



wwPDB X-ray Structure Validation Summary Report ⓘ

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PDB ID : 6Z4V / pdb_00006z4v
Title : Crystal structure of the neurotensin receptor 1 (NTSR1-H4bmx) in complex with NTS8-13
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Deposited on : 2020-05-25
Resolution : 2.60 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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

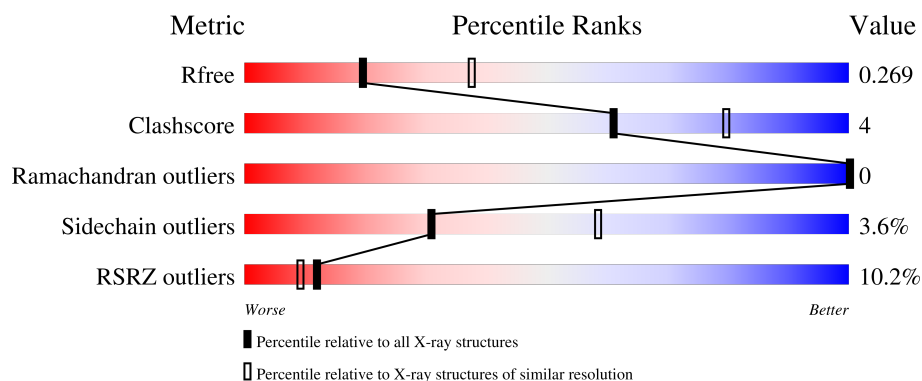
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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	4008 (2.60-2.60)
Clashscore	190562	4347 (2.60-2.60)
Ramachandran outliers	187476	4277 (2.60-2.60)
Sidechain outliers	187428	4277 (2.60-2.60)
RSRZ outliers	180081	4008 (2.60-2.60)

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	AAA	482	10% 83% 11% 5%
2	BBB	6	83% 17%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 6855 atoms, of which 3422 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,Neurotensin receptor type 1,DARPin.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	S			
1	AAA	456	6757	2214	3371	552	608	12	182	0	0

There are 53 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AAA	46	GLY	-	expression tag	UNP P20789
AAA	47	PRO	-	expression tag	UNP P20789
AAA	48	GLY	-	expression tag	UNP P20789
AAA	49	SER	-	expression tag	UNP P20789
AAA	83	GLY	SER	engineered mutation	UNP P20789
AAA	86	LEU	ALA	engineered mutation	UNP P20789
AAA	101	ARG	THR	engineered mutation	UNP P20789
AAA	103	ASP	HIS	engineered mutation	UNP P20789
AAA	105	TYR	HIS	engineered mutation	UNP P20789
AAA	119	PHE	LEU	engineered mutation	UNP P20789
AAA	121	LEU	MET	engineered mutation	UNP P20789
AAA	143	LYS	ARG	engineered mutation	UNP P20789
AAA	161	VAL	ALA	engineered mutation	UNP P20789
AAA	167	LEU	ARG	engineered mutation	UNP P20789
AAA	213	LEU	ARG	engineered mutation	UNP P20789
AAA	234	LEU	VAL	engineered mutation	UNP P20789
AAA	235	ARG	LYS	engineered mutation	UNP P20789
AAA	240	LEU	VAL	engineered mutation	UNP P20789
AAA	253	ALA	ILE	engineered mutation	UNP P20789
AAA	260	ALA	ILE	engineered mutation	UNP P20789
AAA	262	ARG	ASN	engineered mutation	UNP P20789
AAA	263	ARG	LYS	engineered mutation	UNP P20789
AAA	?	-	GLU	deletion	UNP P20789
AAA	?	-	GLN	deletion	UNP P20789
AAA	?	-	GLY	deletion	UNP P20789
AAA	?	-	ARG	deletion	UNP P20789
AAA	?	-	VAL	deletion	UNP P20789

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Chain	Residue	Modelled	Actual	Comment	Reference
AAA	?	-	CYS	deletion	UNP P20789
AAA	?	-	THR	deletion	UNP P20789
AAA	?	-	VAL	deletion	UNP P20789
AAA	?	-	GLY	deletion	UNP P20789
AAA	?	-	THR	deletion	UNP P20789
AAA	?	-	HIS	deletion	UNP P20789
AAA	?	-	ASN	deletion	UNP P20789
AAA	?	-	GLY	deletion	UNP P20789
AAA	?	-	LEU	deletion	UNP P20789
AAA	?	-	GLU	deletion	UNP P20789
AAA	?	-	HIS	deletion	UNP P20789
AAA	?	-	SER	deletion	UNP P20789
AAA	?	-	THR	deletion	UNP P20789
AAA	305	ARG	HIS	engineered mutation	UNP P20789
AAA	332	VAL	CYS	engineered mutation	UNP P20789
AAA	342	ALA	PHE	engineered mutation	UNP P20789
AAA	354	SER	THR	engineered mutation	UNP P20789
AAA	372	ALA	-	linker	UNP P20789
AAA	373	GLU	-	linker	UNP P20789
AAA	374	ASP	-	linker	UNP P20789
AAA	375	LEU	-	linker	UNP P20789
AAA	376	VAL	-	linker	UNP P20789
AAA	377	GLU	-	linker	UNP P20789
AAA	378	ASP	-	linker	UNP P20789
AAA	379	TRP	-	linker	UNP P20789
AAA	380	GLU	-	linker	UNP P20789

- Molecule 2 is a protein called ARG-PRO-TYR-ILE-LEU.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	BBB	5	Total	C	H	N	O	1	0	0
			98	32	51	8	7			

4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	69.22Å 77.53Å 111.86Å 90.00° 107.22° 90.00°	Depositor
Resolution (Å)	29.25 – 2.60 29.25 – 2.60	Depositor EDS
% Data completeness (in resolution range)	80.5 (29.25-2.60) 80.5 (29.25-2.60)	Depositor EDS
R_{merge}	0.45	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.64 (at 2.61Å)	Xtriage
Refinement program	REFMAC 5.8.0258	Depositor
R, R_{free}	0.256 , 0.272 0.257 , 0.269	Depositor DCC
R_{free} test set	723 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å ²)	35.2	Xtriage
Anisotropy	0.052	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 28.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.019 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.88	EDS
Total number of atoms	6855	wwPDB-VP
Average B, all atoms (Å ²)	37.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.94% 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	AAA	0.99	0/3463	1.60	4/4755 (0.1%)
2	BBB	0.87	0/48	0.97	0/63
All	All	0.99	0/3511	1.59	4/4818 (0.1%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AAA	201	ALA	CA-C-N	6.41	124.28	120.24
1	AAA	201	ALA	C-N-CA	6.41	124.28	120.24
1	AAA	412	GLU	CA-C-N	5.24	127.83	120.28
1	AAA	412	GLU	C-N-CA	5.24	127.83	120.28

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	AAA	3386	3371	3272	28	0
2	BBB	47	51	50	0	0
All	All	3433	3422	3322	28	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 4.

The worst 5 of 28 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:AAA:492:HIS:HB3	1:AAA:495:ILE:HD12	1.87	0.57
1:AAA:213:LEU:HD12	1:AAA:224:VAL:HG21	1.88	0.54
1:AAA:432:VAL:HA	1:AAA:435:LYS:HD2	1.89	0.54
1:AAA:108:SER:HB3	1:AAA:159:ASN:HD21	1.75	0.52
1:AAA:149:ARG:O	1:AAA:153:THR:HG23	2.10	0.52

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	AAA	450/482 (93%)	434 (96%)	16 (4%)	0	100	100
2	BBB	3/6 (50%)	3 (100%)	0	0	100	100
All	All	453/488 (93%)	437 (96%)	16 (4%)	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	AAA	333/398 (84%)	321 (96%)	12 (4%)	31	58
2	BBB	5/6 (83%)	5 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	338/404 (84%)	326 (96%)	12 (4%)	31 58

5 of 12 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	AAA	394	ASP
1	AAA	401	LEU
1	AAA	540	LEU
1	AAA	415	PHE
1	AAA	150	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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](#)

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 [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	AAA	456/482 (94%)	0.81	47 (10%) 12 9	10, 35, 58, 72	0
2	BBB	5/6 (83%)	0.49	0 100 100	32, 36, 44, 57	0
All	All	461/488 (94%)	0.81	47 (10%) 12 9	10, 35, 57, 72	0

The worst 5 of 47 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	AAA	294	THR	5.0
1	AAA	335	SER	4.4
1	AAA	172	CYS	4.3
1	AAA	102	VAL	4.1
1	AAA	369	TYR	3.3

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.