



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 11:29 PM GMT

PDB ID : 1XI1
Title : Phi29 DNA polymerase ssDNA complex, monoclinic crystal form
Authors : Kamtekar, S.; Berman, A.J.; Wang, J.; Lazaro, J.M.; de Vega, M.; Blanco, L.; Salas, M.; Steitz, T.A.
Deposited on : 2004-09-21
Resolution : 2.20 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
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
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) : trunk26865

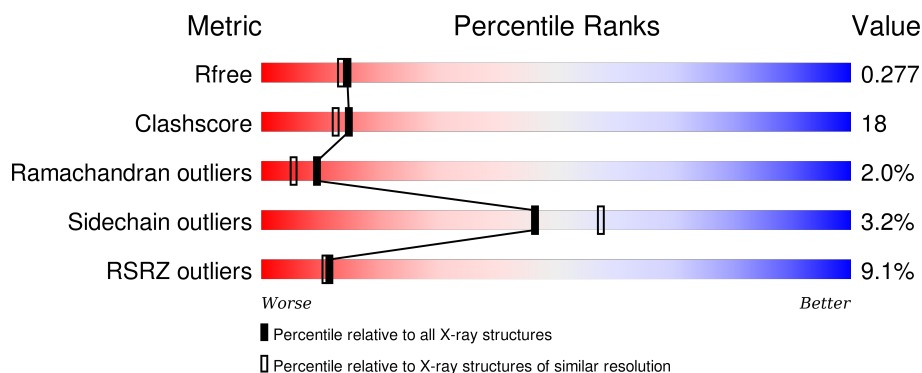
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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}	91344	3774 (2.20-2.20)
Clashscore	102246	4477 (2.20-2.20)
Ramachandran outliers	100387	4404 (2.20-2.20)
Sidechain outliers	100360	4405 (2.20-2.20)
RSRZ outliers	91569	3781 (2.20-2.20)

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	C	5	<div> <div>60%</div> <div> <div></div> <div>60%</div> <div>40%</div> </div> </div>
1	D	5	<div> <div>60%</div> <div> <div>20%</div> <div>40%</div> <div>40%</div> </div> </div>
2	A	575	<div> <div>10%</div> <div> <div>65%</div> <div>31%</div> <div>• •</div> </div> </div>
2	B	575	<div> <div>7%</div> <div> <div>66%</div> <div>30%</div> <div>• •</div> </div> </div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 9693 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 DNA chain called 5'-D(P*TP*TP*TP*TP*T)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	C	3	Total	C	N	O	P	0	0	0
			60	30	6	21	3			
1	D	3	Total	C	N	O	P	0	0	0
			60	30	6	21	3			

- Molecule 2 is a protein called DNA polymerase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	A	571	Total	C	N	O	S	0	0	0
			4668	3041	754	852	21			
2	B	571	Total	C	N	O	S	0	0	0
			4668	3041	754	852	21			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	12	ALA	ASP	ENGINEERED	UNP P03680
A	66	ALA	ASP	ENGINEERED	UNP P03680
B	12	ALA	ASP	ENGINEERED	UNP P03680
B	66	ALA	ASP	ENGINEERED	UNP P03680

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total	Mg	0	0
			1	1		
3	A	1	Total	Mg	0	0
			1	1		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	110	Total 110	O 110	0	0
4	B	125	Total 125	O 125	0	0

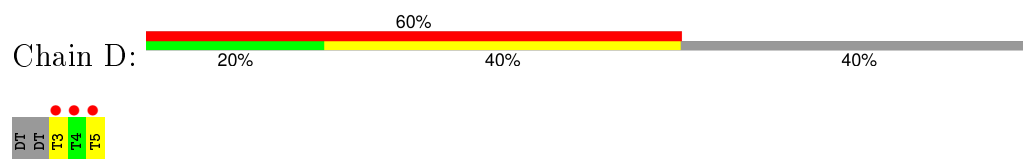
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

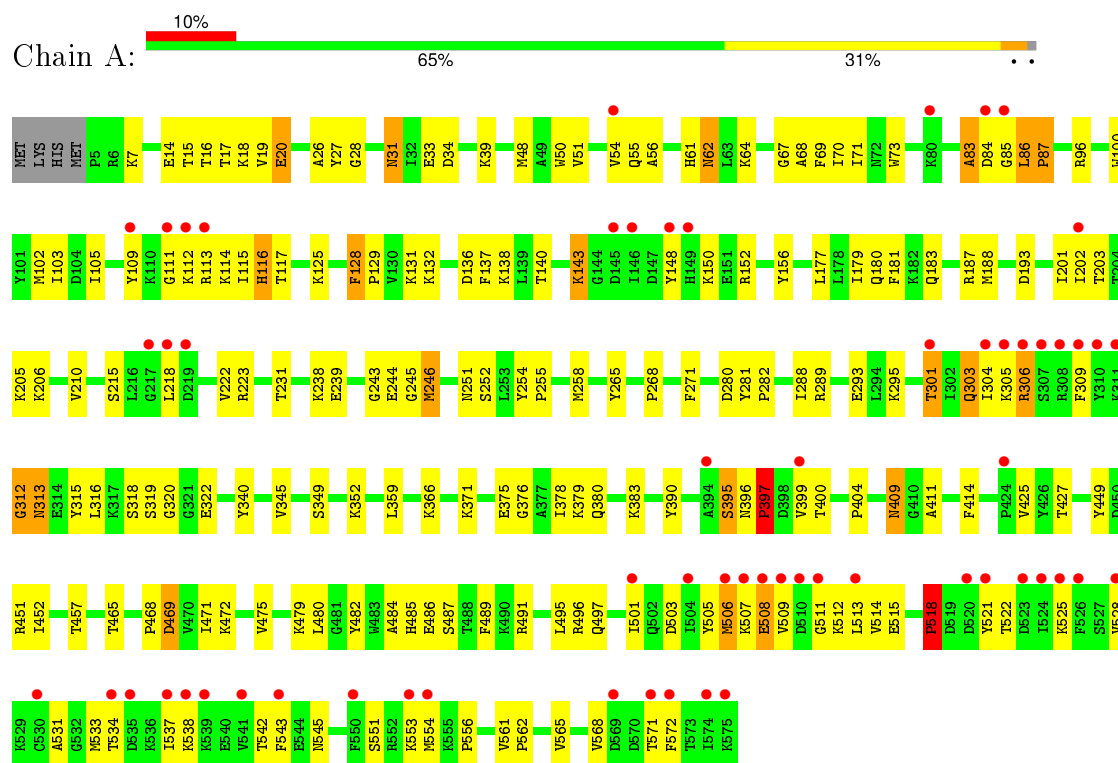
- Molecule 1: 5'-D(P*TP*TP*TP*TP*T)-3'



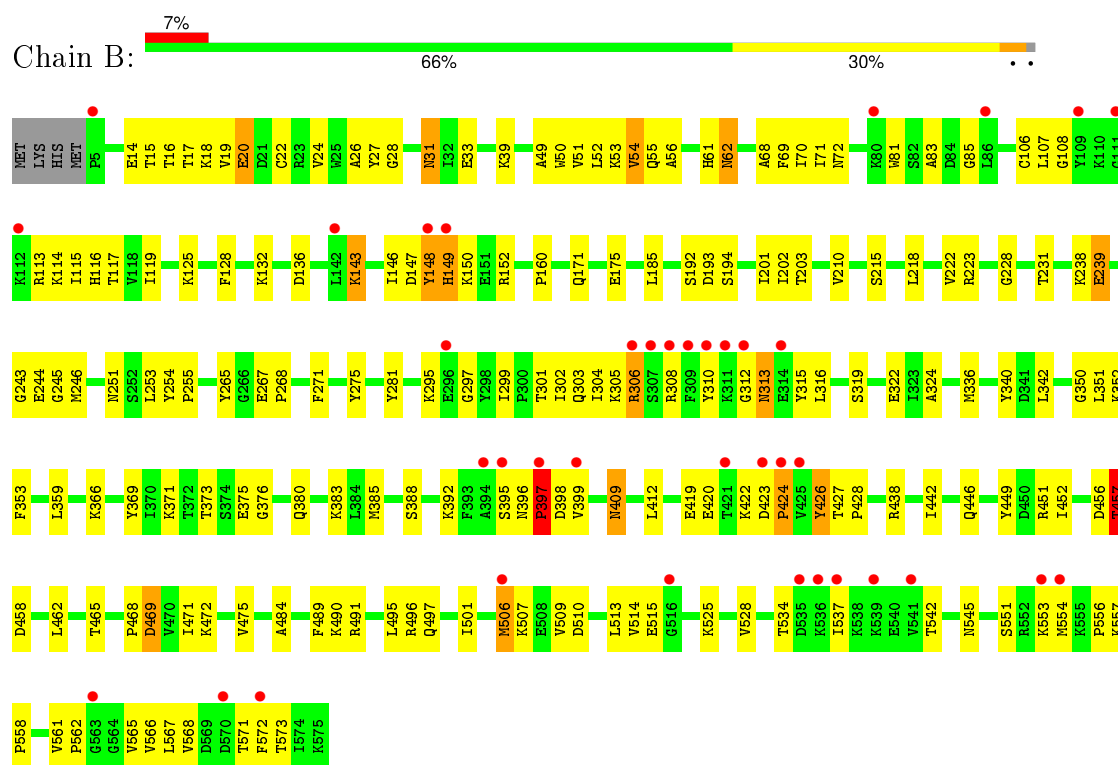
- Molecule 1: 5'-D(P*TP*TP*TP*TP*T)-3'



- Molecule 2: DNA polymerase



- Molecule 2: DNA polymerase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	60.56 Å 170.56 Å 68.81 Å 90.00° 106.99° 90.00°	Depositor
Resolution (Å)	19.71 – 2.20 47.91 – 2.20	Depositor EDS
% Data completeness (in resolution range)	99.1 (19.71-2.20) 99.3 (47.91-2.20)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.31 (at 2.20 Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.243 , 0.277 0.244 , 0.277	Depositor DCC
R_{free} test set	6490 reflections (9.73%)	DCC
Wilson B-factor (Å ²)	44.1	Xtriage
Anisotropy	0.407	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 47.2	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Outliers	1 of 66815 reflections (0.001%)	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	9693	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 4.78% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: MG

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	C	0.71	0/65	0.85	0/98
1	D	0.86	0/65	1.33	0/98
2	A	0.59	2/4788 (0.0%)	0.70	1/6459 (0.0%)
2	B	0.45	0/4788	0.71	1/6459 (0.0%)
All	All	0.53	2/9706 (0.0%)	0.71	2/13114 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	397	PRO	N-CD	-18.59	1.21	1.47
2	A	87	PRO	N-CD	-17.82	1.23	1.47

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	424	PRO	CA-N-CD	-12.43	94.10	111.50
2	A	518	PRO	CA-N-CD	-8.54	99.54	111.50

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	C	60	0	37	4	0
1	D	60	0	37	5	0
2	A	4668	0	4676	180	0
2	B	4668	0	4676	154	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	110	0	0	7	0
4	B	125	0	0	0	0
All	All	9693	0	9426	334	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 18.

All (334) 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)
2:A:305:LYS:HG2	2:A:306:ARG:HG3	1.24	1.20
2:B:305:LYS:HG2	2:B:306:ARG:H	1.09	1.17
2:B:143:LYS:HD2	2:B:143:LYS:H	1.09	1.13
2:A:143:LYS:HD2	2:A:143:LYS:H	1.12	1.10
2:B:369:TYR:O	2:B:373:THR:HG22	1.69	0.92
2:A:505:TYR:CE1	2:A:518:PRO:HG3	2.05	0.91
2:A:243:GLY:HA2	2:A:491:ARG:HA	1.53	0.90
2:B:143:LYS:H	2:B:143:LYS:CD	1.84	0.90
2:A:305:LYS:CG	2:A:306:ARG:H	1.85	0.89
2:A:305:LYS:CG	2:A:306:ARG:HG3	2.03	0.88
2:A:288:ILE:HD11	2:A:345:VAL:HG13	1.55	0.87
2:B:506:MET:CE	2:B:525:LYS:HB3	2.05	0.87
2:B:305:LYS:HG2	2:B:306:ARG:N	1.88	0.87
1:C:3:DT:H2''	1:C:4:DT:O5'	1.75	0.85
2:A:396:ASN:HB3	2:A:397:PRO:HD2	1.59	0.85
2:B:52:LEU:O	2:B:107:LEU:HD11	1.77	0.85
2:B:243:GLY:HA2	2:B:491:ARG:HA	1.58	0.84
2:A:150:LYS:HD3	2:A:152:ARG:HH12	1.43	0.83
2:A:505:TYR:CD1	2:A:518:PRO:HD3	2.13	0.83
2:A:105:ILE:O	2:A:116:HIS:HB2	1.78	0.82
2:A:50:TRP:CE2	2:A:54:VAL:HG21	2.14	0.82
2:B:506:MET:HE3	2:B:525:LYS:HB3	1.61	0.82
2:A:305:LYS:CG	2:A:306:ARG:N	2.42	0.81
2:A:143:LYS:N	2:A:143:LYS:HD2	1.96	0.81
2:A:509:VAL:HG23	2:A:512:LYS:N	1.95	0.80
2:B:305:LYS:HG3	2:B:313:ASN:ND2	1.98	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:305:LYS:HG2	2:A:306:ARG:N	1.99	0.77
2:B:514:VAL:HG12	2:B:515:GLU:H	1.48	0.76
2:A:305:LYS:HG3	2:A:306:ARG:H	1.48	0.76
2:B:147:ASP:C	2:B:149:HIS:H	1.89	0.75
2:A:304:ILE:HD11	2:A:316:LEU:HD11	1.67	0.75
2:B:143:LYS:N	2:B:143:LYS:HD2	1.94	0.74
2:A:511:GLY:O	2:A:512:LYS:HG3	1.87	0.74
2:B:542:THR:OG1	2:B:545:ASN:HB2	1.87	0.74
2:B:50:TRP:CE2	2:B:54:VAL:HG21	2.21	0.74
2:A:143:LYS:H	2:A:143:LYS:CD	1.88	0.73
2:A:509:VAL:HG23	2:A:512:LYS:CA	2.18	0.73
2:B:471:ILE:O	2:B:475:VAL:HG23	1.88	0.73
2:A:305:LYS:HG2	2:A:306:ARG:CG	2.14	0.72
2:B:534:THR:HG23	2:B:537:ILE:H	1.53	0.72
2:B:210:VAL:HG13	2:B:265:TYR:HB2	1.71	0.72
2:B:336:MET:CE	2:B:342:LEU:HD21	2.18	0.72
2:B:336:MET:HE2	2:B:342:LEU:HD21	1.70	0.72
2:B:396:ASN:OD1	2:B:397:PRO:HD2	1.90	0.71
2:A:511:GLY:C	2:A:512:LYS:HG3	2.11	0.71
2:A:534:THR:HG23	2:A:537:ILE:H	1.56	0.70
2:A:554:MET:O	2:A:556:PRO:HD3	1.91	0.70
2:A:128:PHE:HB3	2:A:132:LYS:HD3	1.72	0.70
2:B:54:VAL:O	2:B:54:VAL:HG12	1.90	0.70
2:A:55:GLN:NE2	2:A:115:ILE:HG23	2.07	0.69
2:A:86:LEU:HD12	2:A:87:PRO:HD2	1.73	0.69
2:B:72:ASN:OD1	2:B:412:LEU:HG	1.93	0.69
2:A:508:GLU:HG2	2:A:522:THR:OG1	1.93	0.68
2:A:496:ARG:HG3	2:A:496:ARG:HH11	1.59	0.68
2:A:495:LEU:O	2:A:496:ARG:HG3	1.94	0.68
2:B:336:MET:CE	2:B:342:LEU:CD2	2.72	0.67
2:B:106:CYS:HB2	2:B:114:LYS:HE2	1.76	0.67
2:A:150:LYS:HD3	2:A:152:ARG:NH1	2.10	0.67
2:A:238:LYS:HG2	2:A:239:GLU:HG3	1.75	0.67
2:B:495:LEU:O	2:B:496:ARG:HG3	1.95	0.66
2:B:514:VAL:HG12	2:B:515:GLU:N	2.09	0.66
2:B:238:LYS:HG2	2:B:239:GLU:HG3	1.78	0.66
2:B:305:LYS:CG	2:B:306:ARG:H	1.89	0.66
2:A:313:ASN:H	2:A:313:ASN:HD22	1.43	0.65
2:A:140:THR:HG21	4:A:669:HOH:O	1.97	0.65
2:A:210:VAL:HG13	2:A:265:TYR:HB2	1.79	0.64
2:B:50:TRP:NE1	2:B:54:VAL:HG21	2.13	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:553:LYS:HG2	2:B:571:THR:OG1	1.97	0.64
2:A:542:THR:OG1	2:A:545:ASN:HB2	1.98	0.64
2:B:54:VAL:O	2:B:56:ALA:N	2.32	0.63
1:D:3:DT:H5''	1:D:3:DT:H6	1.63	0.62
2:A:281:TYR:HB3	2:A:352:LYS:HB3	1.80	0.62
2:B:31:ASN:C	2:B:31:ASN:HD22	2.01	0.62
2:B:303:GLN:HB3	2:B:315:TYR:CE2	2.35	0.62
2:B:554:MET:O	2:B:556:PRO:HD3	2.00	0.61
2:A:83:ALA:O	2:A:84:ASP:CG	2.39	0.61
2:B:336:MET:HE3	2:B:342:LEU:CD2	2.31	0.60
2:A:31:ASN:HD22	2:A:31:ASN:C	2.04	0.60
2:B:299:ILE:HG13	2:B:446:GLN:OE1	2.00	0.60
2:B:281:TYR:HB3	2:B:352:LYS:HB3	1.83	0.60
2:A:246:MET:HG2	2:A:465:THR:HA	1.83	0.60
2:B:336:MET:HE2	2:B:342:LEU:CD2	2.31	0.60
2:B:399:VAL:O	2:B:399:VAL:HG12	2.02	0.60
2:A:507:LYS:HB3	2:A:514:VAL:HG23	1.83	0.60
2:A:471:ILE:O	2:A:475:VAL:HG23	2.01	0.59
2:A:203:THR:HG22	2:A:205:LYS:H	1.67	0.59
2:A:305:LYS:HE2	2:A:306:ARG:HE	1.67	0.59
2:A:553:LYS:HG2	2:A:571:THR:OG1	2.03	0.59
2:B:147:ASP:C	2:B:149:HIS:N	2.55	0.59
2:A:409:ASN:O	2:A:562:PRO:HG3	2.03	0.59
2:A:218:LEU:HD21	2:A:268:PRO:HG2	1.85	0.58
2:B:496:ARG:HG3	2:B:496:ARG:HH11	1.67	0.58
2:A:511:GLY:O	2:A:512:LYS:CG	2.51	0.58
2:B:244:GLU:HA	2:B:489:PHE:O	2.03	0.58
2:B:202:ILE:O	2:B:203:THR:OG1	2.12	0.58
2:B:150:LYS:HD3	2:B:152:ARG:HH12	1.67	0.57
2:A:506:MET:HG3	2:A:513:LEU:HD22	1.86	0.57
2:B:147:ASP:O	2:B:149:HIS:N	2.37	0.57
2:B:245:GLY:HA3	2:B:489:PHE:CZ	2.39	0.57
2:B:556:PRO:HA	2:B:568:VAL:O	2.05	0.57
2:B:506:MET:HE3	2:B:525:LYS:CB	2.35	0.57
1:D:5:DT:N3	2:B:567:LEU:HD12	2.20	0.57
2:A:509:VAL:HG22	2:A:511:GLY:H	1.71	0.56
2:B:128:PHE:HB3	2:B:132:LYS:HD3	1.87	0.56
2:B:113:ARG:O	2:B:113:ARG:HG3	2.06	0.56
2:A:399:VAL:HG12	2:A:399:VAL:O	2.05	0.56
1:D:5:DT:O3'	2:B:15:THR:N	2.35	0.56
2:A:16:THR:HG22	2:A:17:THR:N	2.21	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:509:VAL:CG2	2:A:512:LYS:N	2.69	0.56
2:B:106:CYS:HB2	2:B:114:LYS:CE	2.36	0.56
2:A:20:GLU:CD	2:A:20:GLU:H	2.09	0.56
2:B:72:ASN:ND2	2:B:562:PRO:O	2.39	0.56
2:A:479:LYS:HD2	2:A:482:TYR:CE2	2.41	0.56
2:B:246:MET:HG2	2:B:465:THR:HA	1.87	0.56
2:A:68:ALA:CB	2:A:565:VAL:HG23	2.36	0.55
1:C:3:DT:H5'	2:A:129:PRO:HG3	1.88	0.55
2:B:201:ILE:HD11	2:B:366:LYS:HD3	1.88	0.55
2:B:507:LYS:HG2	2:B:509:VAL:HG23	1.88	0.55
2:B:210:VAL:HG11	2:B:359:LEU:HD21	1.89	0.55
2:B:210:VAL:CG1	2:B:265:TYR:HB2	2.37	0.55
2:B:396:ASN:OD1	2:B:397:PRO:CD	2.54	0.55
2:A:55:GLN:HA	2:A:116:HIS:O	2.06	0.55
2:A:210:VAL:HG11	2:A:359:LEU:HD21	1.87	0.55
2:A:244:GLU:HA	2:A:489:PHE:O	2.07	0.55
2:B:22:CYS:SG	2:B:566:VAL:HG23	2.47	0.55
2:A:143:LYS:NZ	4:A:668:HOH:O	2.40	0.54
2:A:14:GLU:HB2	2:A:26:ALA:HB3	1.88	0.54
1:D:5:DT:H2'	2:B:148:TYR:CD2	2.41	0.54
2:A:50:TRP:CE2	2:A:54:VAL:CG2	2.90	0.54
2:A:215:SER:OG	2:A:218:LEU:HB2	2.07	0.54
2:A:48:MET:HE1	2:A:70:ILE:HG12	1.89	0.54
2:B:20:GLU:H	2:B:20:GLU:CD	2.09	0.54
2:B:456:ASP:OD1	2:B:457:THR:HG23	2.08	0.54
2:B:506:MET:HE2	2:B:525:LYS:HB3	1.85	0.53
2:B:215:SER:OG	2:B:218:LEU:HB2	2.08	0.53
2:A:222:VAL:HG12	2:A:427:THR:HG22	1.91	0.53
2:A:313:ASN:HD22	2:A:313:ASN:N	2.02	0.53
2:A:451:ARG:NH1	2:A:468:PRO:HG3	2.23	0.53
2:A:109:TYR:HA	2:A:114:LYS:HA	1.91	0.53
2:A:313:ASN:ND2	2:A:313:ASN:H	2.05	0.53
2:B:501:ILE:HG22	2:B:528:VAL:HG22	1.90	0.52
2:A:295:LYS:HE3	2:A:340:TYR:O	2.08	0.52
2:A:507:LYS:O	2:A:508:GLU:C	2.45	0.52
2:A:7:LYS:O	2:A:56:ALA:HB1	2.09	0.52
2:A:303:GLN:HG3	2:A:304:ILE:N	2.24	0.52
2:A:202:ILE:O	2:A:203:THR:CB	2.58	0.52
2:B:231:THR:HG22	2:B:497:GLN:HG2	1.90	0.52
2:A:288:ILE:HG12	2:A:289:ARG:N	2.25	0.52
2:A:61:HIS:O	2:A:62:ASN:HB3	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:409:ASN:N	2:B:409:ASN:HD22	2.08	0.52
2:B:469:ASP:HA	2:B:472:LYS:HE3	1.92	0.52
2:B:303:GLN:HE21	2:B:305:LYS:HB2	1.75	0.51
2:B:305:LYS:HG3	2:B:313:ASN:HD21	1.71	0.51
2:A:245:GLY:HA3	2:A:489:PHE:CZ	2.44	0.51
2:A:496:ARG:HG3	2:A:496:ARG:NH1	2.24	0.51
2:B:350:GLY:O	2:B:351:LEU:HD23	2.10	0.51
2:B:427:THR:N	2:B:428:PRO:CD	2.73	0.51
2:B:222:VAL:HG12	2:B:427:THR:HG22	1.91	0.51
2:B:409:ASN:H	2:B:409:ASN:HD22	1.58	0.51
2:B:31:ASN:ND2	2:B:33:GLU:H	2.09	0.51
2:B:15:THR:HG21	2:B:69:PHE:CZ	2.46	0.51
2:A:506:MET:CG	2:A:513:LEU:HD22	2.40	0.51
2:B:171:GLN:O	2:B:175:GLU:HG3	2.10	0.51
2:B:51:VAL:HG13	2:B:117:THR:HG21	1.92	0.51
2:A:50:TRP:CZ2	2:A:54:VAL:HG21	2.45	0.51
2:A:31:ASN:HD22	2:A:33:GLU:H	1.58	0.51
2:A:501:ILE:HG22	2:A:528:VAL:HG22	1.92	0.51
2:A:280:ASP:C	2:A:282:PRO:HD3	2.31	0.51
2:A:48:MET:CE	2:A:70:ILE:HG12	2.41	0.51
2:A:187:ARG:HB2	2:A:193:ASP:OD1	2.11	0.51
2:A:506:MET:HE2	2:A:525:LYS:HB3	1.92	0.50
2:A:251:ASN:OD1	2:A:484:ALA:HB2	2.11	0.50
2:A:303:GLN:HE21	2:A:305:LYS:HB2	1.77	0.50
2:B:305:LYS:O	2:B:306:ARG:C	2.49	0.50
2:B:49:ALA:O	2:B:53:LYS:HG3	2.11	0.50
2:A:231:THR:HG22	2:A:497:GLN:HG2	1.94	0.50
1:C:5:DT:H2'	2:A:148:TYR:CD2	2.46	0.50
2:A:508:GLU:CB	2:A:522:THR:OG1	2.60	0.50
2:A:201:ILE:HD11	2:A:366:LYS:HD3	1.94	0.50
2:A:556:PRO:HA	2:A:568:VAL:O	2.11	0.50
2:A:471:ILE:HG22	2:A:475:VAL:HG23	1.92	0.50
2:B:305:LYS:CG	2:B:306:ARG:N	2.60	0.50
2:B:336:MET:CE	2:B:342:LEU:HD22	2.42	0.49
2:B:313:ASN:HD22	2:B:313:ASN:H	1.59	0.49
2:B:313:ASN:HD22	2:B:313:ASN:N	2.10	0.49
2:B:295:LYS:HE3	2:B:340:TYR:O	2.12	0.49
2:B:313:ASN:H	2:B:313:ASN:ND2	2.11	0.49
1:C:3:DT:C2'	1:C:4:DT:O5'	2.53	0.49
2:A:469:ASP:HA	2:A:472:LYS:HE3	1.93	0.49
2:B:375:GLU:HG2	2:B:376:GLY:N	2.28	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:254:TYR:HB2	2:B:255:PRO:HD3	1.95	0.49
2:B:68:ALA:CB	2:B:565:VAL:HG23	2.43	0.49
2:A:125:LYS:HE3	2:A:180:GLN:OE1	2.12	0.49
2:A:304:ILE:CD1	2:A:316:LEU:HD11	2.41	0.48
2:A:55:GLN:CD	2:A:115:ILE:HG23	2.33	0.48
2:B:244:GLU:N	2:B:490:LYS:O	2.46	0.48
2:A:48:MET:HG3	2:A:73:TRP:CD2	2.48	0.48
2:A:380:GLN:OE1	2:A:383:LYS:HE2	2.13	0.48
2:A:16:THR:HG22	2:A:18:LYS:H	1.78	0.48
2:A:471:ILE:HG22	2:A:475:VAL:CG2	2.44	0.48
2:B:28:GLY:HA2	2:B:39:LYS:O	2.13	0.48
2:B:449:TYR:O	2:B:452:ILE:HG22	2.13	0.48
2:B:551:SER:HA	2:B:572:PHE:O	2.13	0.48
2:A:67:GLY:O	2:A:71:ILE:HG12	2.14	0.48
2:A:509:VAL:HG23	2:A:512:LYS:C	2.34	0.48
2:B:253:LEU:HD22	2:B:458:ASP:HB3	1.96	0.48
2:A:243:GLY:O	2:A:244:GLU:HB2	2.12	0.48
2:A:409:ASN:ND2	2:A:411:ALA:H	2.12	0.47
2:B:451:ARG:NH1	2:B:468:PRO:HG3	2.29	0.47
2:A:222:VAL:CG1	2:A:427:THR:HG22	2.43	0.47
2:B:14:GLU:HB2	2:B:26:ALA:HB3	1.97	0.47
2:A:515:GLU:CD	2:A:515:GLU:H	2.17	0.47
2:A:396:ASN:HA	2:A:397:PRO:HD3	1.59	0.47
2:B:319:SER:HB2	2:B:322:GLU:O	2.15	0.47
2:A:508:GLU:CG	2:A:522:THR:OG1	2.61	0.47
2:A:404:PRO:HB3	2:A:414:PHE:CE2	2.50	0.47
2:B:19:VAL:HG13	2:B:561:VAL:HG11	1.97	0.47
2:A:312:GLY:O	2:A:313:ASN:C	2.53	0.47
2:A:542:THR:OG1	2:A:545:ASN:CB	2.63	0.47
2:B:31:ASN:HD22	2:B:33:GLU:H	1.63	0.47
2:B:15:THR:HG22	2:B:24:VAL:HG22	1.97	0.47
2:B:70:ILE:HD13	2:B:119:ILE:HD13	1.96	0.47
2:B:542:THR:H	2:B:545:ASN:HB3	1.80	0.47
2:B:275:TYR:CE1	2:B:352:LYS:HG2	2.50	0.47
2:B:16:THR:HG22	2:B:17:THR:N	2.29	0.47
2:A:96:ARG:HH12	2:A:400:THR:HB	1.80	0.47
2:A:102:MET:HG2	2:A:103:ILE:N	2.30	0.47
2:A:375:GLU:HG2	2:A:376:GLY:N	2.31	0.46
2:B:496:ARG:HG3	2:B:496:ARG:NH1	2.31	0.46
2:A:137:PHE:O	2:A:138:LYS:HB2	2.16	0.46
2:B:336:MET:HE3	2:B:342:LEU:HD21	1.92	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:551:SER:HA	2:A:572:PHE:O	2.16	0.46
2:A:409:ASN:HD22	2:A:409:ASN:N	2.12	0.46
2:A:156:TYR:HB3	4:A:601:HOH:O	2.15	0.46
2:A:378:ILE:HG12	4:A:638:HOH:O	2.16	0.46
2:B:108:GLY:O	2:B:115:ILE:HB	2.15	0.46
2:B:561:VAL:HB	2:B:562:PRO:HD2	1.97	0.45
2:B:16:THR:HG22	2:B:18:LYS:H	1.81	0.45
2:B:27:TYR:C	2:B:27:TYR:CD1	2.89	0.45
2:A:15:THR:HG21	2:A:69:PHE:CZ	2.52	0.45
2:A:449:TYR:O	2:A:452:ILE:HG22	2.16	0.45
2:B:70:ILE:HD13	2:B:119:ILE:CD1	2.46	0.45
2:A:28:GLY:HA2	2:A:39:LYS:O	2.17	0.45
2:B:185:LEU:HG	2:B:385:MET:HE3	1.99	0.45
2:A:113:ARG:HH11	2:A:113:ARG:HG3	1.81	0.45
2:B:506:MET:HG3	2:B:513:LEU:HB3	1.97	0.45
2:A:218:LEU:O	2:A:222:VAL:HG23	2.17	0.45
2:B:228:GLY:O	2:B:438:ARG:HD3	2.17	0.45
2:A:254:TYR:O	2:A:258:MET:HG3	2.16	0.45
2:B:452:ILE:HA	2:B:462:LEU:HD23	1.99	0.45
2:B:223:ARG:NH1	2:B:395:SER:O	2.50	0.45
2:A:507:LYS:HA	2:A:521:TYR:HA	2.00	0.44
2:A:31:ASN:ND2	2:A:33:GLU:H	2.15	0.44
2:A:246:MET:HB3	2:A:485:HIS:HE1	1.81	0.44
2:A:396:ASN:CB	2:A:397:PRO:HD2	2.25	0.44
2:A:379:LYS:O	2:A:383:LYS:HG3	2.17	0.44
2:B:132:LYS:NZ	2:B:136:ASP:OD2	2.46	0.44
2:A:27:TYR:CD1	2:A:27:TYR:C	2.90	0.44
2:B:275:TYR:HE1	2:B:352:LYS:HG2	1.83	0.44
2:A:202:ILE:O	2:A:206:LYS:HB3	2.18	0.44
2:A:188:MET:HG3	4:A:684:HOH:O	2.17	0.44
2:A:31:ASN:HB3	2:A:34:ASP:O	2.18	0.44
2:A:223:ARG:NH1	2:A:395:SER:O	2.51	0.44
2:B:426:TYR:CE2	2:B:428:PRO:HB2	2.53	0.43
2:A:136:ASP:HB3	2:A:380:GLN:HG3	2.00	0.43
2:B:267:GLU:HA	2:B:268:PRO:HD3	1.85	0.43
2:B:514:VAL:CG1	2:B:515:GLU:H	2.25	0.43
2:A:179:ILE:O	2:A:183:GLN:HG2	2.18	0.43
2:B:61:HIS:O	2:B:62:ASN:HB3	2.17	0.43
2:A:491:ARG:NE	2:A:503:ASP:OD2	2.44	0.43
2:A:505:TYR:CZ	2:A:518:PRO:HG3	2.51	0.43
2:A:252:SER:HB2	2:A:480:LEU:HD12	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:305:LYS:O	2:A:306:ARG:C	2.58	0.43
2:A:508:GLU:HA	2:A:522:THR:CB	2.48	0.43
2:B:31:ASN:C	2:B:31:ASN:ND2	2.72	0.43
2:A:471:ILE:O	2:A:471:ILE:HG22	2.19	0.43
2:A:64:LYS:HA	2:A:100:TRP:CG	2.54	0.43
2:A:320:GLY:HA3	2:B:310:TYR:OH	2.18	0.43
2:A:288:ILE:HD11	2:A:345:VAL:CG1	2.39	0.43
2:B:419:GLU:HG2	2:B:420:GLU:N	2.33	0.43
2:A:319:SER:HB2	2:A:322:GLU:O	2.19	0.42
2:A:111:GLY:O	2:A:112:LYS:HB2	2.18	0.42
2:B:194:SER:OG	2:B:388:SER:HB2	2.19	0.42
2:A:271:PHE:CD2	2:A:352:LYS:HG3	2.54	0.42
2:A:177:LEU:O	2:A:181:PHE:HD1	2.03	0.42
2:A:305:LYS:HE2	2:A:306:ARG:CG	2.49	0.42
2:A:48:MET:HG3	2:A:73:TRP:CG	2.55	0.42
2:A:61:HIS:O	2:A:62:ASN:CB	2.68	0.42
2:B:125:LYS:NZ	2:B:193:ASP:OD2	2.51	0.42
2:B:514:VAL:CG1	2:B:515:GLU:N	2.79	0.42
2:A:271:PHE:O	2:A:349:SER:HB2	2.19	0.42
2:B:281:TYR:HA	2:B:353:PHE:O	2.20	0.42
2:A:506:MET:HE3	2:A:525:LYS:HD3	2.02	0.42
2:B:422:LYS:O	2:B:423:ASP:OD1	2.37	0.42
2:A:85:GLY:O	2:A:86:LEU:HB3	2.20	0.42
2:A:301:THR:HB	2:A:340:TYR:HE1	1.84	0.42
2:B:468:PRO:O	2:B:472:LYS:HG3	2.19	0.42
2:A:309:PHE:HZ	2:B:324:ALA:HB2	1.85	0.42
2:A:303:GLN:CG	2:A:304:ILE:N	2.83	0.42
2:A:505:TYR:CE1	2:A:518:PRO:CG	2.90	0.42
2:B:271:PHE:CD2	2:B:352:LYS:HG3	2.54	0.42
2:A:51:VAL:HG13	2:A:117:THR:HG21	2.02	0.42
2:B:304:ILE:HD12	2:B:316:LEU:HD21	2.00	0.42
2:A:534:THR:CG2	2:A:537:ILE:HG13	2.50	0.42
2:A:508:GLU:HA	2:A:522:THR:HB	2.01	0.42
2:A:254:TYR:HB2	2:A:255:PRO:HD3	2.02	0.42
2:B:251:ASN:OD1	2:B:484:ALA:HB2	2.20	0.42
2:B:551:SER:HB3	2:B:573:THR:OG1	2.20	0.41
2:A:525:LYS:HG3	4:A:656:HOH:O	2.21	0.41
2:A:452:ILE:O	2:A:452:ILE:HG23	2.20	0.41
2:B:557:LYS:HA	2:B:558:PRO:HD3	1.85	0.41
2:A:131:LYS:HE3	4:A:651:HOH:O	2.20	0.41
2:B:81:TRP:CH2	2:B:83:ALA:HB2	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:146:ILE:O	2:B:148:TYR:N	2.53	0.41
2:A:143:LYS:N	2:A:143:LYS:CD	2.67	0.41
2:B:336:MET:HE3	2:B:342:LEU:HD22	2.00	0.41
2:A:309:PHE:CZ	2:B:324:ALA:HB2	2.56	0.41
1:D:5:DT:C3'	2:B:15:THR:H	2.32	0.41
2:A:293:GLU:OE2	2:A:318:SER:HB2	2.20	0.41
2:B:192:SER:HA	2:B:392:LYS:HE3	2.02	0.41
2:A:132:LYS:NZ	2:A:136:ASP:OD2	2.50	0.41
2:A:19:VAL:HG13	2:A:561:VAL:HG11	2.02	0.41
2:B:380:GLN:OE1	2:B:383:LYS:HE2	2.20	0.41
2:B:297:GLY:HA2	2:B:449:TYR:CE2	2.55	0.41
2:A:533:MET:HG2	2:A:538:LYS:HG3	2.03	0.41
2:B:452:ILE:HG23	2:B:452:ILE:O	2.21	0.40
2:A:486:GLU:O	2:A:487:SER:HB3	2.21	0.40
2:B:301:THR:HG22	2:B:442:ILE:HD13	2.04	0.40
2:B:534:THR:CG2	2:B:537:ILE:HG13	2.51	0.40
2:B:302:ILE:HD11	2:B:336:MET:SD	2.61	0.40
2:B:312:GLY:O	2:B:313:ASN:C	2.60	0.40
2:A:303:GLN:HB2	2:A:315:TYR:CE2	2.56	0.40
2:A:508:GLU:CA	2:A:522:THR:OG1	2.70	0.40
2:B:422:LYS:HB2	2:B:422:LYS:HE3	1.84	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	
2	A	569/575 (99%)	513 (90%)	46 (8%)	10 (2%)	11	7
2	B	569/575 (99%)	516 (91%)	40 (7%)	13 (2%)	8	4
All	All	1138/1150 (99%)	1029 (90%)	86 (8%)	23 (2%)	9	5

All (23) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	A	397	PRO
2	A	531	ALA
2	B	55	GLN
2	B	426	TYR
2	A	306	ARG
2	A	313	ASN
2	B	397	PRO
2	A	62	ASN
2	A	83	ALA
2	B	148	TYR
2	B	306	ARG
2	B	308	ARG
2	B	313	ASN
2	B	457	THR
2	A	86	LEU
2	B	62	ASN
2	A	457	THR
2	B	85	GLY
2	B	510	ASP
2	B	239	GLU
2	B	54	VAL
2	A	425	VAL
2	A	312	GLY

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	
2	A	502/506 (99%)	485 (97%)	17 (3%)	44	54
2	B	502/506 (99%)	487 (97%)	15 (3%)	48	60
All	All	1004/1012 (99%)	972 (97%)	32 (3%)	46	57

All (32) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	A	20	GLU
2	A	31	ASN
2	A	116	HIS
2	A	128	PHE
2	A	143	LYS
2	A	246	MET
2	A	301	THR
2	A	303	GLN
2	A	371	LYS
2	A	390	TYR
2	A	395	SER
2	A	409	ASN
2	A	469	ASP
2	A	506	MET
2	A	508	GLU
2	A	518	PRO
2	A	543	PHE
2	B	20	GLU
2	B	31	ASN
2	B	71	ILE
2	B	116	HIS
2	B	143	LYS
2	B	149	HIS
2	B	160	PRO
2	B	371	LYS
2	B	397	PRO
2	B	398	ASP
2	B	409	ASN
2	B	424	PRO
2	B	457	THR
2	B	469	ASP
2	B	506	MET

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
2	A	31	ASN
2	A	313	ASN
2	A	409	ASN
2	A	485	HIS
2	B	31	ASN
2	B	171	GLN
2	B	313	ASN

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Mol	Chain	Res	Type
2	B	409	ASN
2	B	485	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 ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	C	3/5 (60%)	3.86	3 (100%) 0 0	121, 121, 130, 131	0
1	D	3/5 (60%)	2.78	3 (100%) 0 0	124, 124, 127, 139	0
2	A	571/575 (99%)	0.72	60 (10%) 8 7	33, 54, 95, 128	0
2	B	571/575 (99%)	0.62	38 (6%) 21 20	33, 53, 90, 128	0
All	All	1148/1160 (98%)	0.68	104 (9%) 11 11	33, 54, 94, 139	0

All (104) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	A	305	LYS	7.1
2	B	310	TYR	6.4
2	A	112	LYS	6.2
2	A	310	TYR	6.1
2	A	148	TYR	5.8
2	A	510	ASP	5.8
2	A	306	ARG	5.7
2	A	508	GLU	5.7
2	A	399	VAL	5.1
2	B	306	ARG	5.1
1	C	4	DT	4.7
2	B	424	PRO	4.7
1	C	3	DT	4.5
2	B	148	TYR	4.4
2	A	554	MET	4.4
2	A	524	ILE	4.3
2	A	113	ARG	4.3
2	A	572	PHE	4.2
2	A	537	ILE	4.2
2	A	507	LYS	4.1
2	A	553	LYS	4.1

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Mol	Chain	Res	Type	RSRZ
2	A	149	HIS	4.1
2	A	511	GLY	4.1
2	A	520	ASP	4.0
2	A	111	GLY	4.0
2	A	509	VAL	4.0
2	A	84	ASP	3.9
2	A	541	VAL	3.8
2	A	543	PHE	3.7
2	A	109	TYR	3.6
2	A	309	PHE	3.6
2	B	312	GLY	3.6
2	A	506	MET	3.4
2	B	111	GLY	3.4
1	D	4	DT	3.4
2	B	109	TYR	3.3
2	A	218	LEU	3.2
2	A	523	ASP	3.2
2	B	399	VAL	3.1
2	B	535	ASP	3.1
2	B	307	SER	3.1
2	A	304	ILE	3.1
2	B	309	PHE	3.0
2	A	575	LYS	3.0
2	A	513	LEU	3.0
2	B	554	MET	3.0
2	B	394	ALA	3.0
2	A	311	LYS	2.9
2	A	424	PRO	2.9
1	D	5	DT	2.9
2	B	112	LYS	2.9
2	A	85	GLY	2.9
2	A	550	PHE	2.8
2	B	423	ASP	2.7
2	B	142	LEU	2.7
2	B	308	ARG	2.7
2	A	308	ARG	2.7
2	A	569	ASP	2.7
2	A	538	LYS	2.7
2	B	536	LYS	2.7
2	A	525	LYS	2.6
2	B	149	HIS	2.6
2	B	572	PHE	2.6

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Mol	Chain	Res	Type	RSRZ
2	A	574	ILE	2.6
2	B	314	GLU	2.5
2	A	539	LYS	2.5
2	B	80	LYS	2.5
2	B	86	LEU	2.4
2	A	146	ILE	2.4
2	A	526	PHE	2.4
2	A	535	ASP	2.4
2	A	571	THR	2.4
1	C	5	DT	2.4
2	B	397	PRO	2.4
2	B	5	PRO	2.3
2	B	425	VAL	2.3
2	A	145	ASP	2.3
2	A	307	SER	2.3
2	A	504	ILE	2.3
2	A	217	GLY	2.3
2	B	395	SER	2.3
2	B	541	VAL	2.3
2	A	80	LYS	2.3
2	B	311	LYS	2.2
2	A	219	ASP	2.2
2	A	501	ILE	2.2
2	B	570	ASP	2.2
2	A	534	THR	2.2
2	A	521	TYR	2.2
2	B	506	MET	2.2
2	B	296	GLU	2.2
2	A	394	ALA	2.1
2	B	421	THR	2.1
2	B	539	LYS	2.1
1	D	3	DT	2.1
2	A	301	THR	2.1
2	A	202	ILE	2.1
2	B	537	ILE	2.1
2	B	553	LYS	2.1
2	A	530	CYS	2.0
2	A	54	VAL	2.0
2	B	516	GLY	2.0
2	B	563	GLY	2.0
2	A	528	VAL	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](#)

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(\AA^2)	Q<0.9
3	MG	A	576	1/1	0.79	0.20	-0.46	85,85,85,85	0
3	MG	B	576	1/1	0.57	0.20	-	97,97,97,97	0

6.5 Other polymers [i](#)

There are no such residues in this entry.