



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 12:32 PM UTC

PDB ID : 4C99 / pdb_00004c99
Title : Mouse ZNRF3 ectodomain in complex with mouse RSPO2 Fu1-Fu2 crystal form I
Authors : Zebisch, M.; Jones, E.Y.
Deposited on : 2013-10-02
Resolution : 2.80 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:

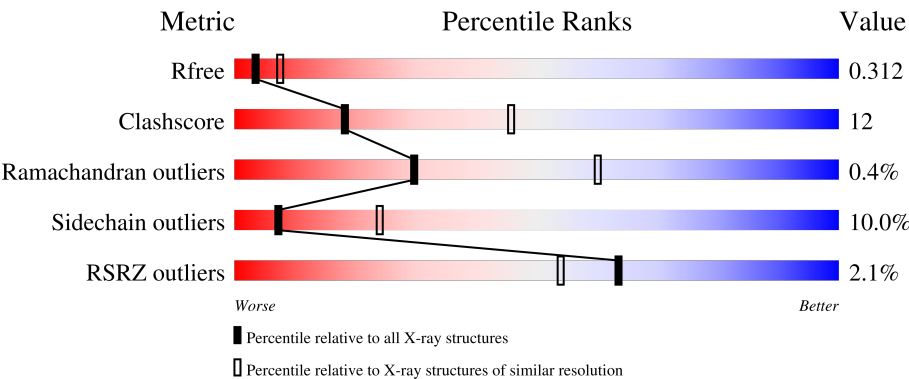
MolProbity : 4-5-2 with Phenix2.0
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

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 2.80 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}	180053	3866 (2.80-2.80)
Clashscore	190562	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)
RSRZ outliers	180081	3869 (2.80-2.80)

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 $\leq 5\%$. 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	165	% 62% 28% • 7%
1	C	165	% 67% 24% • 7%
2	B	122	4% 51% 30% • 16%
2	D	122	2% 63% 20% •• 14%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 3968 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 E3 UBIQUITIN-PROTEIN LIGASE ZNR3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	153	Total	C	N	O	S	0	0	0
			1178	740	205	228	5			
1	C	153	Total	C	N	O	S	0	0	0
			1178	740	205	228	5			

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	50	GLU	-	expression tag	UNP Q5SSZ7
A	51	THR	-	expression tag	UNP Q5SSZ7
A	52	GLY	-	expression tag	UNP Q5SSZ7
A	206	GLY	-	expression tag	UNP Q5SSZ7
A	207	THR	-	expression tag	UNP Q5SSZ7
A	208	LYS	-	expression tag	UNP Q5SSZ7
A	209	HIS	-	expression tag	UNP Q5SSZ7
A	210	HIS	-	expression tag	UNP Q5SSZ7
A	211	HIS	-	expression tag	UNP Q5SSZ7
A	212	HIS	-	expression tag	UNP Q5SSZ7
A	213	HIS	-	expression tag	UNP Q5SSZ7
A	214	HIS	-	expression tag	UNP Q5SSZ7
C	50	GLU	-	expression tag	UNP Q5SSZ7
C	51	THR	-	expression tag	UNP Q5SSZ7
C	52	GLY	-	expression tag	UNP Q5SSZ7
C	206	GLY	-	expression tag	UNP Q5SSZ7
C	207	THR	-	expression tag	UNP Q5SSZ7
C	208	LYS	-	expression tag	UNP Q5SSZ7
C	209	HIS	-	expression tag	UNP Q5SSZ7
C	210	HIS	-	expression tag	UNP Q5SSZ7
C	211	HIS	-	expression tag	UNP Q5SSZ7
C	212	HIS	-	expression tag	UNP Q5SSZ7
C	213	HIS	-	expression tag	UNP Q5SSZ7
C	214	HIS	-	expression tag	UNP Q5SSZ7

- Molecule 2 is a protein called R-SPONDIN-2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	103	Total	C	N	O	S	0	0	0
			797	484	146	148	19			
2	D	105	Total	C	N	O	S	0	0	0
			814	498	146	151	19			

There are 28 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	34	GLU	-	expression tag	UNP Q8BFU0
B	35	THR	-	expression tag	UNP Q8BFU0
B	36	GLY	-	expression tag	UNP Q8BFU0
B	145	THR	-	expression tag	UNP Q8BFU0
B	146	HIS	-	expression tag	UNP Q8BFU0
B	147	HIS	-	expression tag	UNP Q8BFU0
B	148	HIS	-	expression tag	UNP Q8BFU0
B	149	HIS	-	expression tag	UNP Q8BFU0
B	150	HIS	-	expression tag	UNP Q8BFU0
B	151	HIS	-	expression tag	UNP Q8BFU0
B	152	HIS	-	expression tag	UNP Q8BFU0
B	153	HIS	-	expression tag	UNP Q8BFU0
B	154	HIS	-	expression tag	UNP Q8BFU0
B	155	HIS	-	expression tag	UNP Q8BFU0
D	34	GLU	-	expression tag	UNP Q8BFU0
D	35	THR	-	expression tag	UNP Q8BFU0
D	36	GLY	-	expression tag	UNP Q8BFU0
D	145	THR	-	expression tag	UNP Q8BFU0
D	146	HIS	-	expression tag	UNP Q8BFU0
D	147	HIS	-	expression tag	UNP Q8BFU0
D	148	HIS	-	expression tag	UNP Q8BFU0
D	149	HIS	-	expression tag	UNP Q8BFU0
D	150	HIS	-	expression tag	UNP Q8BFU0
D	151	HIS	-	expression tag	UNP Q8BFU0
D	152	HIS	-	expression tag	UNP Q8BFU0
D	153	HIS	-	expression tag	UNP Q8BFU0
D	154	HIS	-	expression tag	UNP Q8BFU0
D	155	HIS	-	expression tag	UNP Q8BFU0

- Molecule 3 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Cl	0	0
			1	1		

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4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	59.80Å 77.21Å 130.61Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	66.46 – 2.80 66.46 – 2.80	Depositor EDS
% Data completeness (in resolution range)	99.9 (66.46-2.80) 99.9 (66.46-2.80)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.36 (at 2.81Å)	Xtriage
Refinement program	REFMAC 5.7.0029	Depositor
R, R_{free}	0.236 , 0.323 0.236 , 0.312	Depositor DCC
R_{free} test set	772 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	75.6	Xtriage
Anisotropy	0.114	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 66.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	3968	wwPDB-VP
Average B, all atoms (Å ²)	86.0	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 31.31 % 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 1.1304e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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

Bond lengths and bond angles in the following residue types are not validated in this section:
CL

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	0.92	0/1198	1.07	1/1623 (0.1%)
1	C	0.86	0/1198	1.03	1/1623 (0.1%)
2	B	0.81	0/815	1.02	4/1089 (0.4%)
2	D	0.84	0/832	1.16	1/1111 (0.1%)
All	All	0.86	0/4043	1.07	7/5446 (0.1%)

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
2	D	0	1

There are no bond length outliers.

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	C	152	ILE	CB-CA-C	-6.14	104.27	111.09
2	D	141	CYS	N-CA-C	6.02	118.31	108.55
2	B	110	CYS	N-CA-C	5.54	118.84	107.69
2	B	61	PHE	N-CA-C	5.27	117.34	108.96
2	B	43	CYS	N-CA-C	5.27	117.66	108.76
1	A	121	VAL	N-CA-CB	-5.24	107.41	112.65
2	B	90	MET	N-CA-C	5.08	115.86	108.14

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	D	141	CYS	Peptide

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	1178	0	1178	35	0
1	C	1178	0	1178	33	0
2	B	797	0	698	23	0
2	D	814	0	727	13	0
3	A	1	0	0	0	0
All	All	3968	0	3781	94	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 12.

All (94) 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:B:129:PRO:HD2	2:B:141:CYS:SG	1.91	1.08
1:C:155:VAL:CG2	1:C:179:TYR:HB2	1.93	0.97
1:C:155:VAL:HG21	1:C:179:TYR:HB2	1.51	0.90
2:B:113:CYS:SG	2:B:117:PHE:HB3	2.19	0.82
2:B:113:CYS:SG	2:B:117:PHE:CB	2.74	0.76
1:C:154:ASP:OD1	1:C:154:ASP:C	2.36	0.69
1:A:54:GLU:HB2	1:A:88:MET:HE1	1.74	0.68
1:A:128:LEU:HD13	2:B:45:SER:OG	1.94	0.66
1:A:124:GLU:OE1	2:B:47:SER:HB3	1.96	0.65
2:B:129:PRO:CD	2:B:141:CYS:SG	2.80	0.64
1:A:160:GLU:O	1:A:164:GLN:HG3	1.97	0.64
2:B:83:TYR:HB3	2:B:104:CYS:HB2	1.78	0.64
2:D:87:ALA:HB1	2:D:88:PRO:CD	2.28	0.63
1:C:155:VAL:HG12	1:C:158:ASN:O	2.00	0.60
2:D:49:ASP:C	2:D:69:ARG:HH22	2.10	0.59
2:B:82:TYR:HA	2:B:94:ALA:O	2.02	0.59
1:C:155:VAL:HG21	1:C:179:TYR:CB	2.29	0.59
1:A:122:LYS:O	2:B:50:ASN:ND2	2.33	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:155:VAL:HG21	1:A:162:ILE:CG1	2.33	0.59
2:B:113:CYS:SG	2:B:117:PHE:HB2	2.43	0.58
2:D:87:ALA:HB3	2:D:90:MET:O	2.03	0.58
1:C:57:PHE:CE1	1:C:205:LEU:HD12	2.38	0.58
1:A:149:THR:OG1	1:A:175:ARG:NH1	2.38	0.56
1:C:157:GLU:HA	1:C:157:GLU:OE1	2.06	0.56
2:D:43:CYS:HB2	2:D:45:SER:O	2.07	0.55
1:A:128:LEU:HD22	2:B:45:SER:HB2	1.86	0.55
2:D:42:GLY:O	2:D:56:GLN:HB2	2.07	0.55
1:C:85:ALA:HB2	1:C:165:LEU:O	2.07	0.55
2:D:87:ALA:HB1	2:D:88:PRO:HD2	1.88	0.54
1:A:125:GLN:HB2	1:A:128:LEU:HG	1.88	0.54
2:B:64:ARG:HH21	2:B:73:GLU:HG2	1.73	0.53
2:B:135:LEU:O	2:B:139:MET:N	2.41	0.53
2:D:82:TYR:HA	2:D:94:ALA:O	2.09	0.53
1:C:97:GLN:HE22	2:D:69:ARG:HH12	1.56	0.53
1:A:135:THR:O	1:A:138:GLY:N	2.41	0.53
1:C:155:VAL:HG23	1:C:179:TYR:HB2	1.83	0.52
1:C:161:ALA:O	1:C:165:LEU:N	2.42	0.52
2:D:129:PRO:O	2:D:132:PHE:HB2	2.10	0.52
1:A:171:ASP:OD1	1:A:171:ASP:N	2.43	0.52
2:B:83:TYR:CE2	2:B:85:HIS:HB2	2.46	0.51
2:B:87:ALA:HB1	2:B:88:PRO:HD2	1.93	0.51
1:A:78:LEU:HD21	1:A:188:LEU:HB2	1.92	0.50
1:A:155:VAL:HG21	1:A:162:ILE:HG12	1.91	0.50
2:B:83:TYR:CD2	2:B:84:GLY:O	2.64	0.50
2:B:64:ARG:NH2	2:B:73:GLU:HG2	2.26	0.50
1:C:189:MET:O	1:C:193:ASN:HB2	2.11	0.50
1:C:99:HIS:ND1	1:C:100:PRO:HD2	2.27	0.49
1:A:98:MET:CE	1:A:103:LEU:HD21	2.42	0.49
1:C:125:GLN:O	1:C:126:PRO:C	2.55	0.49
1:A:117:TRP:H	1:A:117:TRP:CD1	2.31	0.48
1:C:193:ASN:ND2	2:D:49:ASP:OD1	2.46	0.48
1:C:126:PRO:HD3	1:C:158:ASN:HB2	1.94	0.48
1:A:182:GLY:O	1:A:186:ILE:HG12	2.14	0.48
1:C:160:GLU:CD	1:C:160:GLU:H	2.21	0.48
1:C:55:THR:HG23	1:C:79:THR:HG23	1.95	0.48
1:C:144:VAL:HA	1:C:148:ALA:HB3	1.96	0.47
1:C:136:VAL:HG13	1:C:137:LEU:H	1.79	0.47
2:B:135:LEU:O	2:B:138:THR:N	2.47	0.46
2:B:127:GLU:O	2:B:128:CYS:C	2.57	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:76:THR:HG22	1:C:77:GLY:N	2.31	0.46
2:D:60:PHE:CZ	2:D:84:GLY:HA3	2.51	0.46
2:B:87:ALA:HB3	2:B:90:MET:O	2.16	0.46
2:D:46:CYS:SG	2:D:47:SER:N	2.89	0.45
1:C:154:ASP:HA	1:C:180:VAL:HG23	1.98	0.45
1:A:71:TYR:CE2	1:C:115:TYR:HB2	2.52	0.45
1:A:92:GLU:OE2	1:C:149:THR:OG1	2.31	0.45
1:C:136:VAL:HG13	1:C:137:LEU:N	2.31	0.45
1:A:144:VAL:HG21	1:A:173:LEU:HD13	1.98	0.44
1:A:100:PRO:C	1:A:102:GLY:H	2.25	0.44
1:C:135:THR:O	1:C:136:VAL:C	2.58	0.44
1:A:159:PRO:O	1:A:162:ILE:N	2.50	0.44
2:B:80:SER:HA	2:B:102:ASP:OD1	2.17	0.44
1:A:185:ALA:O	1:A:186:ILE:C	2.61	0.44
1:A:193:ASN:ND2	2:B:49:ASP:OD1	2.50	0.44
1:A:114:GLU:N	1:A:114:GLU:OE1	2.51	0.43
1:A:115:TYR:HB2	1:C:71:TYR:CE1	2.53	0.43
1:A:143:ALA:O	1:A:144:VAL:C	2.61	0.43
1:A:116:GLY:O	1:A:149:THR:HG22	2.19	0.42
1:A:98:MET:HB2	1:A:121:VAL:HG22	2.02	0.42
1:C:135:THR:O	1:C:138:GLY:N	2.52	0.42
1:A:189:MET:O	1:A:193:ASN:HB2	2.20	0.42
1:A:178:VAL:HG12	1:A:179:TYR:N	2.34	0.41
1:C:76:THR:HG22	1:C:77:GLY:H	1.85	0.41
1:A:98:MET:HE2	1:A:103:LEU:HD21	2.02	0.41
1:C:57:PHE:CZ	1:C:205:LEU:HD12	2.55	0.41
2:D:120:HIS:HB3	2:D:125:PHE:CE1	2.56	0.41
1:A:126:PRO:O	1:A:129:ASP:C	2.63	0.41
2:B:113:CYS:HB2	2:B:124:CYS:HB2	2.00	0.41
1:C:120:VAL:HG12	1:C:189:MET:HE1	2.03	0.41
1:A:167:GLN:OE1	1:A:167:GLN:O	2.39	0.40
1:A:147:GLY:O	1:A:148:ALA:C	2.63	0.40
1:C:158:ASN:OD1	1:C:158:ASN:C	2.64	0.40
1:A:110:GLU:OE2	1:A:142:ARG:NH2	2.50	0.40
1:C:120:VAL:CG1	1:C:189:MET:HE1	2.51	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	151/165 (92%)	135 (89%)	15 (10%)	1 (1%)	18	47
1	C	151/165 (92%)	141 (93%)	10 (7%)	0	100	100
2	B	101/122 (83%)	87 (86%)	13 (13%)	1 (1%)	12	38
2	D	103/122 (84%)	93 (90%)	10 (10%)	0	100	100
All	All	506/574 (88%)	456 (90%)	48 (10%)	2 (0%)	30	60

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	55	CYS
1	A	130	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	128/138 (93%)	120 (94%)	8 (6%)	16	45
1	C	128/138 (93%)	117 (91%)	11 (9%)	10	31
2	B	86/108 (80%)	73 (85%)	13 (15%)	3	10
2	D	89/108 (82%)	78 (88%)	11 (12%)	4	16
All	All	431/492 (88%)	388 (90%)	43 (10%)	7	24

All (43) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	78	LEU
1	A	79	THR
1	A	92	GLU
1	A	109	GLU
1	A	134	LEU
1	A	171	ASP
1	A	181	LYS
1	A	193	ASN
2	B	40	CYS
2	B	43	CYS
2	B	46	CYS
2	B	52	CYS
2	B	53	SER
2	B	54	ARG
2	B	55	CYS
2	B	76	HIS
2	B	101	CYS
2	B	103	SER
2	B	120	HIS
2	B	124	CYS
2	B	125	PHE
1	C	64	GLU
1	C	78	LEU
1	C	79	THR
1	C	94	GLU
1	C	123	LEU
1	C	133	CYS
1	C	146	ARG
1	C	155	VAL
1	C	184	ASP
1	C	191	ILE
1	C	193	ASN
2	D	43	CYS
2	D	48	LYS
2	D	52	CYS
2	D	56	GLN
2	D	58	LYS
2	D	66	GLU
2	D	68	MET
2	D	76	HIS
2	D	78	CYS
2	D	115	VAL
2	D	141	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	145	GLN
1	A	193	ASN
2	B	85	HIS
2	B	100	ASN
2	B	120	HIS
1	C	190	ASN
2	D	120	HIS

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 1 ligands modelled in this entry, 1 is 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 [i](#)

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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	153/165 (92%)	0.08	2 (1%) 75 66	38, 71, 117, 182	0
1	C	153/165 (92%)	0.08	1 (0%) 84 77	44, 77, 139, 184	0
2	B	103/122 (84%)	0.62	5 (4%) 35 27	63, 101, 136, 162	0
2	D	105/122 (86%)	0.27	3 (2%) 53 43	57, 82, 123, 143	0
All	All	514/574 (89%)	0.23	11 (2%) 63 54	38, 81, 130, 184	0

All (11) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	133	ALA	3.3
2	D	39	ILE	3.2
2	B	134	PRO	2.7
2	B	73	GLU	2.6
2	D	44	LEU	2.5
2	D	56	GLN	2.5
2	B	132	PHE	2.5
1	A	85	ALA	2.2
1	C	69	GLY	2.1
1	A	143	ALA	2.1
2	B	131	GLY	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 oligosaccharides in this entry.

6.4 Ligands

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. 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	B-factors($\text{\AA}^2$)	Q<0.9
3	CL	A	1206	1/1	0.93	0.11	79,79,79,79	0

6.5 Other polymers

There are no such residues in this entry.