:309:HOH:O	2.09	0.52
1:C:209:LYS:HG3	2:C:316:HOH:O	2.08	0.52
1:B:151:ILE:HG12	1:B:152:GLN:HG2	1.91	0.52
1:D:222:SER:HB2	1:D:235:LEU:HB2	1.92	0.51
1:A:258:SER:HB3	2:A:356:HOH:O	2.09	0.51
1:A:195:THR:OG1	1:A:198:GLU:HG3	2.10	0.51
1:A:211:HIS:HE1	2:A:296:HOH:O	1.93	0.51
1:C:255:ASN:HD22	1:C:258:SER:N	2.06	0.51
1:D:152:GLN:CD	1:D:152:GLN:H	2.14	0.51
1:B:151:ILE:HD13	2:B:340:HOH:O	2.10	0.51
1:A:154:GLN:HG3	1:A:247:ASN:OD1	2.11	0.51
1:B:232:ARG:NH1	1:D:286:PRO:HA	2.26	0.51
1:B:278:LYS:HD2	1:B:281:GLU:OE1	2.11	0.50
1:D:181:LEU:HD21	2:D:327:HOH:O	2.11	0.50
1:B:163:THR:CG2	1:B:271:SER:HB3	2.43	0.49
1:B:233:THR:HG21	2:B:344:HOH:O	2.12	0.49
1:B:277:LEU:HD12	2:B:356:HOH:O	2.13	0.49
1:C:287:PHE:O	1:C:288:ASP:HB2	2.11	0.49
1:A:286:PRO:O	1:A:287:PHE:CB	2.60	0.48
1:C:190:ILE:HG12	2:C:306:HOH:O	2.12	0.48
1:A:204:GLN:HE21	1:A:208:ASN:HD21	1.60	0.48
1:A:204:GLN:HE21	1:A:208:ASN:ND2	2.12	0.47
1:D:285:ASP:HB3	2:D:312:HOH:O	2.14	0.47
1:B:204:GLN:OE1	1:B:216:ILE:HG12	2.14	0.47
1:C:282:LYS:NZ	1:C:282:LYS:HB3	2.29	0.47
1:A:244:ARG:NE	2:A:337:HOH:O	2.48	0.47
1:B:246:LYS:HE2	2:B:303:HOH:O	2.13	0.47
1:A:287:PHE:O	1:A:288:ASP:CB	2.62	0.47
1:C:287:PHE:HD2	1:D:231:PHE:CE2	2.33	0.46
1:A:169:LEU:HD22	1:A:276:VAL:O	2.15	0.46
1:D:214:TYR:OH	1:D:278:LYS:CE	2.63	0.46
1:D:152:GLN:CD	1:D:152:GLN:N	2.69	0.46
1:D:278:LYS:HB2	1:D:278:LYS:HE3	1.44	0.46
1:D:181:LEU:HD13	2:D:326:HOH:O	2.15	0.46
1:D:169:LEU:HD23	1:D:277:LEU:CD2	2.47	0.45
1:A:180:LYS:HA	2:D:294:HOH:O	2.17	0.45
1:A:222:SER:OG	1:A:272:GLU:OE2	2.29	0.45
1:C:179:LEU:HD23	2:C:367:HOH:O	2.17	0.45
1:A:238:ASP:HB2	2:A:362:HOH:O	2.16	0.44
1:A:176:ARG:HD3	1:D:252:TYR:CE1	2.52	0.44
1:C:288:ASP:HB3	1:D:234:ILE:HD11	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:281:GLU:CD	1:D:281:GLU:H	2.19	0.44
1:A:287:PHE:O	1:A:288:ASP:HB2	2.17	0.44
1:C:222:SER:HB2	1:C:235:LEU:HB2	2.00	0.44
1:B:163:THR:O	1:B:271:SER:HA	2.18	0.43
1:D:214:TYR:CE1	1:D:278:LYS:CE	3.00	0.43
1:C:151:ILE:HD12	1:C:151:ILE:N	2.32	0.43
1:D:204:GLN:HE21	1:D:208:ASN:ND2	2.16	0.43
1:B:232:ARG:NH1	1:D:286:PRO:O	2.50	0.43
1:A:185:LEU:HD12	1:A:185:LEU:HA	1.87	0.43
1:C:190:ILE:HG23	1:C:247:ASN:HA	2.00	0.43
1:C:151:ILE:HG12	1:C:247:ASN:ND2	2.34	0.43
1:D:210:ASN:HB3	1:D:211:HIS:CE1	2.54	0.43
1:A:237:MET:HG3	2:A:309:HOH:O	2.17	0.43
1:D:169:LEU:HD13	1:D:169:LEU:HA	1.68	0.43
1:C:253:ARG:NE	1:C:264:ILE:HG21	2.31	0.42
1:D:265:ASN:HD22	1:D:265:ASN:HA	1.64	0.42
1:B:211:HIS:CE1	2:B:294:HOH:O	2.73	0.42
1:C:251:ALA:N	1:C:266:ASN:HD21	2.10	0.42
1:B:204:GLN:HE21	1:B:208:ASN:ND2	2.18	0.42
1:D:237:MET:HA	2:D:332:HOH:O	2.20	0.42
1:A:226:HIS:HE1	1:A:233:THR:HG23	1.68	0.41
1:B:169:LEU:HD12	1:B:169:LEU:HA	1.83	0.41
1:A:284:TYR:CZ	1:A:288:ASP:HA	2.56	0.41
1:D:217:TYR:CG	1:D:277:LEU:HD23	2.56	0.41
1:C:170:ASN:O	1:C:170:ASN:OD1	2.38	0.41
1:D:264:ILE:HB	2:D:316:HOH:O	2.21	0.41
1:D:185:LEU:HA	1:D:185:LEU:HD12	1.81	0.41
1:A:284:TYR:HD2	1:A:284:TYR:HA	1.73	0.40
1:C:186:LYS:HG3	1:C:188:LEU:HG	2.03	0.40
1:A:179:LEU:HD23	2:A:323:HOH:O	2.20	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:232:ARG:NH1	1:D:286:PRO:CB[1_455]	2.00	0.20

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	136/138 (99%)	124 (91%)	8 (6%)	4 (3%)	5	3
1	B	131/138 (95%)	123 (94%)	8 (6%)	0	100	100
1	C	136/138 (99%)	127 (93%)	8 (6%)	1 (1%)	25	30
1	D	136/138 (99%)	127 (93%)	6 (4%)	3 (2%)	8	6
All	All	539/552 (98%)	501 (93%)	30 (6%)	8 (2%)	12	11

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	285	ASP
1	D	281	GLU
1	D	283	PRO
1	A	287	PHE
1	A	171	PRO
1	D	286	PRO
1	A	283	PRO
1	C	245	VAL

5.3.2 Protein sidechains

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	126/128 (98%)	116 (92%)	10 (8%)	14	18
1	B	123/128 (96%)	116 (94%)	7 (6%)	24	32

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	C	128/128 (100%)	120 (94%)	8 (6%)	21	28
1	D	127/128 (99%)	117 (92%)	10 (8%)	14	18
All	All	504/512 (98%)	469 (93%)	35 (7%)	18	23

All (35) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	153	ASN
1	A	157	SER
1	A	169	LEU
1	A	181	LEU
1	A	185	LEU
1	A	197	GLN
1	A	233	THR
1	A	284	TYR
1	A	286	PRO
1	A	288	ASP
1	B	151	ILE
1	B	156	LYS
1	B	169	LEU
1	B	173	ASP
1	B	181	LEU
1	B	233	THR
1	B	282	LYS
1	C	169	LEU
1	C	181	LEU
1	C	185	LEU
1	C	197	GLN
1	C	233	THR
1	C	249	GLU
1	C	253	ARG
1	C	282	LYS
1	D	157	SER
1	D	169	LEU
1	D	170	ASN
1	D	181	LEU
1	D	197	GLN
1	D	233	THR
1	D	237	MET
1	D	278	LYS
1	D	283	PRO

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Mol	Chain	Res	Type
1	D	285	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (28) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	197	GLN
1	A	208	ASN
1	A	226	HIS
1	A	228	ASN
1	A	255	ASN
1	A	266	ASN
1	B	154	GLN
1	B	208	ASN
1	B	226	HIS
1	B	228	ASN
1	B	266	ASN
1	C	154	GLN
1	C	170	ASN
1	C	197	GLN
1	C	208	ASN
1	C	226	HIS
1	C	228	ASN
1	C	255	ASN
1	C	266	ASN
1	D	153	ASN
1	D	170	ASN
1	D	197	GLN
1	D	208	ASN
1	D	226	HIS
1	D	228	ASN
1	D	255	ASN
1	D	265	ASN
1	D	266	ASN

5.3.3 RNA ⓘ

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 carbohydrates 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	138/138 (100%)	0.51	13 (9%) 9 12	27, 43, 84, 99	0
1	B	133/138 (96%)	0.13	6 (4%) 34 41	24, 39, 79, 96	0
1	C	138/138 (100%)	0.17	8 (5%) 24 30	26, 41, 74, 81	0
1	D	138/138 (100%)	0.55	17 (12%) 5 7	26, 42, 87, 100	0
All	All	547/552 (99%)	0.34	44 (8%) 13 17	24, 41, 80, 100	0

All (44) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	287	PHE	15.5
1	D	286	PRO	8.9
1	B	151	ILE	8.3
1	A	286	PRO	8.3
1	D	152	GLN	6.0
1	A	173	ASP	5.8
1	D	284	TYR	5.7
1	B	283	PRO	4.4
1	D	151	ILE	4.3
1	A	284	TYR	4.2
1	C	151	ILE	4.2
1	B	280	GLY	3.8
1	D	281	GLU	3.6
1	C	256	LYS	3.5
1	D	257	LYS	3.4
1	A	238	ASP	3.4
1	C	257	LYS	3.2
1	D	283	PRO	3.2
1	D	171	PRO	3.1
1	A	256	LYS	3.1
1	B	257	LYS	3.1

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Mol	Chain	Res	Type	RSRZ
1	C	170	ASN	3.0
1	B	256	LYS	3.0
1	D	173	ASP	3.0
1	A	174	ASP	2.9
1	D	280	GLY	2.9
1	A	285	ASP	2.8
1	D	256	LYS	2.7
1	A	257	LYS	2.6
1	D	288	ASP	2.5
1	D	255	ASN	2.4
1	A	153	ASN	2.4
1	C	280	GLY	2.4
1	A	151	ILE	2.4
1	C	244	ARG	2.3
1	C	173	ASP	2.2
1	D	270	ILE	2.2
1	C	153	ASN	2.2
1	D	278	LYS	2.1
1	A	216	ILE	2.0
1	D	172	ASP	2.0
1	B	237	MET	2.0
1	A	152	GLN	2.0
1	D	282	LYS	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 carbohydrates 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.