



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2018 – 12:19 PM EST

PDB ID : 5N9A
Title : Crystal Structure of Drosophila DHX36 helicase in complex with GT-TAGGGTT
Authors : Chen, W.-F.; Rety, S.; Guo, H.-L.; Wu, W.-Q.; Liu, N.-N.; Liu, Q.-W.; Dai, Y.-X.; Xi, X.-G.
Deposited on : 2017-02-24
Resolution : 3.04 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

<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	:	rb-20030736
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)	:	rb-20030736

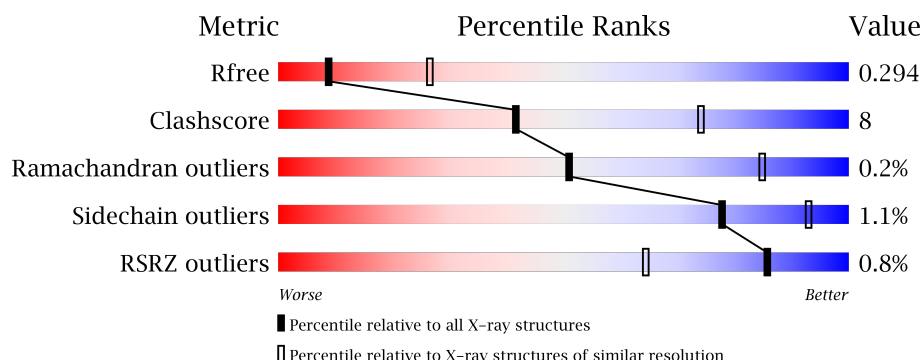
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.04 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}	100719	2176 (3.08-3.00)
Clashscore	112137	2542 (3.08-3.00)
Ramachandran outliers	110173	2458 (3.08-3.00)
Sidechain outliers	110143	2461 (3.08-3.00)
RSRZ outliers	101464	2202 (3.08-3.00)

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	944	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, green 71%, yellow 18%, grey 10%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> 1% 71% 18% 10% </div> </div>
1	B	944	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, green 72%, yellow 18%, grey 10%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> 72% 18% 10% </div> </div>
2	C	9	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 33%, green 56%, yellow 44%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> 33% 56% 44% </div> </div>
2	D	9	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 11%, green 22%, yellow 78%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> 11% 22% 78% </div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 14012 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 CG9323, isoform A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	849	Total	C	N	O	S	0	0	0
			6814	4304	1200	1265	45			
1	B	853	Total	C	N	O	S	0	0	0
			6848	4324	1207	1272	45			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	943	VAL	-	expression tag	UNP Q8SWT2
A	944	ASP	-	expression tag	UNP Q8SWT2
B	943	VAL	-	expression tag	UNP Q8SWT2
B	944	ASP	-	expression tag	UNP Q8SWT2

- Molecule 2 is a DNA chain called DNA (5'-D(P*GP*TP*TP*AP*GP*GP*GP*TP*T)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	9	Total	C	N	O	P	0	0	0
			174	81	31	53	9			
2	D	9	Total	C	N	O	P	0	0	0
			173	80	31	53	9			

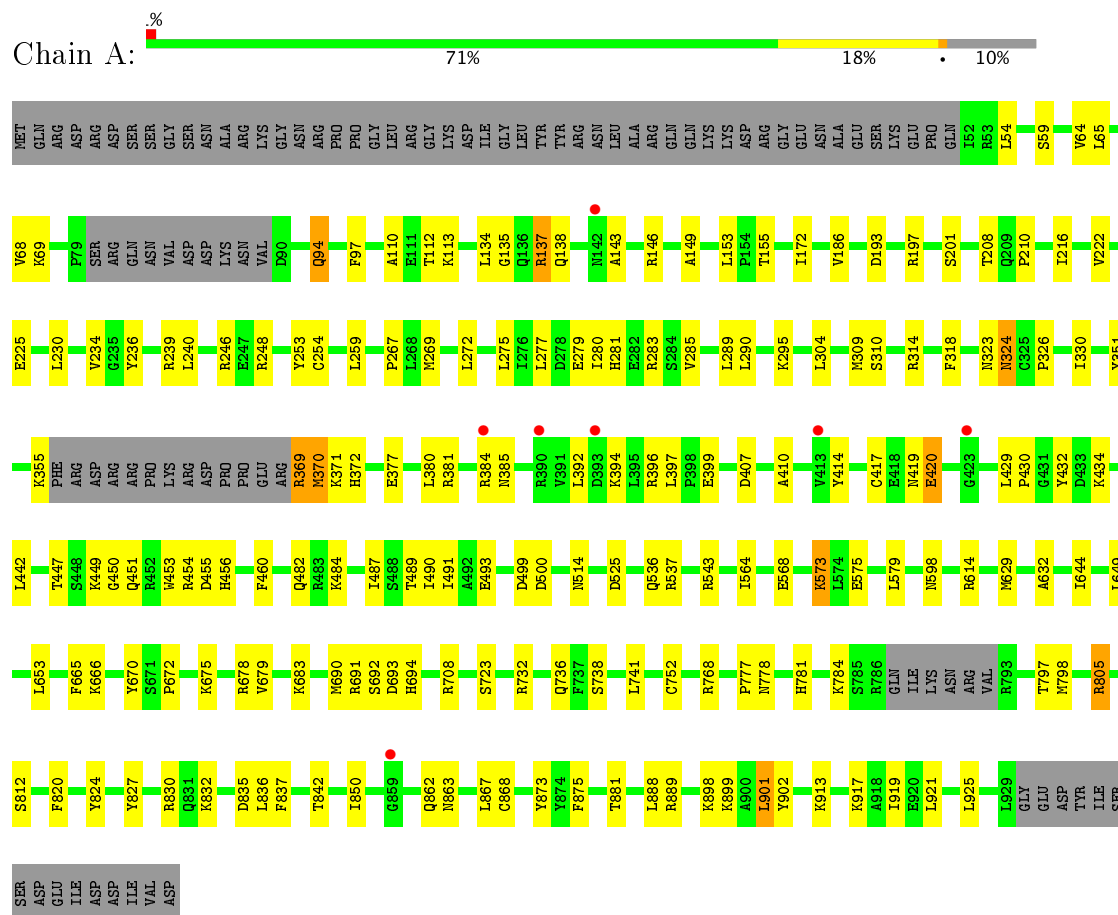
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	2	Total	O	0	0
			2	2		
3	B	1	Total	O	0	0
			1	1		

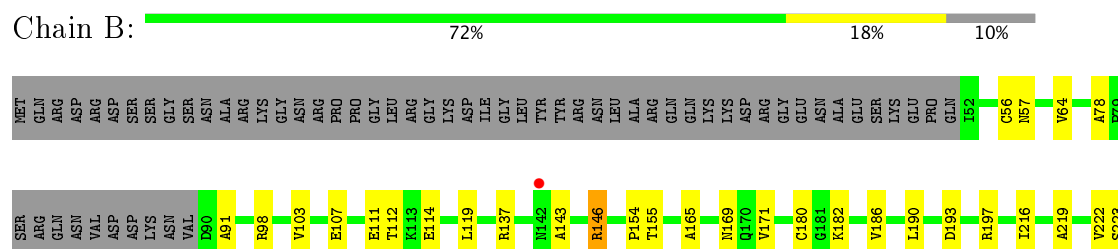
3 Residue-property plots

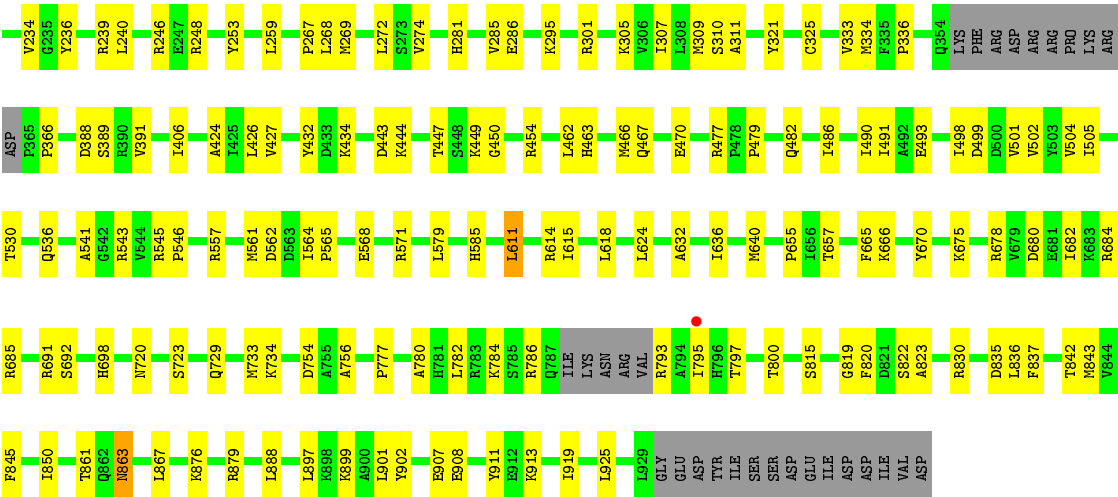
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are 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: CG9323, isoform A



• Molecule 1: CG9323, isoform A





• Molecule 2: DNA (5'-D(P*GP*TP*TP*AP*GP*GP*GP*TP*T)-3')



• Molecule 2: DNA (5'-D(P*GP*TP*TP*AP*GP*GP*GP*TP*T)-3')



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	305.57Å 51.42Å 165.36Å 90.00° 114.94° 90.00°	Depositor
Resolution (Å)	69.27 – 3.04 149.94 – 3.04	Depositor EDS
% Data completeness (in resolution range)	96.1 (69.27-3.04) 96.1 (149.94-3.04)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.94 (at 3.01Å)	Xtriage
Refinement program	PHENIX (dev_2427: ???)	Depositor
R, R_{free}	0.215 , 0.297 0.214 , 0.294	Depositor DCC
R_{free} test set	2168 reflections (4.91%)	DCC
Wilson B-factor (Å ²)	62.3	Xtriage
Anisotropy	0.237	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 64.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.27$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.88	EDS
Total number of atoms	14012	wwPDB-VP
Average B, all atoms (Å ²)	66.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 17.00% 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

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	0.49	0/6933	0.72	4/9353 (0.0%)
1	B	0.51	1/6969 (0.0%)	0.72	2/9403 (0.0%)
2	C	1.09	0/193	1.13	0/298
2	D	1.24	0/193	1.08	0/298
All	All	0.53	1/14288 (0.0%)	0.73	6/19352 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	56	CYS	CB-SG	-6.04	1.72	1.82

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	863	ASN	C-N-CA	7.31	139.97	121.70
1	A	708	ARG	NE-CZ-NH1	-5.94	117.33	120.30
1	B	611	LEU	CA-CB-CG	5.65	128.29	115.30
1	A	921	LEU	CA-CB-CG	5.13	127.10	115.30
1	B	897	LEU	CA-CB-CG	5.08	126.98	115.30
1	A	370	MET	C-N-CA	5.06	134.36	121.70

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	6814	0	6913	117	0
1	B	6848	0	6942	106	0
2	C	174	0	91	4	0
2	D	173	0	91	8	0
3	A	2	0	0	0	0
3	B	1	0	0	0	0
All	All	14012	0	14037	225	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 8.

All (225) 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:A:370:MET:HA	1:A:372:HIS:H	1.25	0.99
1:B:675:LYS:HE2	1:B:678:ARG:HH12	1.45	0.79
1:A:146:ARG:HH21	1:A:225:GLU:HG2	1.45	0.79
1:A:239:ARG:HG2	1:A:240:LEU:HG	1.63	0.79
1:B:193:ASP:OD2	1:B:197:ARG:NH1	2.14	0.79
1:B:657:THR:OG1	1:B:734:LYS:NZ	2.18	0.76
1:A:738:SER:OG	1:A:752:CYS:HB3	1.88	0.73
1:A:514:ASN:ND2	1:A:525:ASP:OD2	2.20	0.73
1:A:805:ARG:NH1	1:A:835:ASP:OD1	2.23	0.72
1:A:323:ASN:O	1:A:324:ASN:HB2	1.88	0.72
1:A:172:ILE:HG22	1:A:326:PRO:HG2	1.73	0.70
1:B:830:ARG:HD2	1:B:836:LEU:HD21	1.73	0.70
1:B:239:ARG:HG2	1:B:240:LEU:HG	1.72	0.69
1:B:786:ARG:HB2	1:B:795:ILE:HG22	1.76	0.68
1:A:370:MET:HA	1:A:372:HIS:N	2.05	0.67
1:B:286:GLU:OE1	2:D:7:DG:N2	2.29	0.66
1:A:283:ARG:NH2	1:A:598:ASN:OD1	2.28	0.66
1:B:295:LYS:NZ	1:B:321:TYR:O	2.27	0.66
1:B:499:ASP:OD2	1:B:543:ARG:NH1	2.28	0.66
1:B:680:ASP:O	1:B:684:ARG:HG2	1.97	0.65
1:A:377:GLU:OE2	1:A:396:ARG:NE	2.31	0.64
1:B:692:SER:HB2	1:B:842:THR:HG23	1.78	0.64
1:A:222:VAL:HG12	1:A:234:VAL:HG21	1.81	0.62
1:B:239:ARG:HB2	2:D:9:DT:H3'	1.82	0.62
1:A:694:HIS:ND1	1:A:842:THR:OG1	2.31	0.62
1:B:491:ILE:HB	2:D:6:DG:H5''	1.82	0.62
1:B:154:PRO:HG2	1:B:180:CYS:HA	1.81	0.62
1:A:693:ASP:OD2	1:A:812:SER:OG	2.14	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:530:THR:HG22	1:B:562:ASP:HB2	1.82	0.61
1:B:655:PRO:HA	1:B:698:HIS:ND1	2.16	0.61
1:B:820:PHE:HD1	1:B:843:MET:CE	2.14	0.60
1:A:216:ILE:HG23	1:A:236:TYR:CE2	2.37	0.59
1:B:467:GLN:HG2	1:B:670:TYR:CD2	2.37	0.59
1:A:239:ARG:HB2	2:C:9:DT:H3'	1.85	0.58
1:B:222:VAL:HG12	1:B:234:VAL:HG21	1.85	0.58
1:A:285:VAL:HG23	1:A:568:GLU:HG3	1.85	0.58
1:B:493:GLU:HG2	1:B:536:GLN:HG2	1.84	0.58
1:B:470:GLU:OE1	1:B:670:TYR:OH	2.12	0.58
1:A:193:ASP:OD2	1:A:197:ARG:NE	2.34	0.58
1:B:424:ALA:HB3	1:B:501:VAL:HA	1.86	0.58
1:A:429:LEU:O	1:A:489:THR:HA	2.04	0.56
1:B:486:ILE:HD13	1:B:498:ILE:HD13	1.87	0.56
1:B:182:LYS:NZ	1:B:310:SER:O	2.37	0.56
1:A:614:ARG:NH1	1:A:777:PRO:HG3	2.20	0.56
1:B:432:TYR:CD1	2:D:4:DT:H72	2.40	0.56
1:B:463:HIS:HB3	1:B:466:MET:HG3	1.88	0.56
1:A:239:ARG:HG3	2:C:10:DT:OP1	2.07	0.55
1:B:685:ARG:NH2	1:B:720:ASN:OD1	2.35	0.55
1:B:388:ASP:OD1	1:B:389:SER:N	2.40	0.55
1:A:134:LEU:O	1:A:138:GLN:HG3	2.07	0.54
1:A:850:ILE:HD13	1:A:867:LEU:HD23	1.89	0.54
1:A:351:TYR:O	1:A:394:LYS:NZ	2.21	0.54
1:A:240:LEU:HD21	1:A:736:GLN:HB2	1.90	0.54
1:A:417:CYS:HB3	1:A:453:TRP:CZ3	2.42	0.54
1:B:286:GLU:OE2	1:B:286:GLU:N	2.37	0.54
1:A:155:THR:HA	1:A:330:ILE:HD13	1.89	0.54
1:A:778:ASN:HB3	1:A:827:TYR:CZ	2.42	0.54
1:A:269:MET:HE3	1:A:304:LEU:HD21	1.88	0.54
1:B:269:MET:O	1:B:301:ARG:NH1	2.39	0.54
1:A:778:ASN:HB3	1:A:827:TYR:CE1	2.43	0.53
1:A:493:GLU:HG2	1:A:536:GLN:HG2	1.89	0.53
1:B:190:LEU:HD11	1:B:307:ILE:HD11	1.90	0.53
1:A:280:ILE:HD11	1:A:310:SER:HB2	1.90	0.53
1:B:754:ASP:OD1	1:B:756:ALA:N	2.41	0.53
1:B:274:VAL:HG22	1:B:305:LYS:HB2	1.90	0.53
1:A:449:LYS:O	1:A:453:TRP:HD1	1.91	0.52
1:A:447:THR:O	1:A:451:GLN:HG3	2.08	0.52
1:B:336:PRO:HD2	1:B:546:PRO:HG3	1.91	0.52
1:B:861:THR:O	1:B:863:ASN:N	2.42	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:146:ARG:HA	1:A:146:ARG:NH1	2.24	0.52
1:B:64:VAL:HG11	1:B:925:LEU:HD11	1.91	0.52
1:A:97:PHE:HD1	1:A:629:MET:HE3	1.75	0.52
1:B:665:PHE:CD1	1:B:666:LYS:HG2	2.45	0.52
1:B:784:LYS:HB2	1:B:797:THR:HB	1.90	0.52
1:A:832:LYS:HA	1:A:835:ASP:O	2.10	0.52
1:A:490:ILE:HG13	1:A:537:ARG:HH21	1.74	0.52
1:B:91:ALA:HB2	1:B:902:TYR:HD1	1.74	0.51
1:B:186:VAL:HG21	1:B:309:MET:HE1	1.93	0.51
1:B:670:TYR:CZ	1:B:723:SER:HB2	2.46	0.51
1:A:112:THR:OG1	1:A:267:PRO:HD2	2.11	0.50
1:A:137:ARG:NH2	1:A:143:ALA:HB2	2.26	0.50
1:B:281:HIS:HB3	1:B:310:SER:OG	2.11	0.50
1:B:165:ALA:O	1:B:169:ASN:ND2	2.25	0.50
1:B:729:GLN:O	1:B:733:MET:HG3	2.12	0.50
1:A:210:PRO:HG3	1:A:279:GLU:HB2	1.94	0.50
1:A:380:LEU:HD22	1:A:392:LEU:HB3	1.92	0.50
1:A:898:LYS:HG2	1:A:902:TYR:HD2	1.78	0.49
1:B:155:THR:OG1	1:B:180:CYS:O	2.17	0.49
1:B:793:ARG:NH2	1:B:815:SER:OG	2.42	0.49
1:A:491:ILE:HB	2:C:6:DG:H5"	1.95	0.49
1:A:573:LYS:HB3	1:A:575:GLU:OE1	2.13	0.49
1:A:672:PRO:HG2	1:A:675:LYS:HB2	1.94	0.49
1:B:239:ARG:HG3	2:D:10:DT:OP1	2.12	0.49
1:A:186:VAL:HG21	1:A:309:MET:HE1	1.95	0.49
1:B:119:LEU:HD23	1:B:248:ARG:CZ	2.43	0.49
1:B:143:ALA:HA	1:B:146:ARG:HB2	1.95	0.49
1:B:780:ALA:HA	1:B:800:THR:HA	1.95	0.48
1:A:868:CYS:HA	1:A:873:TYR:O	2.13	0.48
1:B:901:LEU:HA	1:B:901:LEU:HD12	1.62	0.48
1:B:447:THR:HG23	1:B:450:GLY:H	1.79	0.48
1:A:432:TYR:CD1	2:C:4:DT:H72	2.48	0.48
1:A:644:ILE:HG22	1:A:741:LEU:HD21	1.96	0.48
1:B:568:GLU:HG3	1:B:571:ARG:NH2	2.29	0.48
1:A:690:MET:O	1:A:768:ARG:NH2	2.46	0.48
1:A:259:LEU:HD23	1:A:290:LEU:HD11	1.95	0.48
1:B:112:THR:OG1	1:B:267:PRO:HD2	2.14	0.47
1:A:208:THR:HA	1:A:254:CYS:O	2.14	0.47
1:A:230:LEU:HD23	1:A:230:LEU:HA	1.60	0.47
1:B:614:ARG:CZ	1:B:777:PRO:HG3	2.44	0.47
1:A:146:ARG:CZ	1:A:146:ARG:HA	2.44	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:388:ASP:HB3	1:B:391:VAL:HG23	1.97	0.47
1:A:430:PRO:HD2	1:A:434:LYS:HB2	1.96	0.47
1:B:665:PHE:CE1	1:B:666:LYS:HG2	2.48	0.47
1:A:493:GLU:HG2	1:A:536:GLN:CG	2.44	0.47
1:A:830:ARG:HD2	1:A:836:LEU:HD21	1.96	0.47
1:B:443:ASP:O	1:B:454:ARG:NE	2.47	0.47
1:A:830:ARG:HD2	1:A:836:LEU:CD2	2.45	0.47
1:B:406:ILE:HD11	1:B:434:LYS:HD2	1.96	0.47
1:A:384:ARG:HG2	1:A:385:ASN:N	2.30	0.47
1:A:830:ARG:HD2	1:A:836:LEU:HG	1.97	0.47
1:B:579:LEU:HG	1:B:632:ALA:HB2	1.98	0.46
1:B:78:ALA:HB2	1:B:911:TYR:CG	2.51	0.46
1:A:281:HIS:HA	1:A:318:PHE:HZ	1.81	0.46
1:B:655:PRO:HA	1:B:698:HIS:CE1	2.51	0.46
1:A:275:LEU:HD21	1:A:277:LEU:HD21	1.97	0.46
1:B:427:VAL:HG22	1:B:505:ILE:HD12	1.96	0.46
1:B:691:ARG:HH12	1:B:819:GLY:C	2.18	0.46
1:A:419:ASN:O	1:A:420:GLU:O	2.34	0.46
1:A:579:LEU:HG	1:A:632:ALA:HB2	1.96	0.46
1:A:781:HIS:O	1:A:798:MET:HG3	2.16	0.46
1:B:443:ASP:OD2	1:B:444:LYS:NZ	2.49	0.46
1:B:285:VAL:HG23	1:B:568:GLU:OE1	2.16	0.45
1:A:670:TYR:CZ	1:A:723:SER:HB2	2.52	0.45
1:B:107:GLU:O	1:B:111:GLU:HG3	2.17	0.45
1:B:682:ILE:HD13	1:B:720:ASN:HA	1.98	0.45
1:A:236:TYR:HA	1:A:253:TYR:O	2.16	0.45
1:B:907:GLU:O	1:B:913:LYS:HB2	2.16	0.45
1:B:236:TYR:HA	1:B:253:TYR:O	2.17	0.45
1:B:57:ASN:HA	1:B:876:LYS:HB2	1.98	0.45
1:A:201:SER:O	1:A:248:ARG:HD2	2.16	0.45
1:B:835:ASP:HB3	1:B:837:PHE:CZ	2.52	0.45
1:B:502:VAL:O	1:B:541:ALA:HB1	2.17	0.45
1:B:557:ARG:O	1:B:561:MET:HG3	2.17	0.45
1:A:146:ARG:HH12	1:A:149:ALA:HB3	1.82	0.45
1:A:246:ARG:HG3	1:A:248:ARG:O	2.17	0.44
1:A:414:TYR:CZ	1:A:450:GLY:HA2	2.52	0.44
1:A:784:LYS:HB2	1:A:797:THR:HB	2.00	0.44
1:A:888:LEU:HD21	1:A:919:ILE:HG12	1.99	0.44
1:B:119:LEU:HA	1:B:119:LEU:HD23	1.79	0.44
1:B:219:ALA:O	1:B:223:SER:HB2	2.18	0.44
2:D:3:DT:H2"	2:D:4:DT:C7	2.46	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:54:LEU:HA	1:A:54:LEU:HD23	1.75	0.44
1:A:665:PHE:CE1	1:A:666:LYS:HG2	2.53	0.44
1:A:824:TYR:HH	1:A:875:PHE:HE1	1.64	0.44
1:A:240:LEU:HD13	1:A:732:ARG:HB3	1.99	0.44
1:A:281:HIS:HB3	1:A:310:SER:OG	2.18	0.44
1:A:649:LEU:HD22	1:A:899:LYS:HG3	1.99	0.44
1:B:490:ILE:HG22	2:D:5:DA:H2"	2.00	0.44
1:B:822:SER:HB2	1:B:845:PHE:CE1	2.52	0.44
1:B:850:ILE:HD13	1:B:867:LEU:HD23	1.99	0.44
1:A:691:ARG:HD2	1:A:820:PHE:CE1	2.53	0.44
1:B:246:ARG:HG3	1:B:248:ARG:O	2.18	0.43
1:A:692:SER:HB2	1:A:842:THR:HG23	2.00	0.43
1:B:281:HIS:CD2	1:B:311:ALA:H	2.36	0.43
1:A:407:ASP:HA	1:A:410:ALA:HB3	1.99	0.43
1:B:449:LYS:HB2	1:B:449:LYS:HE3	1.80	0.43
1:A:94:GLN:HB2	1:A:901:LEU:HD22	2.01	0.43
1:B:564:ILE:HG13	1:B:565:PRO:O	2.18	0.43
1:A:442:LEU:HD12	1:A:487:ILE:HD11	2.01	0.43
1:A:456:HIS:HA	1:A:482:GLN:HG2	2.00	0.43
1:A:290:LEU:HD23	1:A:290:LEU:HA	1.77	0.43
1:A:397:LEU:HB3	1:A:399:GLU:OE2	2.18	0.43
1:A:460:PHE:CD2	1:A:484:LYS:HG3	2.54	0.43
1:A:614:ARG:CZ	1:A:777:PRO:HG3	2.49	0.43
1:B:692:SER:HA	1:B:842:THR:HA	2.01	0.43
1:A:59:SER:HA	1:A:881:THR:HG21	2.01	0.43
1:A:679:VAL:HG12	1:A:683:LYS:HE3	2.01	0.43
1:A:64:VAL:HG21	1:A:925:LEU:HD21	2.00	0.43
1:B:462:LEU:HA	1:B:462:LEU:HD12	1.80	0.43
1:A:153:LEU:HA	1:A:153:LEU:HD23	1.85	0.43
1:A:913:LYS:HG3	1:A:917:LYS:HE2	2.00	0.43
1:B:618:LEU:HD23	1:B:624:LEU:HA	2.00	0.42
1:B:216:ILE:HG12	1:B:236:TYR:CD1	2.54	0.42
1:A:381:ARG:HD2	1:A:381:ARG:HA	1.73	0.42
1:A:97:PHE:CD1	1:A:629:MET:HE3	2.53	0.42
1:A:135:GLY:HA2	1:A:138:GLN:OE1	2.20	0.42
1:A:289:LEU:HD12	1:A:289:LEU:HA	1.87	0.42
1:A:899:LYS:HA	1:A:899:LYS:HD2	1.85	0.42
1:B:899:LYS:HA	1:B:899:LYS:HD2	1.69	0.42
1:B:171:VAL:O	1:B:325:CYS:HB2	2.20	0.42
1:B:545:ARG:NE	1:B:546:PRO:O	2.53	0.42
1:A:454:ARG:NH1	1:A:455:ASP:OD1	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:888:LEU:HD21	1:B:919:ILE:HG12	2.02	0.42
1:A:281:HIS:HA	1:A:318:PHE:CZ	2.55	0.42
1:A:399:GLU:H	1:A:399:GLU:CD	2.23	0.42
1:B:426:LEU:HB3	1:B:504:VAL:HG22	2.02	0.42
1:B:836:LEU:HD12	1:B:836:LEU:HA	1.75	0.42
1:A:369:ARG:O	1:A:371:LYS:HB2	2.20	0.42
1:B:333:VAL:HG13	1:B:334:MET:N	2.34	0.42
1:B:830:ARG:HD2	1:B:836:LEU:CD2	2.46	0.42
2:D:3:DT:H2"	2:D:4:DT:H71	2.01	0.42
1:A:835:ASP:HB3	1:A:837:PHE:CZ	2.55	0.41
1:B:259:LEU:HA	1:B:259:LEU:HD12	1.75	0.41
1:A:575:GLU:H	1:A:575:GLU:CD	2.23	0.41
1:A:64:VAL:O	1:A:68:VAL:HG23	2.20	0.41
1:A:110:ALA:O	1:A:113:LYS:HB3	2.20	0.41
1:A:901:LEU:HA	1:A:901:LEU:HD23	1.76	0.41
1:B:268:LEU:O	1:B:301:ARG:HD2	2.20	0.41
1:B:908:GLU:O	1:B:913:LYS:HG2	2.20	0.41
1:A:281:HIS:O	1:A:283:ARG:HG2	2.21	0.41
1:A:500:ASP:OD1	1:A:500:ASP:N	2.53	0.41
1:B:611:LEU:O	1:B:615:ILE:HG23	2.20	0.41
1:A:314:ARG:HD3	1:A:564:ILE:HD13	2.02	0.41
1:B:636:ILE:HD11	1:B:640:MET:HE3	2.03	0.41
1:A:499:ASP:HA	1:A:543:ARG:HD3	2.03	0.41
1:A:675:LYS:O	1:A:678:ARG:N	2.54	0.41
1:B:267:PRO:C	1:B:268:LEU:HD12	2.40	0.41
1:B:782:LEU:O	1:B:823:ALA:HB1	2.20	0.41
1:B:103:VAL:O	1:B:585:HIS:NE2	2.53	0.41
1:B:614:ARG:NH1	1:B:777:PRO:HG3	2.36	0.41
1:B:820:PHE:HD1	1:B:843:MET:HE1	1.84	0.41
1:B:479:PRO:HG2	1:B:482:GLN:HB2	2.03	0.41
1:A:850:ILE:O	1:A:889:ARG:HD2	2.21	0.40
1:A:653:LEU:HD23	1:A:752:CYS:HA	2.04	0.40
1:A:65:LEU:O	1:A:69:LYS:HG3	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	841/944 (89%)	811 (96%)	28 (3%)	2 (0%)	51	85
1	B	845/944 (90%)	812 (96%)	31 (4%)	2 (0%)	51	85
All	All	1686/1888 (89%)	1623 (96%)	59 (4%)	4 (0%)	51	85

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	324	ASN
1	A	420	GLU
1	B	863	ASN
1	B	366	PRO

5.3.2 Protein sidechains

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	757/842 (90%)	747 (99%)	10 (1%)	73	91
1	B	761/842 (90%)	754 (99%)	7 (1%)	82	94
All	All	1518/1684 (90%)	1501 (99%)	17 (1%)	78	93

All (17) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	94	GLN
1	A	137	ARG

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Mol	Chain	Res	Type
1	A	272	LEU
1	A	295	LYS
1	A	355	LYS
1	A	369	ARG
1	A	573	LYS
1	A	805	ARG
1	A	862	GLN
1	A	901	LEU
1	B	98	ARG
1	B	114	GLU
1	B	137	ARG
1	B	146	ARG
1	B	272	LEU
1	B	477	ARG
1	B	879	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	262	GLN
1	B	281	HIS
1	B	522	GLN

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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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	A	849/944 (89%)	-0.08	7 (0%) 86 64	31, 61, 114, 156	0
1	B	853/944 (90%)	-0.14	2 (0%) 94 86	30, 57, 98, 164	0
2	C	9/9 (100%)	1.04	3 (33%) 0 0	72, 83, 130, 162	0
2	D	9/9 (100%)	0.80	1 (11%) 6 2	63, 91, 120, 126	0
All	All	1720/1906 (90%)	-0.10	13 (0%) 86 64	30, 59, 109, 164	0

All (13) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	142	ASN	4.5
1	B	142	ASN	4.1
1	A	384	ARG	2.9
2	C	10	DT	2.8
2	C	8	DG	2.7
1	A	390	ARG	2.6
1	A	423	GLY	2.6
1	B	795	ILE	2.5
1	A	393	ASP	2.2
2	D	10	DT	2.1
2	C	7	DG	2.1
1	A	413	VAL	2.1
1	A	859	GLY	2.1

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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.