



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 18, 2026 – 12:21 AM UTC

PDB ID : 3ZEV / pdb_00003zev
Title : Structure of Thermostable Agonist-bound Neurotensin Receptor 1 Mutant without Lysozyme Fusion
Authors : Egloff, P.; Hillenbrand, M.; Schlinkmann, K.M.; Batyuk, A.; Mittl, P.; Plueckthun, A.
Deposited on : 2012-12-07
Resolution : 3.00 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

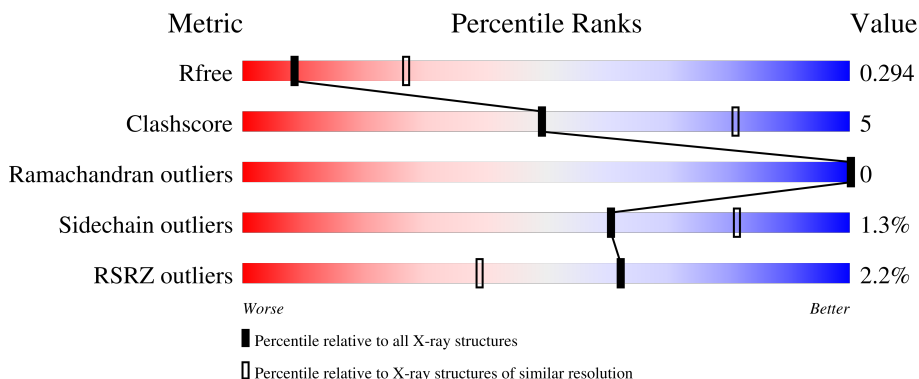
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

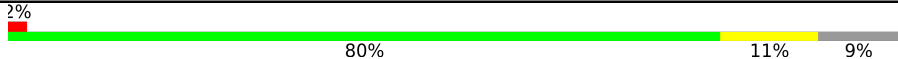
The reported resolution of this entry is 3.00 Å.

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	2672 (3.00-3.00)
Clashscore	190562	2977 (3.00-3.00)
Ramachandran outliers	187476	2877 (3.00-3.00)
Sidechain outliers	187428	2880 (3.00-3.00)
RSRZ outliers	180081	2671 (3.00-3.00)

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 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	338	
1	B	338	
2	C	8	
2	D	8	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4956 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 NEUROTENSIN RECEPTOR 1 TM86V.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	307	Total	C	N	O	S	0	0	0
			2413	1597	388	412	16			
1	B	304	Total	C	N	O	S	0	0	0
			2390	1582	380	412	16			

There are 82 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	46	GLY	-	expression tag	UNP P20789
A	47	PRO	-	expression tag	UNP P20789
A	48	GLY	-	expression tag	UNP P20789
A	49	SER	-	expression tag	UNP P20789
A	391	THR	-	expression tag	UNP P20789
A	392	ARG	-	expression tag	UNP P20789
A	393	GLU	-	expression tag	UNP P20789
A	394	LEU	-	expression tag	UNP P20789
A	395	GLU	-	expression tag	UNP P20789
A	396	VAL	-	expression tag	UNP P20789
A	397	LEU	-	expression tag	UNP P20789
A	398	PHE	-	expression tag	UNP P20789
A	399	GLN	-	expression tag	UNP P20789
A	86	LEU	ALA	engineered mutation	UNP P20789
A	103	ASP	HIS	engineered mutation	UNP P20789
A	105	TYR	HIS	engineered mutation	UNP P20789
A	161	VAL	ALA	engineered mutation	UNP P20789
A	167	LEU	ARG	engineered mutation	UNP P20789
A	213	LEU	ARG	engineered mutation	UNP P20789
A	234	LEU	VAL	engineered mutation	UNP P20789
A	253	ALA	ILE	engineered mutation	UNP P20789
A	?	-	VAL	deletion	UNP P20789
A	?	-	GLY	deletion	UNP P20789
A	?	-	THR	deletion	UNP P20789
A	?	-	HIS	deletion	UNP P20789

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Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	ASN	deletion	UNP P20789
A	?	-	GLY	deletion	UNP P20789
A	?	-	LEU	deletion	UNP P20789
A	?	-	GLU	deletion	UNP P20789
A	?	-	HIS	deletion	UNP P20789
A	?	-	SER	deletion	UNP P20789
A	?	-	THR	deletion	UNP P20789
A	?	-	PHE	deletion	UNP P20789
A	?	-	ASN	deletion	UNP P20789
A	?	-	MET	deletion	UNP P20789
A	?	-	THR	deletion	UNP P20789
A	?	-	ILE	deletion	UNP P20789
A	?	-	THR	deletion	UNP P20789
A	305	ARG	HIS	engineered mutation	UNP P20789
A	358	VAL	PHE	engineered mutation	UNP P20789
A	362	ALA	SER	engineered mutation	UNP P20789
B	46	GLY	-	expression tag	UNP P20789
B	47	PRO	-	expression tag	UNP P20789
B	48	GLY	-	expression tag	UNP P20789
B	49	SER	-	expression tag	UNP P20789
B	391	THR	-	expression tag	UNP P20789
B	392	ARG	-	expression tag	UNP P20789
B	393	GLU	-	expression tag	UNP P20789
B	394	LEU	-	expression tag	UNP P20789
B	395	GLU	-	expression tag	UNP P20789
B	396	VAL	-	expression tag	UNP P20789
B	397	LEU	-	expression tag	UNP P20789
B	398	PHE	-	expression tag	UNP P20789
B	399	GLN	-	expression tag	UNP P20789
B	86	LEU	ALA	engineered mutation	UNP P20789
B	103	ASP	HIS	engineered mutation	UNP P20789
B	105	TYR	HIS	engineered mutation	UNP P20789
B	161	VAL	ALA	engineered mutation	UNP P20789
B	167	LEU	ARG	engineered mutation	UNP P20789
B	213	LEU	ARG	engineered mutation	UNP P20789
B	234	LEU	VAL	engineered mutation	UNP P20789
B	253	ALA	ILE	engineered mutation	UNP P20789
B	?	-	VAL	deletion	UNP P20789
B	?	-	GLY	deletion	UNP P20789
B	?	-	THR	deletion	UNP P20789
B	?	-	HIS	deletion	UNP P20789
B	?	-	ASN	deletion	UNP P20789

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Chain	Residue	Modelled	Actual	Comment	Reference
B	?	-	GLY	deletion	UNP P20789
B	?	-	LEU	deletion	UNP P20789
B	?	-	GLU	deletion	UNP P20789
B	?	-	HIS	deletion	UNP P20789
B	?	-	SER	deletion	UNP P20789
B	?	-	THR	deletion	UNP P20789
B	?	-	PHE	deletion	UNP P20789
B	?	-	ASN	deletion	UNP P20789
B	?	-	MET	deletion	UNP P20789
B	?	-	THR	deletion	UNP P20789
B	?	-	ILE	deletion	UNP P20789
B	?	-	THR	deletion	UNP P20789
B	305	ARG	HIS	engineered mutation	UNP P20789
B	358	VAL	PHE	engineered mutation	UNP P20789
B	362	ALA	SER	engineered mutation	UNP P20789

- Molecule 2 is a protein called NEUROTENSIN.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	7	Total	C	N	O	0	0	0
			62	40	13	9			
2	D	8	Total	C	N	O	0	0	0
			66	42	14	10			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	6	GLY	-	expression tag	UNP P20068
C	7	GLY	-	expression tag	UNP P20068
D	6	GLY	-	expression tag	UNP P20068
D	7	GLY	-	expression tag	UNP P20068

- Molecule 3 is GLYCINE (CCD ID: GLY) (formula: C₂H₅NO₂).

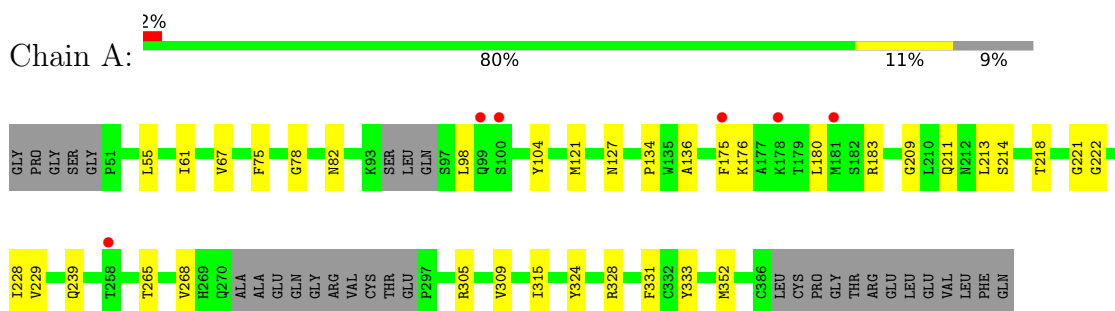


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			5	2	1	2		
3	A	1	Total	C	N	O	0	0
			5	2	1	2		
3	A	1	Total	C	N	O	0	0
			5	2	1	2		
3	A	1	Total	C	N	O	0	0
			5	2	1	2		
3	A	1	Total	C	N	O	0	0
			5	2	1	2		

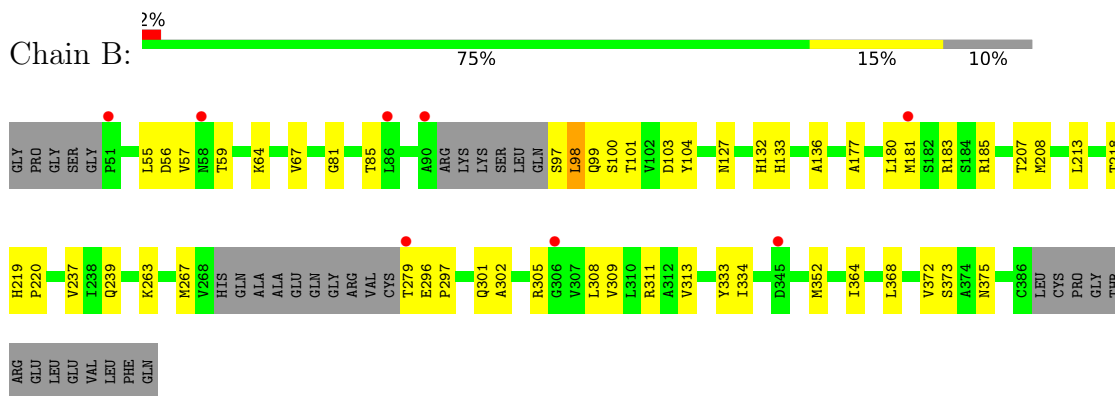
3 Residue-property plots

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.

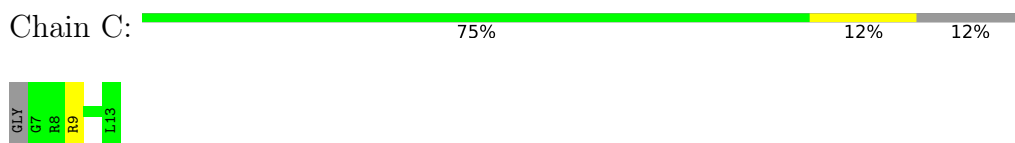
• Molecule 1: NEUROTENSIN RECEPTOR 1 TM86V



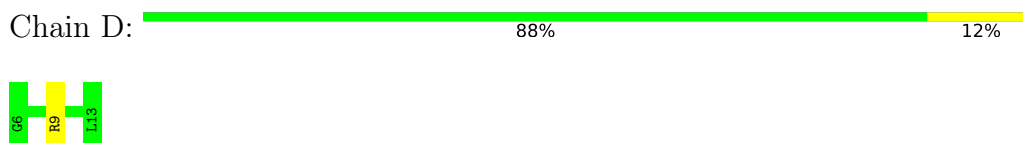
• Molecule 1: NEUROTENSIN RECEPTOR 1 TM86V



• Molecule 2: NEUROTENSIN



• Molecule 2: NEUROTENSIN



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	58.55Å 90.18Å 209.36Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.93 – 3.00 19.93 – 3.00	Depositor EDS
% Data completeness (in resolution range)	98.9 (19.93-3.00) 98.6 (19.93-3.00)	Depositor EDS
R_{merge}	0.01	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.09 (at 3.01Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, R_{free}	0.242 , 0.279 0.270 , 0.294	Depositor DCC
R_{free} test set	1149 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	116.2	Xtriage
Anisotropy	0.289	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.27 , 74.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	4956	wwPDB-VP
Average B, all atoms (Å ²)	125.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.73% 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 [i](#)

5.1 Standard geometry [i](#)

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	0.30	0/2472	0.73	0/3373
1	B	0.33	0/2449	0.75	0/3346
2	C	0.23	0/63	0.75	0/82
2	D	0.23	0/67	0.71	0/87
All	All	0.31	0/5051	0.74	0/6888

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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	2413	0	2478	19	0
1	B	2390	0	2447	35	0
2	C	62	0	66	1	0
2	D	66	0	69	1	0
3	A	25	0	10	0	0
All	All	4956	0	5070	54	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 5.

All (54) 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:97:SER:N	1:B:100:SER:HG	1.57	1.00
1:A:127:ASN:HD21	1:A:136:ALA:H	1.23	0.86
1:A:239:GLN:NE2	1:A:333:TYR:OH	2.19	0.75
1:B:127:ASN:HD21	1:B:136:ALA:H	1.34	0.74
1:B:309:VAL:HG22	1:B:372:VAL:HG11	1.68	0.73
1:B:334:ILE:O	2:D:9:ARG:NH2	2.21	0.73
1:B:239:GLN:NE2	1:B:333:TYR:OH	2.24	0.70
1:B:97:SER:N	1:B:100:SER:OG	2.30	0.64
1:A:61:ILE:H	1:A:61:ILE:HD12	1.64	0.63
1:B:55:LEU:HD21	1:B:213:LEU:HB2	1.81	0.61
1:B:104:TYR:HE2	1:B:183:ARG:HE	1.49	0.60
1:B:305:ARG:O	1:B:309:VAL:HG23	2.01	0.60
1:B:97:SER:O	1:B:101:THR:HG23	2.02	0.60
1:B:56:ASP:OD1	1:B:133:HIS:NE2	2.30	0.58
1:B:305:ARG:NH2	1:B:375:ASN:HD22	2.06	0.54
1:B:100:SER:O	1:B:103:ASP:HB2	2.08	0.52
1:A:209:GLY:HA3	1:A:228:ILE:HD13	1.92	0.52
1:A:331:PHE:O	2:C:9:ARG:NH2	2.43	0.51
1:A:104:TYR:HE2	1:A:183:ARG:HD2	1.74	0.51
1:A:211:GLN:HG3	1:A:228:ILE:HG22	1.92	0.51
1:A:127:ASN:ND2	1:A:136:ALA:H	2.01	0.50
1:B:81:GLY:O	1:B:85:THR:OG1	2.25	0.50
1:B:302:ALA:HA	1:B:305:ARG:HD2	1.95	0.49
1:A:176:LYS:O	1:A:180:LEU:HG	2.13	0.48
1:A:134:PRO:HG3	1:A:221:GLY:HA2	1.95	0.48
1:A:265:THR:O	1:A:268:VAL:HG12	2.14	0.47
1:B:296:GLU:HB2	1:B:297:PRO:HD3	1.95	0.47
1:A:78:GLY:O	1:A:82:ASN:ND2	2.42	0.47
1:B:57:VAL:HB	1:B:132:HIS:CD2	2.50	0.47
1:B:97:SER:OG	1:B:98:LEU:N	2.46	0.47
1:B:308:LEU:HD13	1:B:311:ARG:HE	1.81	0.46
1:A:175:PHE:CE2	1:A:176:LYS:HG3	2.52	0.45
1:B:219:HIS:HA	1:B:220:PRO:HD3	1.86	0.44
1:A:214:SER:HB3	1:A:222:GLY:HA3	1.99	0.44
1:A:75:PHE:HB2	1:A:121:MET:SD	2.57	0.44
1:B:207:THR:HG22	1:B:208:MET:HE2	2.00	0.43
1:B:301:GLN:O	1:B:305:ARG:HG3	2.19	0.43
1:B:181:MET:HA	1:B:185:ARG:NH2	2.34	0.43
1:B:67:VAL:HG21	1:B:352:MET:HB3	2.01	0.42
1:B:98:LEU:C	1:B:98:LEU:HD13	2.45	0.42
1:B:309:VAL:O	1:B:313:VAL:HG23	2.18	0.42
1:A:55:LEU:HD11	1:A:213:LEU:O	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:372:VAL:HG13	1:B:373:SER:H	1.83	0.42
1:B:207:THR:HG21	1:B:237:VAL:HG21	2.00	0.42
1:B:263:LYS:O	1:B:267:MET:HG2	2.20	0.42
1:A:324:TYR:CZ	1:A:328:ARG:HD2	2.55	0.41
1:A:305:ARG:O	1:A:309:VAL:HG23	2.20	0.41
1:B:364:ILE:HG13	1:B:368:LEU:HG	2.02	0.41
1:B:98:LEU:HD13	1:B:99:GLN:N	2.36	0.41
1:A:67:VAL:HG21	1:A:352:MET:HB3	2.03	0.40
1:B:177:ALA:O	1:B:180:LEU:HB2	2.20	0.40
1:B:59:THR:O	1:B:64:LYS:HE2	2.21	0.40
1:B:97:SER:O	1:B:101:THR:N	2.46	0.40
1:B:368:LEU:O	1:B:372:VAL:HG12	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	301/338 (89%)	297 (99%)	4 (1%)	0	100	100
1	B	298/338 (88%)	292 (98%)	6 (2%)	0	100	100
2	C	5/8 (62%)	5 (100%)	0	0	100	100
2	D	6/8 (75%)	6 (100%)	0	0	100	100
All	All	610/692 (88%)	600 (98%)	10 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	265/291 (91%)	261 (98%)	4 (2%)	57	80
1	B	264/291 (91%)	261 (99%)	3 (1%)	65	83
2	C	6/6 (100%)	6 (100%)	0	100	100
2	D	6/6 (100%)	6 (100%)	0	100	100
All	All	541/594 (91%)	534 (99%)	7 (1%)	61	81

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	98	LEU
1	A	218	THR
1	A	229	VAL
1	A	315	ILE
1	B	98	LEU
1	B	218	THR
1	B	279	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	58	ASN
1	A	99	GLN
1	A	127	ASN
1	A	173	HIS
1	A	211	GLN
1	A	239	GLN
1	A	257	ASN
1	B	127	ASN
1	B	211	GLN
1	B	239	GLN
1	B	257	ASN
1	B	370	ASN
1	B	375	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 ⓘ

5 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
3	GLY	A	1388	-	4,4,4	1.15	1 (25%)	3,4,4	1.64	1 (33%)
3	GLY	A	1391	-	4,4,4	1.15	1 (25%)	3,4,4	1.67	1 (33%)
3	GLY	A	1389	-	4,4,4	1.16	1 (25%)	3,4,4	1.64	1 (33%)
3	GLY	A	1390	-	4,4,4	1.14	1 (25%)	3,4,4	1.65	1 (33%)
3	GLY	A	1387	-	4,4,4	1.14	1 (25%)	3,4,4	1.64	1 (33%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	GLY	A	1388	-	-	0/2/2/2	-
3	GLY	A	1391	-	-	0/2/2/2	-
3	GLY	A	1389	-	-	0/2/2/2	-
3	GLY	A	1390	-	-	0/2/2/2	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	GLY	A	1387	-	-	0/2/2/2	-

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1389	GLY	OXT-C	-2.20	1.23	1.30
3	A	1391	GLY	OXT-C	-2.20	1.23	1.30
3	A	1388	GLY	OXT-C	-2.19	1.23	1.30
3	A	1390	GLY	OXT-C	-2.18	1.23	1.30
3	A	1387	GLY	OXT-C	-2.17	1.23	1.30

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1391	GLY	OXT-C-O	-2.11	117.90	123.33
3	A	1390	GLY	OXT-C-O	-2.09	117.95	123.33
3	A	1388	GLY	OXT-C-O	-2.08	117.98	123.33
3	A	1387	GLY	OXT-C-O	-2.07	118.01	123.33
3	A	1389	GLY	OXT-C-O	-2.07	118.02	123.33

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 [i](#)

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	307/338 (90%)	-0.06	6 (1%) 65 41	73, 110, 203, 284	0
1	B	304/338 (89%)	-0.02	8 (2%) 57 34	70, 115, 207, 278	0
2	C	7/8 (87%)	0.23	0 100 100	89, 105, 144, 166	0
2	D	8/8 (100%)	0.53	0 100 100	86, 108, 148, 165	0
All	All	626/692 (90%)	-0.03	14 (2%) 62 39	70, 113, 206, 284	0

All (14) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	181	MET	3.5
1	A	181	MET	2.9
1	A	100	SER	2.8
1	B	86	LEU	2.8
1	A	99	GLN	2.6
1	B	58	ASN	2.6
1	B	345	ASP	2.4
1	A	258	THR	2.3
1	B	279	THR	2.1
1	A	175	PHE	2.1
1	A	178	LYS	2.1
1	B	51	PRO	2.1
1	B	90	ALA	2.1
1	B	306	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 [i](#)

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	GLY	A	1387	5/5	0.40	0.11	120,125,132,139	0
3	GLY	A	1388	5/5	0.46	0.13	139,139,139,215	0
3	GLY	A	1391	5/5	0.77	0.14	118,146,146,146	0
3	GLY	A	1389	5/5	0.78	0.12	129,130,130,130	0
3	GLY	A	1390	5/5	0.83	0.10	121,121,131,138	0

6.5 Other polymers [i](#)

There are no such residues in this entry.