W O R L D W I D E
wwPDB
P R O T E I N   D A T A   B A N K

wwPDB X-ray Structure Validation Summary Report (i)

Sep 17, 2023 – 08:42 PM EDT

PDB ID	:	4XEE
Title	:	Structure of active-like neurotensin receptor
Authors	:	Krumm, B.E.; White, J.F.; Shah, P.; Grisshammer, R.
Deposited on	:	2014-12-23
Resolution	:	2.90 Å(reported)

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

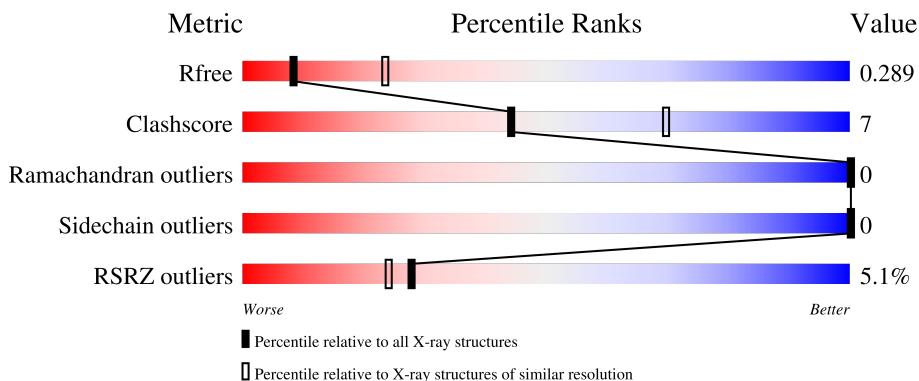|		
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35.1

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 2.90 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	Percentile Ranks	Value
Rfree		0.289
Clashscore		7
Ramachandran outliers		0
Sidechain outliers		0
RSRZ outliers		5.1%

Worse   *Better*

▌ Percentile relative to all X-ray structures
▯ Percentile relative to X-ray structures of similar resolution

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1957 (2.90-2.90)
Clashscore	141614	2172 (2.90-2.90)
Ramachandran outliers	138981	2115 (2.90-2.90)
Sidechain outliers	138945	2117 (2.90-2.90)
RSRZ outliers	127900	1906 (2.90-2.90)

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 <=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	541	4% — 75% / 11% / 14%
2	B	6	83% / 17%

2   Entry composition ⓘ

There are 7 unique types of molecules in this entry. The entry contains 3801 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, Endolysin chimera.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	464	3666	2380	624	643	19	81	0	0

There are 36 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	33	ASP	-	expression tag	UNP P20789
A	34	TYR	-	expression tag	UNP P20789
A	35	LYS	-	expression tag	UNP P20789
A	36	ASP	-	expression tag	UNP P20789
A	37	ASP	-	expression tag	UNP P20789
A	38	ASP	-	expression tag	UNP P20789
A	39	ASP	-	expression tag	UNP P20789
A	40	ALA	-	expression tag	UNP P20789
A	41	THR	-	expression tag	UNP P20789
A	42	SER	-	expression tag	UNP P20789
A	86	LEU	ALA	engineered mutation	UNP P20789
A	215	ALA	GLY	engineered mutation	UNP P20789
A	360	ALA	VAL	engineered mutation	UNP P20789
A	989	ALA	-	linker	UNP P20789
A	990	HIS	-	linker	UNP P20789
A	991	HIS	-	linker	UNP P20789
A	992	HIS	-	linker	UNP P20789
A	993	HIS	-	linker	UNP P20789
A	994	HIS	-	linker	UNP P20789
A	995	HIS	-	linker	UNP P20789
A	996	HIS	-	linker	UNP P20789
A	997	HIS	-	linker	UNP P20789
A	998	HIS	-	linker	UNP P20789
A	999	HIS	-	linker	UNP P20789
A	1000	GLY	-	linker	UNP P20789
A	1001	GLY	-	linker	UNP P20789
A	1012	GLY	ARG	conflict	UNP P00720

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Chain	Residue	Modelled	Actual	Comment	Reference
A	1054	THR	CYS	conflict	UNP P00720
A	1097	ALA	CYS	conflict	UNP P00720
A	1122	ASN	GLN	conflict	UNP P00720
A	1123	ASN	GLN	conflict	UNP P00720
A	1137	ARG	ILE	conflict	UNP P00720
A	1162	GLY	-	expression tag	UNP P00720
A	1163	SER	-	expression tag	UNP P00720
A	1164	GLY	-	expression tag	UNP P00720
A	1165	SER	-	expression tag	UNP P00720

- Molecule 2 is a protein called Neurotensin/neuromedin N.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
2	B	6	58	38	12	8	0	0	0

- Molecule 3 is PENTAETHYLENE GLYCOL (three-letter code: 1PE) (formula: $C_{10}H_{22}O_6$).
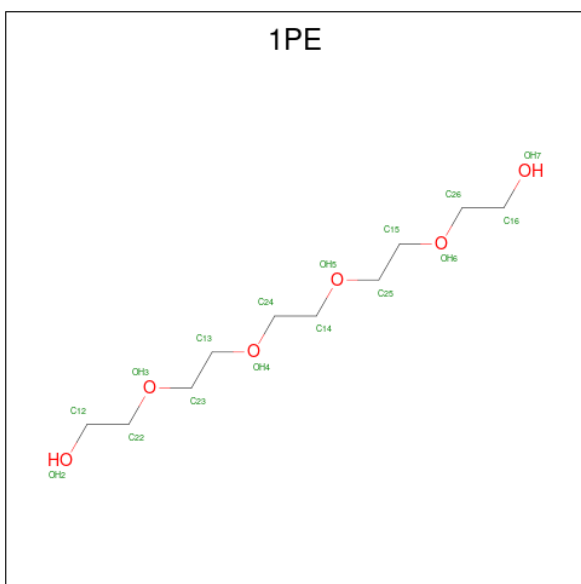
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
3	A	1	16	10	6	0	0
3	A	1	Total	C	O	0	0
			16	10	6		

- Molecule 4 is 4-(2-HYDROXYETHYL)-1-PIPERAZINE ETHANESULFONIC ACID (three-letter code: EPE) (formula: $C_8H_{18}N_2O_4S$).

EPE

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	S	0	0
			15	8	2	4	1		

- Molecule 5 is CITRATE ANION (three-letter code: FLC) (formula: $C_6H_5O_7$).

FLC

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			13	6	7		

- Molecule 6 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: $C_4H_{10}O_3$).

PEG

C4

OH O4

O2

O

C3

C1

HO

C2

O1

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total 7	C 4	O 3	0	0

- Molecule 7 is water.

| Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	10	Total 10	O 10	0	0

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 type 1, Endolysin chimera

Chain A:
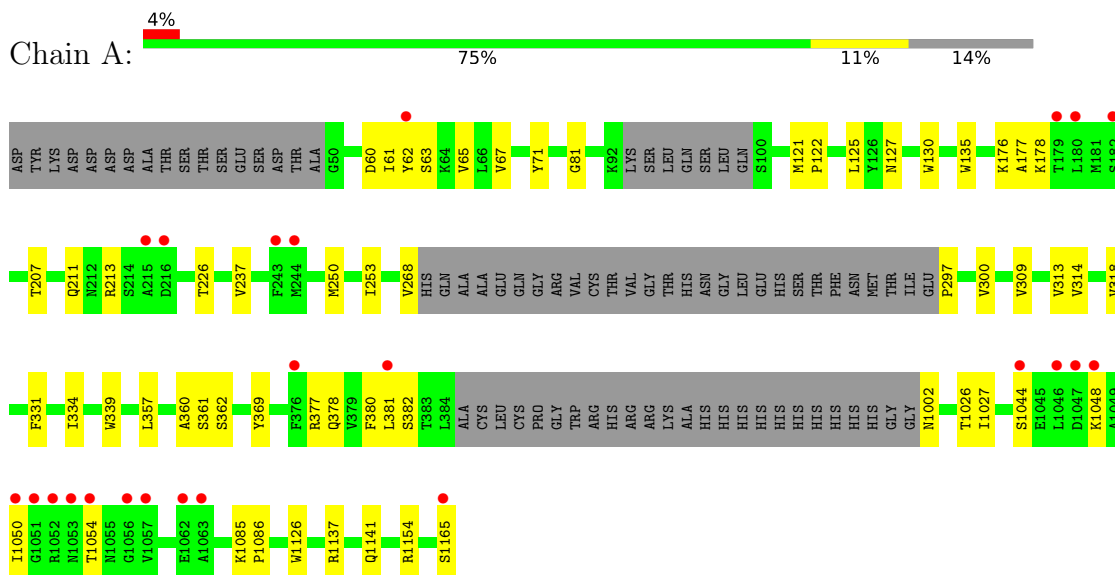
• Molecule 2: Neurotensin/neuromedin N

Chain B:
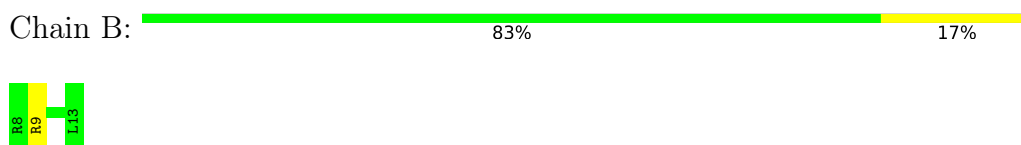
4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 2 21	Depositor
Cell constants a, b, c, α, β, γ	49.07Å 88.11Å 161.29Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	45.00 – 2.90 45.89 – 2.90	Depositor EDS
% Data completeness (in resolution range)	90.2 (45.00-2.90) 90.2 (45.89-2.90)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.68 (at 2.91Å)	Xtriage
Refinement program	REFMAC 5.8.0073	Depositor
R, R_{free}	0.231 , 0.281 0.245 , 0.289	Depositor DCC
R_{free} test set	769 reflections (5.27%)	wwPDB-VP
Wilson B-factor (Å^2)	66.5	Xtriage
Anisotropy	0.359	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.29 , 51.2	EDS
L-test for twinning[2]	$< |L| > = 0.47, < L^2 > = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.88	EDS
Total number of atoms	3801	wwPDB-VP
Average B, all atoms (Å^2)	71.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.50% of the height of the origin peak. No significant pseudotranslation is detected.*

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[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ 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: PEG, FLC, 1PE, EPE

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	0.36	0/3748	0.54	0/5092
2	B	0.38	0/59	0.77	0/77
All	All	0.36	0/3807	0.54	0/5169

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 ⓘ

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	3666	0	3732	49	0
2	B	58	0	63	1	0
3	A	32	0	44	1	0
4	A	15	0	18	0	0
5	A	13	0	5	0	0
6	A	7	0	10	0	0
7	A	10	0	0	0	0
All	All	3801	0	3872	49	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 7.

The worst 5 of 49 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:81:GLY:HA2	1:A:380:PHE:HE1	1.29	0.95
1:A:334:ILE:HG22	1:A:339:TRP:NE1	1.83	0.94
1:A:81:GLY:HA2	1:A:380:PHE:CE1	2.07	0.88
1:A:334:ILE:HG22	1:A:339:TRP:CD1	2.11	0.84
1:A:268:VAL:C	1:A:1002:ASN:N	2.34	0.81

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	456/541 (84%)	430 (94%)	26 (6%)	0	100	100
2	B	4/6 (67%)	4 (100%)	0	0	100	100
All	All	460/547 (84%)	434 (94%)	26 (6%)	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	395/460 (86%)	395 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	B	6/6 (100%)	6 (100%)	0	100	100
All	All	401/466 (86%)	401 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

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

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 monosaccharides 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	#$|Z| > 2$
4	EPE	A	1203	-	15,15,15	1.94	1 (6%)	18,20,20	1.39	1 (5%)
3	1PE	A	1201	-	15,15,15	0.55	0	14,14,14	0.25	0
3	1PE	A	1202	-	15,15,15	0.38	0	14,14,14	0.28	0
6	PEG	A	1205	-	6,6,6	0.26	0	5,5,5	0.57	0
5	FLC	A	1204	-	12,12,12	0.91	0	17,17,17	1.48	2 (11%)

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
4	EPE	A	1203	-	-	5/9/19/19	0/1/1/1
3	1PE	A	1201	-	-	6/13/13/13	-
3	1PE	A	1202	-	-	8/13/13/13	-
6	PEG	A	1205	-	-	2/4/4/4	-
5	FLC	A	1204	-	-	3/16/16/16	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	1203	EPE	C10-S	-7.28	1.67	1.77

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	1204	FLC	OB2-CBC-CB	4.31	120.53	113.05
4	A	1203	EPE	O1S-S-C10	4.24	112.02	106.92
5	A	1204	FLC	OB1-CBC-CB	-2.55	118.64	122.25

There are no chirality outliers.

5 of 24 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	1203	EPE	S-C10-C9-N1
5	A	1204	FLC	CA-CB-CG-CGC
5	A	1204	FLC	CBC-CB-CG-CGC
5	A	1204	FLC	OHB-CB-CG-CGC
3	A	1202	1PE	OH6-C15-C25-OH5

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1202	1PE	1	0

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 ⓘ

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(Å²)	Q<0.9
1	A	464/541 (85%)	0.30	24 (5%)	27	23	25, 71, 110, 138	29 (6%)
2	B	6/6 (100%)	0.02	0	100	100	59, 64, 69, 71	0
All	All	470/547 (85%)	0.30	24 (5%)	28	24	25, 71, 110, 138	29 (6%)

The worst 5 of 24 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1053	ASN	4.6
1	A	179	THR	4.0
1	A	1050	ILE	3.8
1	A	182	SER	3.4
1	A	381	LEU	3.3

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates ⓘ

There are no monosaccharides 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(Å²)	Q<0.9
3	1PE	A	1202	16/16	0.76	0.18	86,101,108,109	0
5	FLC	A	1204	13/13	0.78	0.20	84,91,95,96	0
3	1PE	A	1201	16/16	0.79	0.26	82,93,101,103	0
4	EPE	A	1203	15/15	0.91	0.27	76,81,87,87	0
6	PEG	A	1205	7/7	0.93	0.17	20,20,20,20	0

6.5 Other polymers (i)

There are no such residues in this entry.