



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 27, 2014 – 05:42 AM GMT

PDB ID : 2D10
Title : Crystal structure of the Radixin FERM domain complexed with the NHERF-1 C-terminal tail peptide
Authors : Terawaki, S.; Maesaki, R.; Hakoshima, T.
Deposited on : 2005-08-11
Resolution : 2.50 Å(reported)

This is a full wwPDB 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/ValidationPDFNotes.html>

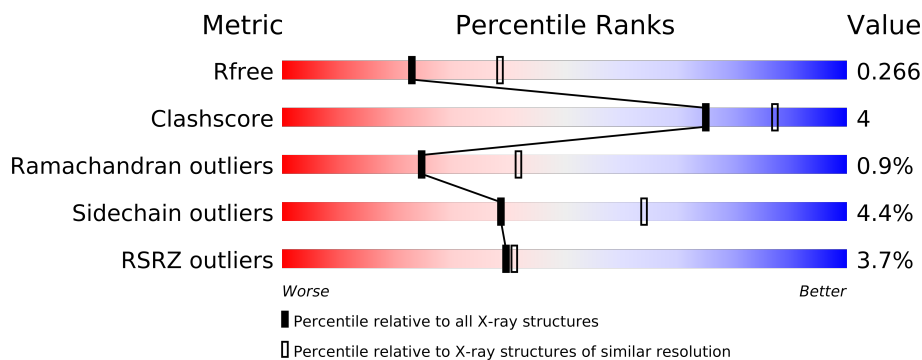
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : stable22639
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

The reported resolution of this entry is 2.50 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}	66092	2784 (2.50-2.50)
Clashscore	79885	3562 (2.50-2.50)
Ramachandran outliers	78287	3480 (2.50-2.50)
Sidechain outliers	78261	3482 (2.50-2.50)
RSRZ outliers	66119	2785 (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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	312	
1	B	312	
1	C	312	
1	D	312	
2	E	28	
2	F	28	
2	G	28	
2	H	28	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 11025 atoms, of which 0 are hydrogen and 0 are deuterium.

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 Radixin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	295	Total	C	N	O	S	0	0	0
			2448	1582	415	442	9			
1	B	297	Total	C	N	O	S	0	0	0
			2456	1585	418	444	9			
1	C	297	Total	C	N	O	S	0	0	0
			2460	1588	419	444	9			
1	D	297	Total	C	N	O	S	0	0	0
			2456	1585	418	444	9			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLY	-	CLONING ARTIFACT	UNP P26043
A	0	SER	-	CLONING ARTIFACT	UNP P26043
B	-1	GLY	-	CLONING ARTIFACT	UNP P26043
B	0	SER	-	CLONING ARTIFACT	UNP P26043
C	-1	GLY	-	CLONING ARTIFACT	UNP P26043
C	0	SER	-	CLONING ARTIFACT	UNP P26043
D	-1	GLY	-	CLONING ARTIFACT	UNP P26043
D	0	SER	-	CLONING ARTIFACT	UNP P26043

- Molecule 2 is a protein called Ezrin-radixin-moesin binding phosphoprotein 50.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	E	20	Total	C	N	O	S	0	0	0
			146	92	25	28	1			
2	F	20	Total	C	N	O	S	0	0	0
			150	94	25	30	1			
2	G	20	Total	C	N	O	S	0	0	0
			146	92	24	29	1			
2	H	20	Total	C	N	O	S	0	0	0
			146	92	25	28	1			

- Molecule 3 is water.

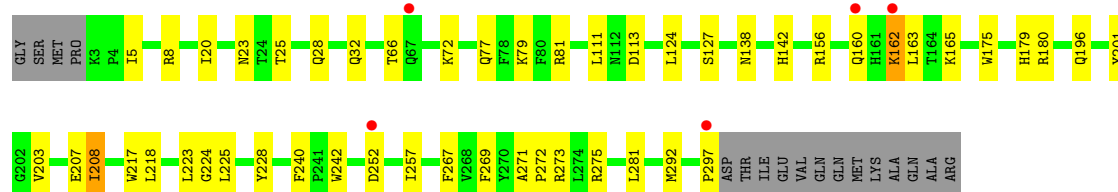
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	160	Total 160	O 160	0	0
3	B	168	Total 168	O 168	0	0
3	C	126	Total 126	O 126	0	0
3	D	153	Total 153	O 153	0	0
3	E	5	Total 5	O 5	0	0
3	F	1	Total 1	O 1	0	0
3	G	1	Total 1	O 1	0	0
3	H	3	Total 3	O 3	0	0

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 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.

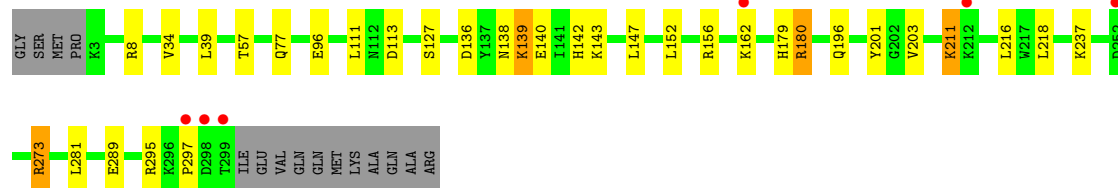
• Molecule 1: Radixin

Chain A: 



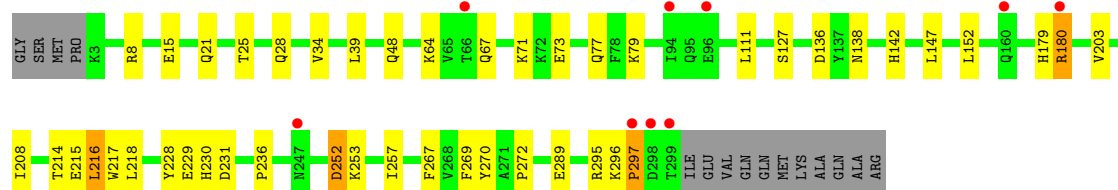
• Molecule 1: Radixin

Chain B: 



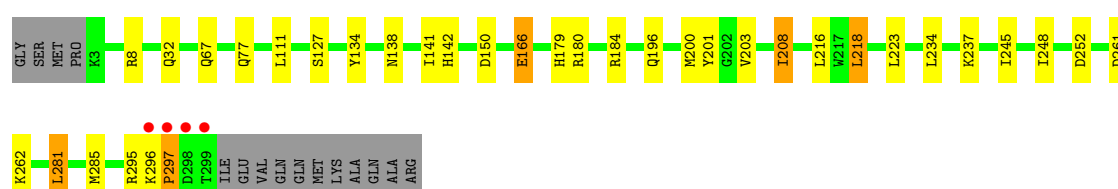
• Molecule 1: Radixin

Chain C: 



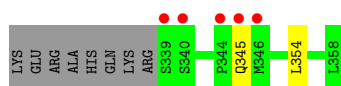
• Molecule 1: Radixin

Chain D: 



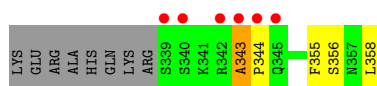
- Molecule 2: Ezrin-radixin-moesin binding phosphoprotein 50

Chain E: 



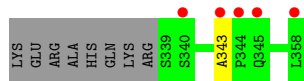
- Molecule 2: Ezrin-radixin-moesin binding phosphoprotein 50

Chain F: 



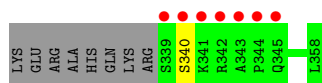
- Molecule 2: Ezrin-radixin-moesin binding phosphoprotein 50

Chain G: 



- Molecule 2: Ezrin-radixin-moesin binding phosphoprotein 50

Chain H: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	69.39Å 146.28Å 177.76Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.93 – 2.50 29.69 – 2.50	Depositor EDS
% Data completeness (in resolution range)	100.0 (29.93-2.50) 99.0 (29.69-2.50)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.91 (at 2.51Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.229 , 0.268 0.229 , 0.266	Depositor DCC
R_{free} test set	1593 reflections (2.60%)	DCC
Wilson B-factor (Å ²)	36.5	Xtriage
Anisotropy	0.020	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 30.1	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 62834 reflections	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	11025	wwPDB-VP
Average B, all atoms (Å ²)	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.00% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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	0.37	0/2507	0.51	1/3387 (0.0%)
1	B	0.37	0/2515	0.53	1/3400 (0.0%)
1	C	0.35	0/2519	0.50	1/3404 (0.0%)
1	D	0.37	0/2515	0.51	1/3400 (0.0%)
2	E	0.33	0/149	0.43	0/201
2	F	0.39	0/153	0.50	0/206
2	G	0.36	0/149	0.44	0/201
2	H	0.37	0/149	0.46	0/201
All	All	0.37	0/10656	0.51	4/14400 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	297	PRO	N-CA-CB	6.28	110.83	103.30
1	C	297	PRO	N-CA-CB	6.26	110.81	103.30
1	A	297	PRO	N-CA-CB	6.19	110.72	103.30
1	B	297	PRO	N-CA-CB	5.79	110.25	103.30

There are no chirality outliers.

There are no planarity outliers.

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2448	0	2426	25	0
1	B	2456	0	2419	18	0
1	C	2460	0	2430	24	0
1	D	2456	0	2419	19	0
2	E	146	0	120	0	0
2	F	150	0	124	3	0
2	G	146	0	118	1	0
2	H	146	0	120	0	0
3	A	160	0	0	1	0
3	B	168	0	0	3	0
3	C	126	0	0	1	0
3	D	153	0	0	2	0
3	E	5	0	0	0	0
3	F	1	0	0	0	0
3	G	1	0	0	0	0
3	H	3	0	0	0	0
All	All	11025	0	10176	83	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 4.

All (83) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:138:ASN:H	1:B:142:HIS:HD1	1.19	0.86
1:C:138:ASN:H	1:C:142:HIS:HD1	1.25	0.84
1:C:8:ARG:HH11	1:C:77:GLN:HE22	1.31	0.76
1:A:138:ASN:H	1:A:142:HIS:HD1	1.34	0.73
1:B:139:LYS:HD2	1:B:139:LYS:H	1.54	0.71
1:B:273:ARG:HH11	1:B:273:ARG:HG2	1.56	0.68
1:D:138:ASN:HD22	1:D:141:ILE:H	1.44	0.65
1:D:252:ASP:O	3:D:430:HOH:O	2.14	0.63
1:C:48:GLN:HG3	1:C:79:LYS:HB2	1.81	0.61
1:C:25:THR:HA	1:C:64:LYS:HA	1.82	0.61
1:A:127:SER:OG	1:A:175:TRP:HB3	2.01	0.61
1:A:32:GLN:NE2	1:D:142:HIS:HE2	1.98	0.61
1:C:136:ASP:OD2	1:C:180:ARG:O	2.19	0.59
1:A:8:ARG:HE	1:A:77:GLN:HE22	1.50	0.58
1:A:257:ILE:HD12	1:A:267:PHE:HD2	1.67	0.58
1:A:217:TRP:HB2	1:A:228:TYR:HB2	1.85	0.58
1:C:25:THR:H	1:C:28:GLN:NE2	2.02	0.58
1:A:32:GLN:HE22	1:D:142:HIS:HE2	1.50	0.57
1:A:257:ILE:HD11	1:A:269:PHE:HE1	1.68	0.57
1:B:273:ARG:HH11	1:B:273:ARG:CG	2.18	0.57

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:D:8:ARG:HH11	1:D:77:GLN:HE22	1.53	0.57
2:F:343:ALA:H	2:F:344:PRO:HA	1.69	0.57
1:A:225:LEU:HB2	1:A:240:PHE:HB2	1.86	0.56
1:A:25:THR:HG22	1:A:28:GLN:CD	2.25	0.56
1:B:295:ARG:NH1	3:B:401:HOH:O	2.39	0.56
1:A:113:ASP:OD1	1:A:156:ARG:HB2	2.07	0.55
1:C:236:PRO:HB2	2:G:343:ALA:HB2	1.89	0.55
1:B:136:ASP:OD2	1:B:180:ARG:O	2.24	0.55
1:C:257:ILE:HD12	1:C:267:PHE:HD2	1.71	0.55
1:C:25:THR:HG23	1:C:28:GLN:H	1.71	0.54
1:C:147:LEU:HB3	1:C:152:LEU:HD11	1.89	0.54
1:B:8:ARG:HH11	1:B:77:GLN:HE22	1.56	0.54
1:C:215:GLU:O	1:C:230:HIS:HB2	2.11	0.51
1:A:162:LYS:HD3	1:A:163:LEU:HD12	1.94	0.50
1:B:147:LEU:HB3	1:B:152:LEU:HD11	1.93	0.50
1:B:295:ARG:CZ	3:B:401:HOH:O	2.59	0.50
1:A:124:LEU:O	1:A:127:SER:HB3	2.11	0.50
1:C:217:TRP:HB2	1:C:228:TYR:HB2	1.93	0.49
1:B:281:LEU:HG	3:B:400:HOH:O	2.13	0.48
1:D:8:ARG:HD3	1:D:77:GLN:HE22	1.79	0.48
1:C:295:ARG:NH1	3:C:430:HOH:O	2.47	0.47
1:A:113:ASP:HB3	1:A:156:ARG:HH21	1.78	0.47
1:C:257:ILE:HD12	1:C:267:PHE:CD2	2.49	0.47
1:D:208:ILE:HG22	1:D:216:LEU:HB2	1.97	0.47
1:C:127:SER:OG	1:C:179:HIS:HE1	1.97	0.47
1:B:113:ASP:OD1	1:B:156:ARG:HB2	2.15	0.47
1:D:281:LEU:O	1:D:285:MET:HG3	2.16	0.46
1:C:257:ILE:HD11	1:C:269:PHE:HE1	1.81	0.45
1:C:216:LEU:HD12	1:C:229:GLU:HA	1.98	0.45
1:D:134:TYR:OH	1:D:150:ASP:OD2	2.25	0.45
1:A:127:SER:OG	1:A:179:HIS:CE1	2.69	0.45
1:D:166:GLU:H	1:D:166:GLU:CD	2.19	0.45
1:B:273:ARG:NH1	1:B:273:ARG:CG	2.79	0.45
1:D:184:ARG:HD2	3:D:458:HOH:O	2.17	0.45
2:F:355:PHE:HA	2:F:358:LEU:HD12	1.99	0.44
1:B:138:ASN:N	1:B:142:HIS:HD1	2.00	0.44
1:B:127:SER:OG	1:B:179:HIS:HE1	1.99	0.44
1:B:143:LYS:HD2	1:C:21:GLN:HG3	1.98	0.44
1:A:32:GLN:NE2	1:D:142:HIS:NE2	2.65	0.43
1:B:211:LYS:HD2	2:F:356:SER:HB3	1.99	0.43
1:A:207:GLU:O	1:A:208:ILE:HD12	2.19	0.43
1:C:253:LYS:O	1:C:270:TYR:HA	2.19	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:D:261:ASP:O	1:D:262:LYS:HB2	2.18	0.43
1:A:5:ILE:HB	1:A:20:ILE:HG13	2.00	0.43
1:A:273:ARG:HD3	1:A:275:ARG:HH12	1.83	0.42
1:D:200:MET:HG3	1:D:234:LEU:HD23	2.00	0.42
1:D:127:SER:OG	1:D:179:HIS:HE1	2.01	0.42
1:A:142:HIS:NE2	1:D:32:GLN:NE2	2.67	0.42
1:D:208:ILE:HD13	1:D:218:LEU:HB2	2.01	0.42
1:C:25:THR:H	1:C:28:GLN:HE21	1.68	0.42
1:C:252:ASP:HB3	1:C:253:LYS:H	1.59	0.42
1:A:224:GLY:HA2	1:A:242:TRP:CE2	2.54	0.42
1:B:196:GLN:HA	1:B:201:TYR:CG	2.55	0.42
1:A:160:GLN:HB3	3:A:336:HOH:O	2.19	0.41
1:B:34:VAL:HG13	1:B:39:LEU:O	2.21	0.41
1:D:245:ILE:HG21	1:D:248:ILE:HD11	2.02	0.41
1:C:8:ARG:HH21	1:C:15:GLU:CD	2.23	0.41
1:D:196:GLN:HA	1:D:201:TYR:CG	2.56	0.41
1:C:71:LYS:O	1:C:73:GLU:HG2	2.21	0.41
1:A:196:GLN:HA	1:A:201:TYR:CG	2.56	0.40
1:A:271:ALA:HA	1:A:272:PRO:HD3	1.79	0.40
1:A:79:LYS:HD3	1:A:81:ARG:NH2	2.37	0.40
1:C:34:VAL:HG13	1:C:39:LEU:O	2.21	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	293/312 (94%)	284 (97%)	7 (2%)	2 (1%)	30	50
1	B	295/312 (95%)	287 (97%)	7 (2%)	1 (0%)	50	73
1	C	295/312 (95%)	284 (96%)	7 (2%)	4 (1%)	16	27
1	D	295/312 (95%)	289 (98%)	4 (1%)	2 (1%)	30	50
2	E	18/28 (64%)	18 (100%)	0	0	100	100
2	F	18/28 (64%)	15 (83%)	2 (11%)	1 (6%)	3	2

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	G	18/28 (64%)	18 (100%)	0	0	100	100
2	H	18/28 (64%)	17 (94%)	0	1 (6%)	3	2
All	All	1250/1360 (92%)	1212 (97%)	27 (2%)	11 (1%)	25	42

All (11) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	180	ARG
1	B	180	ARG
1	C	180	ARG
1	C	296	LYS
1	C	297	PRO
1	D	297	PRO
1	A	252	ASP
1	D	296	LYS
2	F	343	ALA
1	C	272	PRO
2	H	340	SER

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	262/282 (93%)	250 (95%)	12 (5%)	37	62
1	B	261/282 (93%)	248 (95%)	13 (5%)	34	58
1	C	262/282 (93%)	252 (96%)	10 (4%)	44	71
1	D	261/282 (93%)	250 (96%)	11 (4%)	40	66
2	E	13/26 (50%)	11 (85%)	2 (15%)	4	7
2	F	14/26 (54%)	14 (100%)	0	100	100
2	G	13/26 (50%)	13 (100%)	0	100	100
2	H	13/26 (50%)	13 (100%)	0	100	100
All	All	1099/1232 (89%)	1051 (96%)	48 (4%)	39	64

All (48) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	23	ASN
1	A	66	THR
1	A	72	LYS
1	A	111	LEU
1	A	162	LYS
1	A	165	LYS
1	A	203	VAL
1	A	208	ILE
1	A	218	LEU
1	A	223	LEU
1	A	281	LEU
1	A	292	MET
1	B	57	THR
1	B	96	GLU
1	B	111	LEU
1	B	139	LYS
1	B	140	GLU
1	B	162	LYS
1	B	203	VAL
1	B	211	LYS
1	B	216	LEU
1	B	218	LEU
1	B	237	LYS
1	B	273	ARG
1	B	289	GLU
1	C	67	GLN
1	C	111	LEU
1	C	203	VAL
1	C	208	ILE
1	C	214	THR
1	C	216	LEU
1	C	218	LEU
1	C	231	ASP
1	C	252	ASP
1	C	289	GLU
1	D	67	GLN
1	D	111	LEU
1	D	166	GLU
1	D	180	ARG
1	D	203	VAL
1	D	208	ILE
1	D	218	LEU
1	D	223	LEU

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Mol	Chain	Res	Type
1	D	237	LYS
1	D	281	LEU
1	D	295	ARG
2	E	345	GLN
2	E	354	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (34) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	6	ASN
1	A	23	ASN
1	A	32	GLN
1	A	48	GLN
1	A	67	GLN
1	A	77	GLN
1	A	131	GLN
1	A	160	GLN
1	A	179	HIS
1	A	288	HIS
1	B	6	ASN
1	B	23	ASN
1	B	32	GLN
1	B	48	GLN
1	B	62	ASN
1	B	74	ASN
1	B	77	GLN
1	B	131	GLN
1	B	179	HIS
1	B	226	ASN
1	C	6	ASN
1	C	28	GLN
1	C	32	GLN
1	C	48	GLN
1	C	77	GLN
1	C	179	HIS
1	C	230	HIS
1	D	6	ASN
1	D	32	GLN
1	D	48	GLN
1	D	77	GLN
1	D	138	ASN
1	D	179	HIS

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Mol	Chain	Res	Type
2	F	357	ASN

5.3.3 RNA ⓘ

There are no RNA chains 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 ⓘ

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	295/312 (94%)	-0.05	5 (1%) 67 69	20, 36, 49, 57	0
1	B	297/312 (95%)	-0.03	6 (2%) 62 64	21, 33, 52, 61	0
1	C	297/312 (95%)	0.21	9 (3%) 48 50	24, 40, 61, 65	0
1	D	297/312 (95%)	-0.09	4 (1%) 74 76	21, 33, 47, 59	0
2	E	20/28 (71%)	1.20	5 (25%) 1 1	57, 64, 79, 79	0
2	F	20/28 (71%)	1.51	6 (30%) 1 1	61, 68, 83, 84	0
2	G	20/28 (71%)	1.17	5 (25%) 1 1	73, 78, 87, 87	0
2	H	20/28 (71%)	1.40	7 (35%) 1 1	59, 68, 84, 84	0
All	All	1266/1360 (93%)	0.09	47 (3%) 39 41	20, 36, 63, 87	0

All (47) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	H	344	PRO	6.4
2	F	343	ALA	5.5
2	E	339	SER	5.3
2	F	339	SER	5.0
1	B	299	THR	5.0
2	F	342	ARG	4.5
2	G	344	PRO	4.4
1	B	297	PRO	4.3
2	H	343	ALA	4.2
1	B	298	ASP	4.2
1	A	297	PRO	4.1
1	C	297	PRO	3.9
2	F	344	PRO	3.7
1	A	67	GLN	3.6
1	D	297	PRO	3.5
1	C	298	ASP	3.2

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Mol	Chain	Res	Type	RSRZ
1	D	296	LYS	3.2
2	H	345	GLN	3.2
2	E	346	MET	3.1
2	H	341	LYS	3.1
1	A	160	GLN	2.9
2	E	345	GLN	2.7
1	C	299	THR	2.7
2	G	340	SER	2.6
2	H	342	ARG	2.6
2	E	344	PRO	2.6
2	F	340	SER	2.5
1	C	66	THR	2.5
2	G	345	GLN	2.4
2	H	339	SER	2.4
1	D	299	THR	2.4
1	C	94	ILE	2.4
2	E	340	SER	2.4
1	C	160	GLN	2.3
1	C	180	ARG	2.3
1	B	162	LYS	2.3
1	A	252	ASP	2.3
1	D	298	ASP	2.3
2	G	358	LEU	2.3
1	C	96	GLU	2.2
2	F	345	GLN	2.1
2	H	340	SER	2.1
2	G	343	ALA	2.1
1	B	212	LYS	2.1
1	B	252	ASP	2.1
1	A	162	LYS	2.0
1	C	247	ASN	2.0

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 ⓘ

There are no carbohydrates in this entry.

6.4 Ligands

There are no ligands in this entry.

6.5 Other polymers

There are no such residues in this entry.