Full wwPDB X-ray Structure Validation Report ⓘ

Apr 16, 2024 – 12:07 AM JST

PDB ID	:	8JJ9
Title	:	Human FAM91A1 N terminal domain in complex with TBC1D23
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Deposited on	:	2023-05-29
Resolution	:	2.51 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

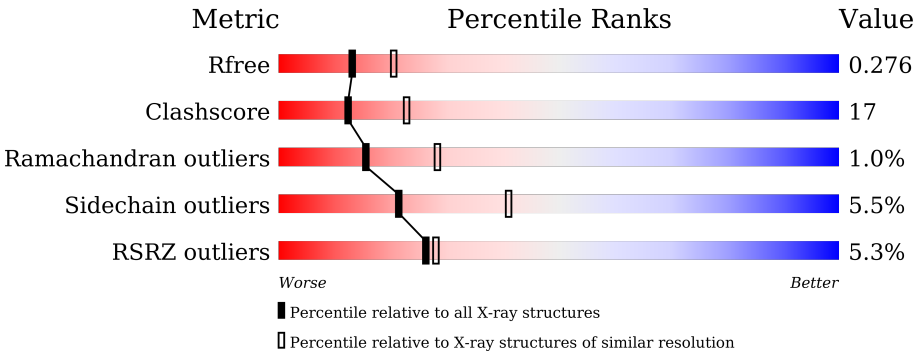
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.51 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	4661 (2.50-2.50)
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)
RSRZ outliers	127900	4559 (2.50-2.50)

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 <=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	312	5% 63% 31%
1	B	312	3% 58% 32% 5%
2	C	21	29% 57% 38% 5%
2	D	21	14% 52% 43% 5%

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 5398 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 Protein FAM91A1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	298	Total	C	N	O	S	0	0	0
			2443	1564	419	447	13			
1	B	299	Total	C	N	O	S	0	0	0
			2460	1577	421	449	13			

- Molecule 2 is a protein called TBC1 domain family member 23.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	21	Total	C	N	O	0	0	0
			166	104	34	28			
2	D	20	Total	C	N	O	0	0	0
			160	101	33	26			

- Molecule 3 is water.

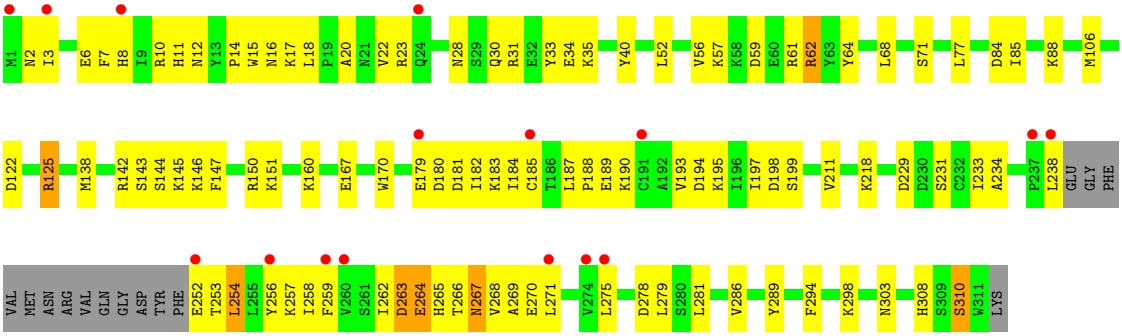
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	81	Total	O	0	0
			81	81		
3	B	84	Total	O	0	0
			84	84		
3	C	1	Total	O	0	0
			1	1		
3	D	3	Total	O	0	0
			3	3		

3 Residue-property plots (i)

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

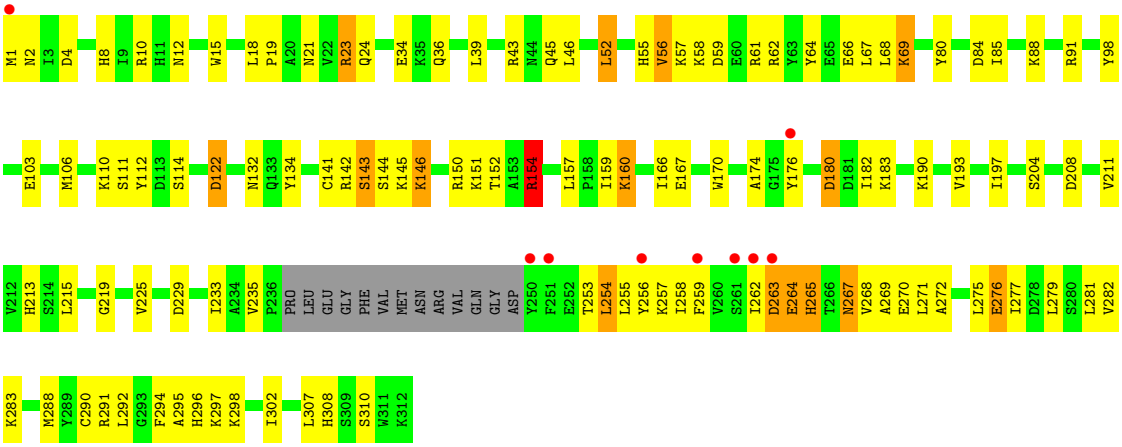
• Molecule 1: Protein FAM91A1

Chain A:



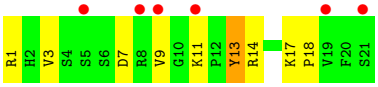
• Molecule 1: Protein FAM91A1

Chain B:



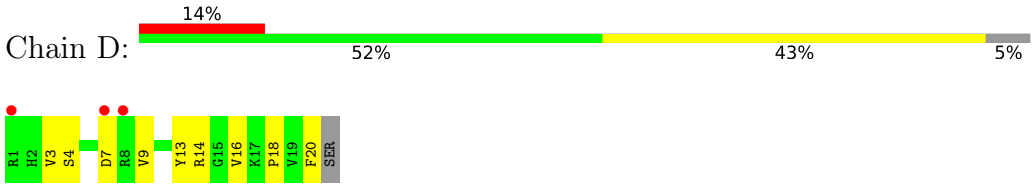
• Molecule 2: TBC1 domain family member 23

Chain C:



• Molecule 2: TBC1 domain family member 23

Chain D:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	88.21Å 93.56Å 111.51Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	41.01 – 2.51 69.18 – 2.51	Depositor EDS
% Data completeness (in resolution range)	99.8 (41.01-2.51) 99.9 (69.18-2.51)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.86 (at 2.51Å)	Xtriage
Refinement program	PHENIX (1.19.2_4158: ???)	Depositor
R, R_{free}	0.225 , 0.277 0.224 , 0.276	Depositor DCC
R_{free} test set	1598 reflections (4.96%)	wwPDB-VP
Wilson B-factor (Å^2)	26.0	Xtriage
Anisotropy	0.000	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.36 , 50.4	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.91	EDS
Total number of atoms	5398	wwPDB-VP
Average B, all atoms (Å^2)	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 63.23 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 9.9866e-06. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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	0.54	0/2497	0.68	1/3380 (0.0%)
1	B	0.56	0/2515	0.69	2/3402 (0.1%)
2	C	0.55	0/170	0.70	0/227
2	D	0.45	0/164	0.74	0/219
All	All	0.55	0/5346	0.69	3/7228 (0.0%)

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	A	0	1
1	B	0	2
All	All	0	3

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	77	LEU	CA-CB-CG	5.47	127.89	115.30
1	B	154	ARG	NE-CZ-NH1	5.37	122.99	120.30
1	B	52	LEU	CB-CG-CD2	-5.25	102.08	111.00

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	125	ARG	Sidechain
1	B	264	GLU	Peptide
1	B	276	GLU	Peptide

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	2443	0	2449	83	0
1	B	2460	0	2462	80	0
2	C	166	0	172	11	0
2	D	160	0	167	12	0
3	A	81	0	0	6	0
3	B	84	0	0	4	0
3	C	1	0	0	0	0
3	D	3	0	0	4	0
All	All	5398	0	5250	177	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 17.

All (177) 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:69:LYS:NZ	3:B:401:HOH:O	1.92	1.03
1:A:190:LYS:NZ	2:C:13:TYR:OH	1.94	1.00
1:A:198:ASP:OD2	2:C:14:ARG:NH2	1.95	0.99
2:D:20:PHE:HB2	3:D:101:HOH:O	1.74	0.87
1:A:15:TRP:CG	1:A:30:GLN:HG3	2.16	0.80
1:B:190:LYS:NZ	2:D:13:TYR:OH	2.15	0.79
1:B:57:LYS:NZ	1:B:66:GLU:OE1	2.15	0.79
1:B:34:GLU:HG2	1:B:56:VAL:HB	1.66	0.77
1:B:1:MET:SD	1:B:43:ARG:NH2	2.58	0.76
1:B:233:ILE:HD11	1:B:262:ILE:HD11	1.69	0.74
1:A:278:ASP:HB3	1:A:281:LEU:HD12	1.71	0.71
1:A:267:ASN:HB3	1:A:270:GLU:HB2	1.74	0.70
2:C:17:LYS:HE2	2:C:18:PRO:HD2	1.74	0.69
1:A:259:PHE:CZ	1:A:294:PHE:HB3	2.27	0.69
1:A:181:ASP:O	1:A:184:ILE:HG22	1.94	0.66
2:C:1:ARG:NH2	2:C:7:ASP:OD2	2.25	0.66
1:A:20:ALA:HA	1:A:23:ARG:HB2	1.77	0.66
2:C:13:TYR:HD1	2:C:14:ARG:N	1.94	0.65
1:A:106:MET:HG2	1:A:138:MET:HE1	1.77	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:30:GLN:HB3	1:A:31:ARG:NH1	2.13	0.64
1:A:234:ALA:HB2	1:A:298:LYS:HD2	1.79	0.64
1:A:15:TRP:CD1	1:A:30:GLN:HG3	2.35	0.62
1:A:34:GLU:HG2	1:A:56:VAL:HG22	1.82	0.62
1:B:254:LEU:HD21	1:B:281:LEU:HD11	1.81	0.62
1:A:122:ASP:OD1	1:A:125:ARG:HD3	2.01	0.61
1:A:254:LEU:O	1:A:258:ILE:HG13	2.01	0.60
1:B:45:GLN:HA	1:B:67:LEU:HD11	1.84	0.60
1:A:2:ASN:ND2	3:A:407:HOH:O	2.35	0.60
1:A:15:TRP:CH2	1:A:23:ARG:HG2	2.38	0.59
1:B:103:GLU:OE1	1:B:154:ARG:NH1	2.36	0.59
1:B:256:TYR:CE2	1:B:257:LYS:HD3	2.37	0.59
1:B:263:ASP:OD2	1:B:265:HIS:HA	2.03	0.59
1:A:84:ASP:O	1:A:88:LYS:HB2	2.04	0.57
1:A:182:ILE:HA	1:A:185:CYS:SG	2.44	0.57
1:B:59:ASP:OD2	1:B:62:ARG:HB2	2.05	0.57
1:B:279:LEU:O	1:B:282:VAL:HG12	2.04	0.57
1:B:1:MET:HE2	1:B:36:GLN:HB3	1.87	0.56
1:B:167:GLU:HB2	1:B:170:TRP:CD1	2.40	0.56
1:A:182:ILE:HD12	2:C:13:TYR:HE2	1.72	0.55
1:B:18:LEU:HB2	1:B:23:ARG:HD3	1.88	0.55
1:A:194:ASP:OD1	2:C:14:ARG:NH1	2.38	0.55
1:B:193:VAL:O	1:B:197:ILE:HG13	2.06	0.54
1:A:198:ASP:CG	2:C:14:ARG:HH22	2.08	0.54
2:D:20:PHE:N	3:D:101:HOH:O	2.35	0.54
1:A:18:LEU:HD11	1:A:33:TYR:CE1	2.43	0.53
1:A:264:GLU:O	1:A:266:THR:OG1	2.22	0.53
1:B:233:ILE:HG22	1:B:297:LYS:HA	1.90	0.53
2:D:4:SER:O	2:D:7:ASP:HB2	2.08	0.53
1:A:144:SER:HA	1:A:147:PHE:HD2	1.73	0.53
1:A:144:SER:HA	1:A:147:PHE:CD2	2.44	0.53
1:A:64:TYR:CD2	1:A:85:ILE:HG21	2.44	0.52
1:A:143:SER:O	1:A:146:LYS:HG3	2.10	0.52
1:A:6:GLU:HG2	1:A:40:TYR:CD1	2.45	0.51
1:A:229:ASP:OD1	1:A:279:LEU:HD21	2.09	0.51
1:B:267:ASN:OD1	1:B:268:VAL:N	2.43	0.51
2:D:16:VAL:O	2:D:18:PRO:HD3	2.11	0.51
1:B:15:TRP:CH2	1:B:23:ARG:HG3	2.44	0.51
1:B:152:THR:HG23	1:B:154:ARG:H	1.75	0.51
1:B:259:PHE:CZ	1:B:294:PHE:HB3	2.46	0.51
1:B:208:ASP:OD2	1:B:211:VAL:HG23	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:229:ASP:OD1	1:B:283:LYS:HE3	2.10	0.51
1:A:167:GLU:HB2	1:A:170:TRP:CD1	2.46	0.50
1:B:19:PRO:HB2	1:B:21:ASN:OD1	2.12	0.50
1:A:286:VAL:HA	1:A:289:TYR:CD2	2.47	0.50
1:A:10:ARG:NH1	1:A:40:TYR:OH	2.44	0.50
1:B:103:GLU:OE2	1:B:154:ARG:HG3	2.12	0.50
1:A:8:HIS:CD2	1:A:22:VAL:HG21	2.47	0.50
1:B:64:TYR:CD2	1:B:85:ILE:HG21	2.47	0.50
1:A:187:LEU:N	1:A:188:PRO:HD2	2.28	0.49
1:A:8:HIS:HB3	1:A:18:LEU:HD21	1.93	0.49
1:B:255:LEU:HD22	1:B:288:MET:HE1	1.94	0.49
2:D:20:PHE:CB	3:D:101:HOH:O	2.47	0.49
1:A:142:ARG:NH2	3:A:402:HOH:O	2.45	0.49
1:A:12:ASN:OD1	1:A:52:LEU:N	2.43	0.48
2:D:13:TYR:CE1	2:D:14:ARG:HG3	2.48	0.48
1:A:14:PRO:HG2	1:A:17:LYS:HG2	1.95	0.48
1:B:112:TYR:HB2	1:B:134:TYR:CD2	2.49	0.48
1:B:229:ASP:OD1	1:B:279:LEU:HD21	2.14	0.48
1:B:254:LEU:O	1:B:258:ILE:HG13	2.14	0.48
1:A:151:LYS:NZ	3:A:413:HOH:O	2.46	0.48
1:A:193:VAL:O	1:A:197:ILE:HG13	2.14	0.48
1:B:64:TYR:CG	1:B:85:ILE:HG21	2.49	0.48
1:B:277:ILE:HG21	1:B:281:LEU:HD12	1.96	0.48
1:B:91:ARG:HH11	1:B:176:TYR:HD2	1.61	0.48
1:B:267:ASN:OD1	1:B:269:ALA:N	2.47	0.47
1:A:252:GLU:OE2	1:A:253:THR:HG23	2.14	0.47
1:B:1:MET:HG3	1:B:36:GLN:OE1	2.15	0.47
1:B:150:ARG:NH1	3:B:405:HOH:O	2.31	0.47
1:B:271:LEU:O	1:B:275:LEU:HD12	2.14	0.47
1:A:16:ASN:OD1	1:A:17:LYS:N	2.47	0.47
1:A:189:GLU:OE2	1:A:218:LYS:HE2	2.15	0.47
1:B:80:TYR:OH	1:B:122:ASP:OD2	2.21	0.47
1:B:144:SER:HB3	1:B:151:LYS:H	1.80	0.47
1:B:167:GLU:O	1:B:204:SER:OG	2.30	0.47
1:A:263:ASP:O	1:A:265:HIS:N	2.47	0.47
1:B:21:ASN:OD1	1:B:21:ASN:N	2.48	0.47
1:A:265:HIS:CG	1:A:265:HIS:O	2.68	0.47
1:A:264:GLU:N	1:A:264:GLU:OE1	2.48	0.46
2:D:9:VAL:O	2:D:9:VAL:HG13	2.14	0.46
1:A:35:LYS:NZ	3:A:401:HOH:O	2.25	0.46
1:B:132:ASN:ND2	3:B:411:HOH:O	2.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:218:LYS:O	2:C:3:VAL:HG13	2.14	0.46
1:A:57:LYS:HE3	1:A:62:ARG:HB3	1.98	0.46
1:A:265:HIS:O	1:A:265:HIS:ND1	2.49	0.46
1:A:269:ALA:HA	1:A:279:LEU:HD13	1.99	0.45
1:A:303:ASN:ND2	3:A:415:HOH:O	2.49	0.45
1:A:189:GLU:HA	1:A:211:VAL:HG13	1.97	0.45
1:B:12:ASN:OD1	1:B:52:LEU:N	2.45	0.45
1:B:308:HIS:ND1	1:B:310:SER:OG	2.41	0.45
1:A:15:TRP:O	1:A:18:LEU:HB2	2.16	0.45
1:A:195:LYS:HE2	1:A:199:SER:HB2	1.98	0.45
1:B:296:HIS:ND1	1:B:298:LYS:HE2	2.31	0.45
1:B:225:VAL:HG21	1:B:291:ARG:HB2	1.98	0.45
1:A:7:PHE:CE2	1:A:11:HIS:CD2	3.05	0.44
1:A:189:GLU:O	1:A:193:VAL:HG23	2.17	0.44
1:B:166:ILE:HD12	1:B:213:HIS:CE1	2.52	0.44
1:A:271:LEU:HD12	1:A:275:LEU:HD23	1.99	0.44
1:A:308:HIS:CE1	1:A:310:SER:HG	2.36	0.44
1:B:272:ALA:HB2	1:B:282:VAL:HG11	2.00	0.44
1:B:106:MET:HE1	1:B:157:LEU:HD21	2.00	0.44
1:B:106:MET:HE2	1:B:106:MET:HB2	1.67	0.44
1:B:277:ILE:CG2	1:B:281:LEU:HD12	2.48	0.44
2:D:20:PHE:CA	3:D:101:HOH:O	2.65	0.44
1:B:159:ILE:HG13	1:B:160:LYS:HD3	2.00	0.43
1:A:278:ASP:OD1	1:A:279:LEU:N	2.51	0.43
1:A:310:SER:HG	1:A:310:SER:H	1.44	0.43
1:A:286:VAL:HA	1:A:289:TYR:HD2	1.83	0.43
1:B:68:LEU:HD12	1:B:68:LEU:HA	1.80	0.43
1:B:143:SER:O	1:B:146:LYS:HG2	2.18	0.43
1:B:308:HIS:CE1	1:B:310:SER:HG	2.33	0.43
1:A:253:THR:O	1:A:257:LYS:HG2	2.19	0.43
1:B:111:SER:O	1:B:114:SER:OG	2.36	0.43
1:B:263:ASP:OD2	1:B:265:HIS:CG	2.71	0.43
1:B:276:GLU:HG3	1:B:277:ILE:HG12	2.00	0.43
2:C:13:TYR:HD1	2:C:13:TYR:C	2.22	0.43
1:A:59:ASP:C	1:A:59:ASP:OD2	2.57	0.43
1:B:55:HIS:O	1:B:58:LYS:NZ	2.51	0.43
1:B:263:ASP:O	1:B:264:GLU:HB2	2.18	0.43
1:A:145:LYS:HG2	1:A:145:LYS:O	2.19	0.43
2:D:13:TYR:CZ	2:D:14:ARG:HG3	2.53	0.43
1:A:61:ARG:NH2	3:A:412:HOH:O	2.45	0.43
1:A:257:LYS:HD3	1:A:257:LYS:HA	1.81	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:262:ILE:CG2	1:A:271:LEU:HD11	2.49	0.42
1:A:308:HIS:ND1	1:A:310:SER:OG	2.47	0.42
1:B:302:ILE:HD13	1:B:307:LEU:HD22	2.00	0.42
1:A:231:SER:O	1:A:268:VAL:HG23	2.20	0.42
1:B:58:LYS:HD2	1:B:58:LYS:HA	1.82	0.42
1:B:84:ASP:OD1	1:B:84:ASP:N	2.52	0.42
1:B:180:ASP:HA	1:B:183:LYS:HD2	2.00	0.42
1:A:179:GLU:H	1:A:179:GLU:CD	2.20	0.42
1:A:258:ILE:O	1:A:262:ILE:HG23	2.19	0.42
1:B:253:THR:O	1:B:257:LYS:HG2	2.20	0.42
1:B:88:LYS:NZ	1:B:174:ALA:O	2.48	0.41
1:B:98:TYR:CZ	1:B:122:ASP:HB3	2.55	0.41
1:B:4:ASP:O	1:B:8:HIS:ND1	2.47	0.41
1:B:219:GLY:HA3	2:D:3:VAL:HG22	2.01	0.41
1:A:31:ARG:HA	1:A:31:ARG:HD3	1.68	0.41
1:A:145:LYS:HA	1:A:150:ARG:HG2	2.02	0.41
1:A:195:LYS:HE2	1:A:199:SER:CB	2.50	0.41
1:B:145:LYS:HB3	1:B:145:LYS:HE2	1.63	0.41
1:B:208:ASP:HB3	1:B:211:VAL:HB	2.01	0.41
1:B:235:VAL:HG21	1:B:262:ILE:CG1	2.50	0.41
1:A:30:GLN:HB3	1:A:31:ARG:HH11	1.81	0.41
1:B:61:ARG:HG3	2:D:20:PHE:CE2	2.56	0.41
1:A:262:ILE:HG22	1:A:271:LEU:HD11	2.02	0.41
1:A:7:PHE:HA	1:A:10:ARG:HH21	1.86	0.41
1:B:46:LEU:HD23	1:B:46:LEU:HA	1.88	0.41
1:A:68:LEU:HD12	1:A:68:LEU:HA	1.83	0.41
1:A:182:ILE:HD11	1:A:190:LYS:HD2	2.03	0.41
1:A:263:ASP:N	1:A:264:GLU:OE1	2.54	0.41
1:B:84:ASP:O	1:B:88:LYS:HB2	2.21	0.41
2:C:13:TYR:C	2:C:13:TYR:CD1	2.94	0.41
1:A:233:ILE:HD11	1:A:262:ILE:HD13	2.03	0.40
1:B:215:LEU:HD23	1:B:215:LEU:HA	1.86	0.40
1:B:290:CYS:HA	1:B:295:ALA:O	2.21	0.40
1:B:182:ILE:HD12	1:B:182:ILE:HA	1.91	0.40
1:B:110:LYS:NZ	3:B:413:HOH:O	2.48	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	294/312 (94%)	279 (95%)	11 (4%)	4 (1%)	11 20
1	B	295/312 (95%)	284 (96%)	9 (3%)	2 (1%)	22 39
2	C	19/21 (90%)	19 (100%)	0	0	100 100
2	D	18/21 (86%)	15 (83%)	3 (17%)	0	100 100
All	All	626/666 (94%)	597 (95%)	23 (4%)	6 (1%)	15 28

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	263	ASP
1	A	267	ASN
1	B	263	ASP
1	A	264	GLU
1	B	265	HIS
1	A	183	LYS

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	274/286 (96%)	264 (96%)	10 (4%)	35 61
1	B	275/286 (96%)	256 (93%)	19 (7%)	15 30
2	C	19/19 (100%)	16 (84%)	3 (16%)	2 4
2	D	18/19 (95%)	18 (100%)	0	100 100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	586/610 (96%)	554 (94%)	32 (6%)	21 41

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

Mol	Chain	Res	Type
1	A	3	ILE
1	A	28	ASN
1	A	62	ARG
1	A	71	SER
1	A	160	LYS
1	A	180	ASP
1	A	238	LEU
1	A	254	LEU
1	A	256	TYR
1	A	310	SER
1	B	2	ASN
1	B	10	ARG
1	B	23	ARG
1	B	24	GLN
1	B	39	LEU
1	B	56	VAL
1	B	69	LYS
1	B	122	ASP
1	B	141	CYS
1	B	142	ARG
1	B	143	SER
1	B	146	LYS
1	B	154	ARG
1	B	160	LYS
1	B	180	ASP
1	B	254	LEU
1	B	267	ASN
1	B	270	GLU
1	B	292	LEU
2	C	9	VAL
2	C	11	LYS
2	C	13	TYR

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

Mol	Chain	Res	Type
1	A	11	HIS
1	A	45	GLN
1	B	132	ASN

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 monosaccharides in this entry.

5.6 Ligand geometry

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, 95^{th} 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	298/312 (95%)	0.41	16 (5%) 25 27	11, 34, 66, 84	0
1	B	299/312 (95%)	0.33	9 (3%) 50 53	9, 29, 58, 75	0
2	C	21/21 (100%)	1.52	6 (28%) 0 0	34, 57, 71, 77	0
2	D	20/21 (95%)	1.12	3 (15%) 2 2	33, 48, 68, 88	0
All	All	638/666 (95%)	0.43	34 (5%) 26 28	9, 32, 65, 88	0

All (34) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	251	PHE	6.5
1	B	250	TYR	5.7
2	C	9	VAL	5.6
1	A	238	LEU	5.4
2	D	8	ARG	4.7
2	D	1	ARG	4.7
1	B	256	TYR	4.0
1	B	176	TYR	3.9
1	A	260	VAL	3.9
1	A	256	TYR	3.8
1	A	1	MET	3.6
2	D	7	ASP	3.3
2	C	11	LYS	3.3
1	B	262	ILE	3.3
2	C	5	SER	3.3
1	B	263	ASP	3.2
2	C	21	SER	3.2
1	A	259	PHE	3.1
1	A	24	GLN	3.1
1	A	179	GLU	2.9
1	B	259	PHE	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	185	CYS	2.7
1	B	1	MET	2.7
1	A	271	LEU	2.7
1	A	8	HIS	2.6
2	C	8	ARG	2.4
1	A	237	PRO	2.4
1	A	3	ILE	2.4
1	A	191	CYS	2.3
1	B	261	SER	2.2
1	A	274	VAL	2.1
1	A	252	GLU	2.1
2	C	19	VAL	2.1
1	A	275	LEU	2.0

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

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

6.4 Ligands (i)

There are no ligands in this entry.

6.5 Other polymers (i)

There are no such residues in this entry.