



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 10:35 AM UTC

PDB ID : 4C9A / pdb_00004c9a
Title : Mouse ZNRF3 ectodomain in complex with Xenopus RSPO2 Fu1-Fu2 (Seleno Met) crystal form I
Authors : Zebisch, M.; Jones, E.Y.
Deposited on : 2013-10-02
Resolution : 2.40 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
Mogul : 2022.3.0, CSD as543be (2022)
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

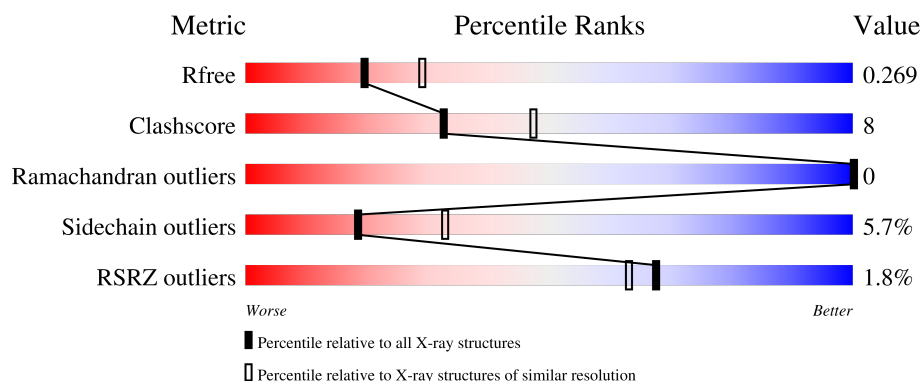
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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	4912 (2.40-2.40)
Clashscore	190562	5391 (2.40-2.40)
Ramachandran outliers	187476	5320 (2.40-2.40)
Sidechain outliers	187428	5321 (2.40-2.40)
RSRZ outliers	180081	4916 (2.40-2.40)

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	73% 17% • 7%
1	C	165	75% 16% • 8%
2	B	121	5% 64% 19% • 15%
2	D	121	70% 12% • 15%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 3815 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
			1170	735	204	226	5			
1	C	152	Total	C	N	O	S	0	0	0
			1159	729	200	225	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	Se	0	0	0
			717	436	134	129	16	2			
2	D	103	Total	C	N	O	S	Se	0	0	0
			769	472	142	137	16	2			

There are 22 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	32	GLU	-	expression tag	UNP Q5M7L6
B	33	THR	-	expression tag	UNP Q5M7L6
B	34	GLY	-	expression tag	UNP Q5M7L6
B	145	THR	-	expression tag	UNP Q5M7L6
B	146	LYS	-	expression tag	UNP Q5M7L6
B	147	HIS	-	expression tag	UNP Q5M7L6
B	148	HIS	-	expression tag	UNP Q5M7L6
B	149	HIS	-	expression tag	UNP Q5M7L6
B	150	HIS	-	expression tag	UNP Q5M7L6
B	151	HIS	-	expression tag	UNP Q5M7L6
B	152	HIS	-	expression tag	UNP Q5M7L6
D	32	GLU	-	expression tag	UNP Q5M7L6
D	33	THR	-	expression tag	UNP Q5M7L6
D	34	GLY	-	expression tag	UNP Q5M7L6
D	145	THR	-	expression tag	UNP Q5M7L6
D	146	LYS	-	expression tag	UNP Q5M7L6
D	147	HIS	-	expression tag	UNP Q5M7L6
D	148	HIS	-	expression tag	UNP Q5M7L6
D	149	HIS	-	expression tag	UNP Q5M7L6
D	150	HIS	-	expression tag	UNP Q5M7L6
D	151	HIS	-	expression tag	UNP Q5M7L6
D	152	HIS	-	expression tag	UNP Q5M7L6

4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	36.36Å 70.96Å 71.99Å 109.15° 101.71° 101.30°	Depositor
Resolution (Å)	38.92 – 2.40 38.92 – 2.40	Depositor EDS
% Data completeness (in resolution range)	78.2 (38.92-2.40) 78.2 (38.92-2.40)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.72 (at 2.39Å)	Xtriage
Refinement program	REFMAC 5.7.0029	Depositor
R, R_{free}	0.195 , 0.273 0.197 , 0.269	Depositor DCC
R_{free} test set	993 reflections (5.09%)	wwPDB-VP
Wilson B-factor (Å ²)	62.2	Xtriage
Anisotropy	0.026	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 44.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.009 for -h,-l,-k	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	3815	wwPDB-VP
Average B, all atoms (Å ²)	79.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.82% 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	1.22	3/1190 (0.3%)	1.21	5/1614 (0.3%)
1	C	1.17	0/1179	1.26	7/1600 (0.4%)
2	B	0.85	0/727	1.10	2/973 (0.2%)
2	D	0.85	0/782	1.02	0/1042
All	All	1.08	3/3878 (0.1%)	1.17	14/5229 (0.3%)

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

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	91	ALA	N-CA	-6.47	1.37	1.45
1	A	121	VAL	C-O	-5.58	1.17	1.24
1	A	79	THR	C-O	5.15	1.30	1.23

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	72	THR	N-CA-C	-7.83	97.38	109.52
1	C	203	GLN	N-CA-C	7.35	121.38	109.40
2	B	65	ARG	CG-CD-NE	-6.63	97.41	112.00
1	C	99	HIS	N-CA-C	-5.97	102.25	109.83
1	A	170	GLU	N-CA-C	-5.86	100.11	109.96
2	B	90	MSE	N-CA-CB	-5.53	103.16	111.56
1	A	99	HIS	CA-C-N	5.38	125.03	119.05
1	A	99	HIS	C-N-CA	5.38	125.03	119.05
1	A	73	THR	N-CA-C	5.36	117.41	109.69

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	197	VAL	N-CA-C	5.35	115.88	108.23
1	C	99	HIS	CA-C-N	5.15	124.59	119.24
1	C	99	HIS	C-N-CA	5.15	124.59	119.24
1	C	183	ALA	N-CA-C	-5.15	105.75	111.36
1	A	188	LEU	N-CA-C	-5.07	105.64	111.07

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	D	42	GLY	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	1170	0	1163	27	0
1	C	1159	0	1150	13	0
2	B	717	0	610	22	0
2	D	769	0	701	9	0
All	All	3815	0	3624	59	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 (59) 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:192:VAL:HG22	2:B:68:MSE:CE	1.98	0.94
1:A:192:VAL:HG22	2:B:68:MSE:HE2	1.67	0.77
2:B:101:CYS:SG	2:B:112:LYS:O	2.47	0.72
2:D:120:HIS:HB2	2:D:141:CYS:SG	2.29	0.72
2:B:133:ALA:H	2:B:142:VAL:HG22	1.56	0.71
1:C:141:LYS:HG2	1:C:145:GLN:HE21	1.56	0.69
1:A:107:ASN:CG	1:A:110:GLU:HG3	2.19	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:136:VAL:HG12	1:C:165:LEU:HD13	1.80	0.64
1:A:114:GLU:O	1:A:117:TRP:HD1	1.82	0.63
1:A:141:LYS:HG3	1:A:173:LEU:HD21	1.81	0.61
1:A:120:VAL:CG1	1:A:189:MET:HE1	2.31	0.61
1:A:192:VAL:HA	2:B:68:MSE:HE2	1.84	0.58
2:B:98:ILE:HG23	2:B:101:CYS:HB3	1.85	0.58
2:B:98:ILE:HD12	2:B:108:ASP:HA	1.86	0.57
1:A:110:GLU:OE1	1:A:142:ARG:NH2	2.37	0.56
2:D:138:THR:OG1	2:D:140:VAL:HG22	2.05	0.56
1:C:161:ALA:O	1:C:165:LEU:HB2	2.09	0.53
2:B:133:ALA:N	2:B:142:VAL:HG22	2.23	0.52
1:C:96:VAL:O	1:C:119:GLY:HA2	2.11	0.51
2:B:104:CYS:HB2	2:B:109:PHE:O	2.11	0.50
1:C:122:LYS:HA	1:C:154:ASP:HB3	1.94	0.49
2:D:43:CYS:SG	2:D:46:CYS:HB2	2.52	0.49
1:A:95:ILE:HG21	2:B:68:MSE:HE3	1.94	0.49
2:D:53:LEU:O	2:D:54:ARG:HG3	2.13	0.48
1:C:117:TRP:O	1:C:149:THR:HG22	2.13	0.48
1:A:65:SER:HB3	1:C:112:LEU:HD21	1.96	0.48
1:A:100:PRO:O	1:A:139:LYS:HE3	2.15	0.47
1:A:106:ASN:OD1	1:A:106:ASN:N	2.46	0.47
2:B:133:ALA:O	2:B:141:CYS:HA	2.15	0.46
1:A:98:MET:HB2	1:A:121:VAL:HG22	1.98	0.46
2:B:81:GLY:O	2:B:96:CYS:HB2	2.15	0.46
1:A:193:ASN:OD1	2:B:69:ARG:NH1	2.48	0.46
1:A:154:ASP:OD1	1:A:154:ASP:C	2.59	0.46
2:B:81:GLY:O	2:B:96:CYS:CB	2.64	0.46
1:A:193:ASN:ND2	2:B:49:ASP:OD1	2.36	0.45
1:A:65:SER:CB	1:C:112:LEU:HD21	2.47	0.45
2:D:88:PRO:HG2	2:D:89:ASP:OD1	2.17	0.45
2:D:89:ASP:OD1	2:D:89:ASP:N	2.49	0.44
2:B:96:CYS:SG	2:B:104:CYS:N	2.91	0.44
1:A:78:LEU:HD21	1:A:188:LEU:HB2	1.99	0.44
1:A:95:ILE:CG2	2:B:68:MSE:HE3	2.48	0.43
1:A:192:VAL:HA	2:B:68:MSE:CE	2.47	0.43
1:C:103:LEU:O	1:C:134:LEU:HD12	2.19	0.43
1:A:192:VAL:CG2	2:B:68:MSE:HE2	2.44	0.43
1:A:142:ARG:O	1:A:146:ARG:HG3	2.19	0.43
2:B:45:SER:HB2	2:B:53:LEU:HB2	2.01	0.42
2:D:65:ARG:NH2	2:D:68:MSE:O	2.53	0.42
2:D:135:LEU:CD1	2:D:142:VAL:HG11	2.49	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:192:VAL:HG22	2:B:68:MSE:HE1	1.94	0.42
2:B:135:LEU:CB	2:B:138:THR:CB	2.97	0.42
1:A:98:MET:HE2	1:A:103:LEU:HD21	2.01	0.41
1:C:136:VAL:CG1	1:C:165:LEU:HD13	2.47	0.41
1:A:190:ASN:HB3	1:A:194:LYS:CE	2.51	0.41
1:A:120:VAL:HG13	1:A:189:MET:HE1	2.00	0.41
1:C:196:LYS:C	1:C:197:VAL:HG13	2.46	0.41
1:C:161:ALA:O	1:C:162:ILE:C	2.62	0.40
2:D:85:VAL:O	2:D:85:VAL:HG12	2.19	0.40
1:A:104:CYS:HB3	1:A:106:ASN:OD1	2.22	0.40
1:C:117:TRP:C	1:C:149:THR:HG22	2.46	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	151/165 (92%)	145 (96%)	6 (4%)	0	100	100
1	C	150/165 (91%)	141 (94%)	9 (6%)	0	100	100
2	B	101/121 (84%)	92 (91%)	9 (9%)	0	100	100
2	D	101/121 (84%)	89 (88%)	12 (12%)	0	100	100
All	All	503/572 (88%)	467 (93%)	36 (7%)	0	100	100

There are no Ramachandran outliers to report.

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	126/138 (91%)	123 (98%)	3 (2%)	43	65
1	C	125/138 (91%)	117 (94%)	8 (6%)	16	28
2	B	69/104 (66%)	62 (90%)	7 (10%)	7	11
2	D	83/104 (80%)	78 (94%)	5 (6%)	17	31
All	All	403/484 (83%)	380 (94%)	23 (6%)	18	33

All (23) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	78	LEU
1	A	106	ASN
1	A	160	GLU
2	B	43	CYS
2	B	68	MSE
2	B	76	GLN
2	B	90	MSE
2	B	99	GLU
2	B	110	CYS
2	B	115	SER
1	C	65	SER
1	C	79	THR
1	C	106	ASN
1	C	110	GLU
1	C	174	LYS
1	C	189	MET
1	C	193	ASN
1	C	196	LYS
2	D	43	CYS
2	D	45	SER
2	D	89	ASP
2	D	90	MSE
2	D	142	VAL

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

Mol	Chain	Res	Type
1	A	74	HIS
1	C	74	HIS

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Mol	Chain	Res	Type
1	C	106	ASN
1	C	107	ASN
1	C	125	GLN
1	C	145	GLN
1	C	166	ASN
1	C	167	GLN
1	C	190	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 oligosaccharides 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 [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%)	-0.19	1 (0%) 84 81	35, 58, 104, 136	0
1	C	152/165 (92%)	-0.18	1 (0%) 84 81	38, 62, 110, 130	0
2	B	100/121 (82%)	0.47	6 (6%) 27 24	53, 106, 153, 186	0
2	D	100/121 (82%)	0.22	1 (1%) 79 76	60, 93, 160, 168	0
All	All	505/572 (88%)	0.02	9 (1%) 67 63	35, 71, 142, 186	0

All (9) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	40	CYS	3.3
2	B	88	PRO	3.1
2	B	117	PHE	3.1
1	A	105	ASN	2.9
2	B	86	ARG	2.6
2	B	87	GLY	2.4
1	C	127	GLU	2.0
2	B	57	PRO	2.0
2	B	118	TYR	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 [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.