



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 13, 2017 – 10:00 pm GMT

PDB ID : 4BV0
Title : High Resolution Structure of Evolved Agonist-bound Neurotensin Receptor 1
Mutant without Lysozyme Fusion
Authors : Egloff, P.; Hillenbrand, M.; Scott, D.J.; Schlinkmann, K.M.; Heine, P.; Balada,
S.; Batyuk, A.; Mittl, P.; Schuetz, M.; Plueckthun, A.
Deposited on : 2013-06-24
Resolution : 3.10 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

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.9-1692
EDS	:	trunk28620
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	recalc28949

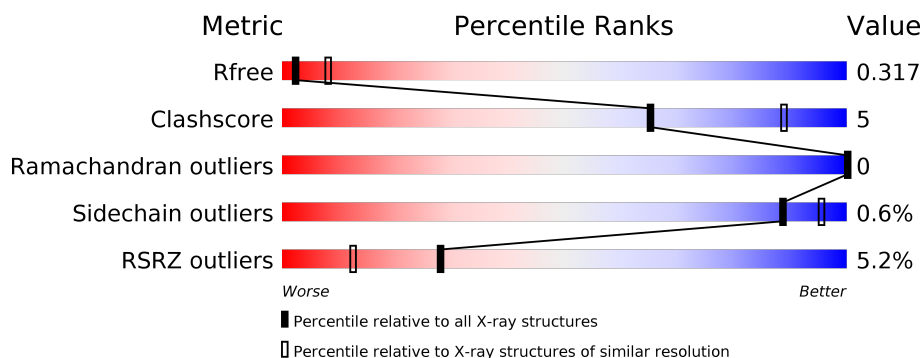
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.10 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}	100719	1001 (3.12-3.08)
Clashscore	112137	1099 (3.12-3.08)
Ramachandran outliers	110173	1057 (3.12-3.08)
Sidechain outliers	110143	1057 (3.12-3.08)
RSRZ outliers	101464	1006 (3.12-3.08)

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. 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	<div> <div>4%</div> <div> <div></div> <div>78%</div> <div>9%</div> <div>12%</div> </div> </div>
1	B	338	<div> <div>5%</div> <div> <div></div> <div>78%</div> <div>11%</div> <div>11%</div> </div> </div>
2	C	10	<div> <div></div> <div> <div>50%</div> <div>20%</div> <div>30%</div> </div> </div>
2	D	10	<div> <div></div> <div> <div>40%</div> <div>30%</div> <div>30%</div> </div> </div>

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 4865 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 TYPE 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	297	Total	C	N	O	S	0	0	0
			2348	1555	384	396	13			
1	B	302	Total	C	N	O	S	0	0	0
			2393	1585	391	403	14			

There are 116 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	83	GLY	SER	ENGINEERED MUTATION	UNP P20789
A	86	LEU	ALA	ENGINEERED MUTATION	UNP P20789
A	101	ARG	THR	ENGINEERED MUTATION	UNP P20789
A	103	ASP	HIS	ENGINEERED MUTATION	UNP P20789
A	105	TYR	HIS	ENGINEERED MUTATION	UNP P20789
A	119	PHE	LEU	ENGINEERED MUTATION	UNP P20789
A	121	LEU	MET	ENGINEERED MUTATION	UNP P20789
A	124	ASP	GLU	ENGINEERED MUTATION	UNP P20789
A	125	VAL	LEU	ENGINEERED MUTATION	UNP P20789
A	143	LYS	ARG	ENGINEERED MUTATION	UNP P20789
A	150	GLU	ASP	ENGINEERED MUTATION	UNP P20789
A	161	VAL	ALA	ENGINEERED MUTATION	UNP P20789
A	167	LEU	ARG	ENGINEERED MUTATION	UNP P20789
A	172	ARG	CYS	ENGINEERED MUTATION	UNP P20789
A	177	HIS	ALA	ENGINEERED MUTATION	UNP P20789
A	208	VAL	MET	ENGINEERED MUTATION	UNP P20789
A	213	LEU	ARG	ENGINEERED MUTATION	UNP P20789
A	234	LEU	VAL	ENGINEERED MUTATION	UNP P20789
A	240	LEU	VAL	ENGINEERED MUTATION	UNP P20789
A	253	ALA	ILE	ENGINEERED MUTATION	UNP P20789
A	262	ARG	ASN	ENGINEERED MUTATION	UNP P20789

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Chain	Residue	Modelled	Actual	Comment	Reference
A	263	ARG	LYS	ENGINEERED MUTATION	UNP P20789
A	.	-	VAL	DELETION	UNP P20789
A	.	-	GLY	DELETION	UNP P20789
A	.	-	THR	DELETION	UNP P20789
A	.	-	HIS	DELETION	UNP P20789
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	305	ARG	HIS	ENGINEERED MUTATION	UNP P20789
A	313	MET	VAL	ENGINEERED MUTATION	UNP P20789
A	332	VAL	CYS	ENGINEERED MUTATION	UNP P20789
A	342	ALA	PHE	ENGINEERED MUTATION	UNP P20789
A	354	SER	THR	ENGINEERED MUTATION	UNP P20789
A	358	VAL	PHE	ENGINEERED MUTATION	UNP P20789
A	362	ALA	SER	ENGINEERED MUTATION	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
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	83	GLY	SER	ENGINEERED MUTATION	UNP P20789
B	86	LEU	ALA	ENGINEERED MUTATION	UNP P20789
B	101	ARG	THR	ENGINEERED MUTATION	UNP P20789
B	103	ASP	HIS	ENGINEERED MUTATION	UNP P20789
B	105	TYR	HIS	ENGINEERED MUTATION	UNP P20789

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Chain	Residue	Modelled	Actual	Comment	Reference
B	119	PHE	LEU	ENGINEERED MUTATION	UNP P20789
B	121	LEU	MET	ENGINEERED MUTATION	UNP P20789
B	124	ASP	GLU	ENGINEERED MUTATION	UNP P20789
B	125	VAL	LEU	ENGINEERED MUTATION	UNP P20789
B	143	LYS	ARG	ENGINEERED MUTATION	UNP P20789
B	150	GLU	ASP	ENGINEERED MUTATION	UNP P20789
B	161	VAL	ALA	ENGINEERED MUTATION	UNP P20789
B	167	LEU	ARG	ENGINEERED MUTATION	UNP P20789
B	172	ARG	CYS	ENGINEERED MUTATION	UNP P20789
B	177	HIS	ALA	ENGINEERED MUTATION	UNP P20789
B	208	VAL	MET	ENGINEERED MUTATION	UNP P20789
B	213	LEU	ARG	ENGINEERED MUTATION	UNP P20789
B	234	LEU	VAL	ENGINEERED MUTATION	UNP P20789
B	240	LEU	VAL	ENGINEERED MUTATION	UNP P20789
B	253	ALA	ILE	ENGINEERED MUTATION	UNP P20789
B	262	ARG	ASN	ENGINEERED MUTATION	UNP P20789
B	263	ARG	LYS	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
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	305	ARG	HIS	ENGINEERED MUTATION	UNP P20789
B	313	MET	VAL	ENGINEERED MUTATION	UNP P20789
B	332	VAL	CYS	ENGINEERED MUTATION	UNP P20789
B	342	ALA	PHE	ENGINEERED MUTATION	UNP P20789
B	354	SER	THR	ENGINEERED MUTATION	UNP P20789
B	358	VAL	PHE	ENGINEERED MUTATION	UNP P20789
B	362	ALA	SER	ENGINEERED MUTATION	UNP P20789
B	391	THR	-	EXPRESSION TAG	UNP P20789
B	392	ARG	-	EXPRESSION TAG	UNP P20789

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Chain	Residue	Modelled	Actual	Comment	Reference
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

- Molecule 2 is a protein called NEUROTENSIN/NEUROMEDIN N.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	7	Total	C	N	O	0	0	0
			62	40	13	9			
2	D	7	Total	C	N	O	0	0	0
			62	40	13	9			

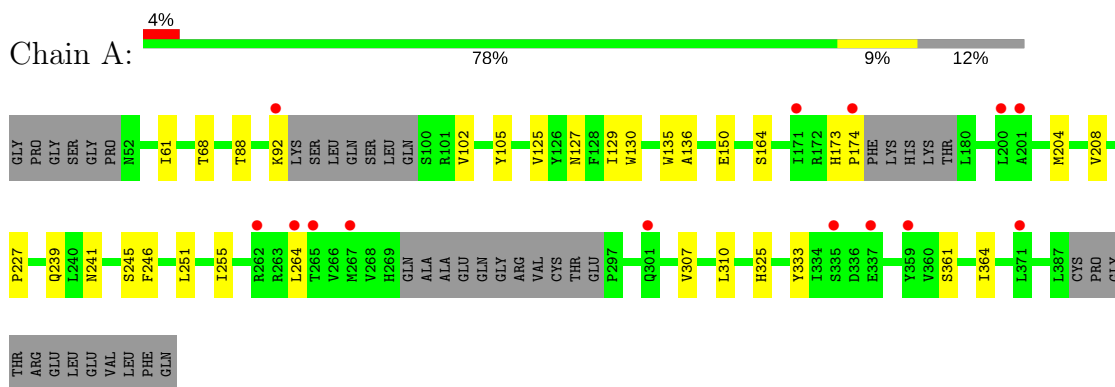
There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	4	GLY	-	EXPRESSION TAG	UNP P20068
C	5	PRO	-	EXPRESSION TAG	UNP P20068
C	6	GLY	-	EXPRESSION TAG	UNP P20068
C	7	GLY	-	EXPRESSION TAG	UNP P20068
D	4	GLY	-	EXPRESSION TAG	UNP P20068
D	5	PRO	-	EXPRESSION TAG	UNP P20068
D	6	GLY	-	EXPRESSION TAG	UNP P20068
D	7	GLY	-	EXPRESSION TAG	UNP P20068

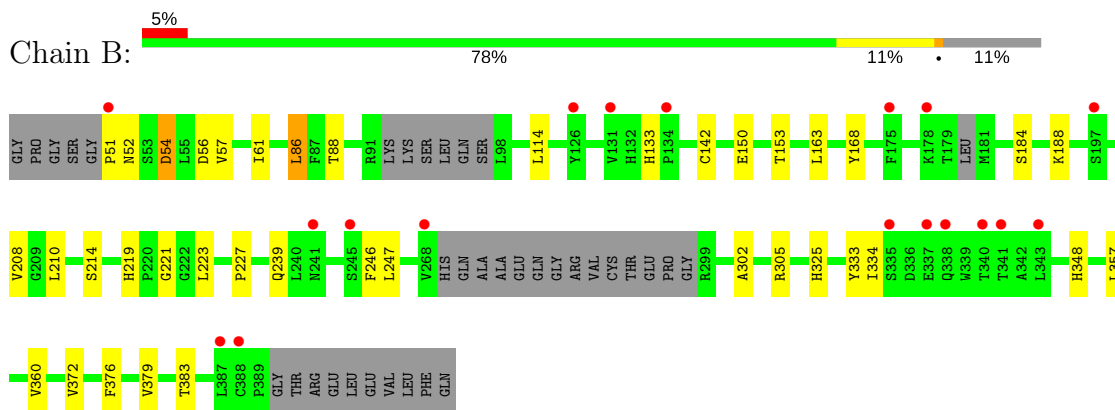
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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 TYPE 1



• Molecule 1: NEUROTENSIN RECEPTOR TYPE 1



• Molecule 2: NEUROTENSIN/NEUROMEDIN N



• Molecule 2: NEUROTENSIN/NEUROMEDIN N



GLY	PRO	GLY	GLY	R8	R9	L13

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	60.58Å 91.56Å 208.58Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.88 – 3.10 49.10 – 3.10	Depositor EDS
% Data completeness (in resolution range)	95.2 (19.88-3.10) 95.3 (49.10-3.10)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.05 (at 3.12Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, R_{free}	0.284 , 0.310 0.286 , 0.317	Depositor DCC
R_{free} test set	1040 reflections (5.01%)	DCC
Wilson B-factor (Å ²)	113.7	Xtriage
Anisotropy	0.229	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.26 , 42.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.86	EDS
Total number of atoms	4865	wwPDB-VP
Average B, all atoms (Å ²)	82.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.31% 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	0.22	0/2405	0.36	0/3281
1	B	0.23	0/2452	0.38	0/3345
2	C	0.17	0/63	0.38	0/82
2	D	0.17	0/63	0.38	0/82
All	All	0.22	0/4983	0.37	0/6790

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	2348	0	2416	19	0
1	B	2393	0	2462	27	0
2	C	62	0	66	1	0
2	D	62	0	66	3	0
All	All	4865	0	5010	46	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 (46) 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:150:GLU:HG3	1:A:204:MET:HG3	1.73	0.70
1:B:54:ASP:O	2:D:8:ARG:NH2	2.30	0.64
1:A:208:VAL:HA	1:A:227:PRO:HA	1.84	0.60
1:B:239:GLN:OE1	1:B:333:TYR:OH	2.20	0.60
1:A:102:VAL:HA	1:A:105:TYR:HD2	1.69	0.58
1:B:246:PHE:HD2	1:B:247:LEU:HD12	1.68	0.58
1:B:334:ILE:O	2:D:9:ARG:NH2	2.36	0.57
1:A:127:ASN:HD21	1:A:136:ALA:H	1.55	0.54
1:A:239:GLN:OE1	1:A:333:TYR:OH	2.24	0.54
1:B:56:ASP:HB3	1:B:133:HIS:HE1	1.72	0.54
1:B:184:SER:OG	1:B:188:LYS:NZ	2.40	0.54
1:A:241:ASN:O	1:A:245:SER:OG	2.27	0.53
1:A:125:VAL:HG23	1:A:129:ILE:HD11	1.92	0.51
1:A:68:THR:OG1	1:A:130:TRP:NE1	2.45	0.49
1:B:51:PRO:HD3	1:B:214:SER:HA	1.94	0.49
1:B:227:PRO:HD3	2:D:13:LEU:HD22	1.95	0.49
1:B:305:ARG:HB2	1:B:372:VAL:HG12	1.93	0.48
1:B:208:VAL:HA	1:B:227:PRO:HA	1.95	0.48
1:A:264:LEU:HD22	1:A:307:VAL:HG21	1.96	0.48
1:A:88:THR:O	1:A:92:LYS:HG2	2.14	0.47
1:B:376:PHE:HA	1:B:379:VAL:HG22	1.97	0.47
1:B:150:GLU:HA	1:B:153:THR:HG22	1.96	0.47
1:B:246:PHE:HB2	1:B:325:HIS:CE1	2.51	0.46
1:B:51:PRO:HG3	1:B:219:HIS:HB3	1.97	0.46
1:B:54:ASP:OD1	1:B:54:ASP:N	2.49	0.46
1:A:255:ILE:HD12	1:B:168:TYR:CE1	2.51	0.46
1:B:88:THR:HG22	1:B:383:THR:HG21	1.98	0.45
1:B:210:LEU:HB3	1:B:223:LEU:HD11	1.98	0.45
1:A:251:LEU:O	1:A:255:ILE:HG12	2.16	0.45
1:B:219:HIS:CD2	1:B:221:GLY:H	2.33	0.45
1:A:246:PHE:HB2	1:A:325:HIS:CE1	2.51	0.45
1:A:127:ASN:HD21	1:A:135:TRP:HA	1.82	0.45
1:B:51:PRO:HB2	1:B:52:ASN:H	1.57	0.44
1:B:61:ILE:H	1:B:61:ILE:HD12	1.82	0.44
1:B:302:ALA:O	1:B:305:ARG:HG2	2.18	0.44
1:B:57:VAL:HG11	1:B:348:HIS:CD2	2.52	0.44
1:A:164:SER:HA	1:A:310:LEU:HD21	2.00	0.43
1:A:61:ILE:HD12	1:A:61:ILE:H	1.84	0.42
1:B:86:LEU:HD23	1:B:114:LEU:HD12	2.00	0.42
1:B:163:LEU:HD23	1:B:163:LEU:HA	1.94	0.42
1:B:86:LEU:HD13	1:B:86:LEU:HA	1.87	0.42
1:A:127:ASN:ND2	1:A:136:ALA:H	2.17	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:173:HIS:N	1:A:174:PRO:HD3	2.35	0.41
1:B:357:LEU:HA	1:B:360:VAL:HB	2.03	0.41
2:C:9:ARG:HA	2:C:10:PRO:HD3	1.98	0.40
1:A:361:SER:O	1:A:364:ILE:HG22	2.21	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	289/338 (86%)	278 (96%)	11 (4%)	0	100	100
1	B	294/338 (87%)	286 (97%)	8 (3%)	0	100	100
2	C	5/10 (50%)	5 (100%)	0	0	100	100
2	D	5/10 (50%)	5 (100%)	0	0	100	100
All	All	593/696 (85%)	574 (97%)	19 (3%)	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	256/290 (88%)	256 (100%)	0	100	100
1	B	262/290 (90%)	259 (99%)	3 (1%)	78	92

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	C	6/7 (86%)	6 (100%)	0	100	100
2	D	6/7 (86%)	6 (100%)	0	100	100
All	All	530/594 (89%)	527 (99%)	3 (1%)	89	95

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	54	ASP
1	B	86	LEU
1	B	142	CYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	127	ASN
1	A	325	HIS
1	B	219	HIS
1	B	325	HIS

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 carbohydrates in this entry.

5.6 Ligand geometry ⓘ

There are no ligands in this entry.

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

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	297/338 (87%)	0.15	14 (4%)	32 14	24, 67, 153, 199	0
1	B	302/338 (89%)	0.22	18 (5%)	23 9	25, 77, 152, 256	0
2	C	7/10 (70%)	-0.20	0	100 100	53, 55, 105, 131	0
2	D	7/10 (70%)	0.49	0	100 100	58, 66, 100, 116	0
All	All	613/696 (88%)	0.18	32 (5%)	28 12	24, 73, 153, 256	0

All (32) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	340	THR	4.8
1	B	387	LEU	4.7
1	B	343	LEU	4.2
1	B	268	VAL	3.6
1	B	341	THR	3.3
1	A	265	THR	3.2
1	B	338	GLN	3.2
1	B	245	SER	3.2
1	A	359	TYR	3.1
1	B	388	CYS	3.1
1	B	337	GLU	2.9
1	A	171	ILE	2.9
1	A	264	LEU	2.9
1	B	178	LYS	2.9
1	A	335	SER	2.9
1	A	262	ARG	2.8
1	B	131	VAL	2.8
1	B	335	SER	2.6
1	B	126	TYR	2.6
1	A	337	GLU	2.6
1	B	241	ASN	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	267	MET	2.5
1	A	371	LEU	2.5
1	B	51	PRO	2.4
1	A	92	LYS	2.4
1	A	301	GLN	2.3
1	B	197	SER	2.3
1	A	200	LEU	2.2
1	B	175	PHE	2.2
1	A	201	ALA	2.2
1	A	174	PRO	2.1
1	B	134	PRO	2.1

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 carbohydrates 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.