



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 04:55 AM GMT

PDB ID : 2ORZ
Title : Structural Basis for Ligand Binding and Heparin Mediated Activation of Neuropilin
Authors : Vander Kooi, C.W.; Jusino, M.A.; Perman, B.; Neau, D.B.; Bellamy, H.D.; Leahy, D.J.
Deposited on : 2007-02-05
Resolution : 2.15 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
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
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) : trunk26865

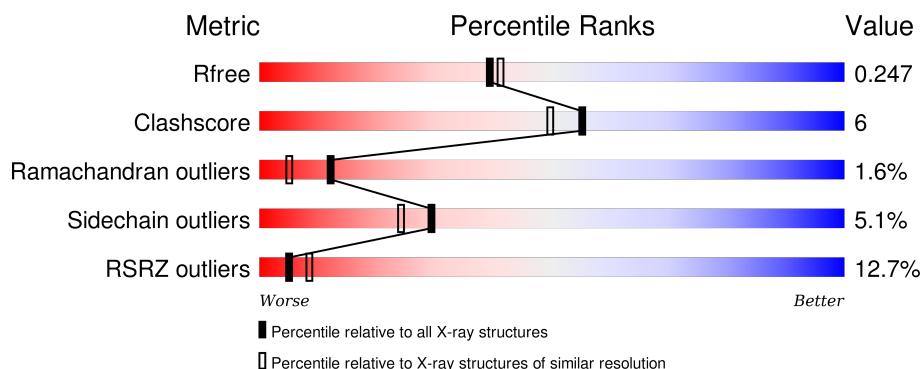
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.15 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}	91344	1045 (2.16-2.16)
Clashscore	102246	1152 (2.16-2.16)
Ramachandran outliers	100387	1131 (2.16-2.16)
Sidechain outliers	100360	1131 (2.16-2.16)
RSRZ outliers	91569	1050 (2.16-2.16)

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	314	<div> <div>12%</div> <div>85%</div> <div>13%</div> <div>.</div> </div>
2	B	4	<div> <div>50%</div> <div>25%</div> <div>25%</div> <div>25%</div> <div>25%</div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 2802 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 Neuropilin-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	313	Total	C	N	O	S	0	2	0
			2513	1589	439	471	14			

- Molecule 2 is a protein called Tuftsin.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	B	3	Total	C	N	O	0	0	0
			28	17	7	4			

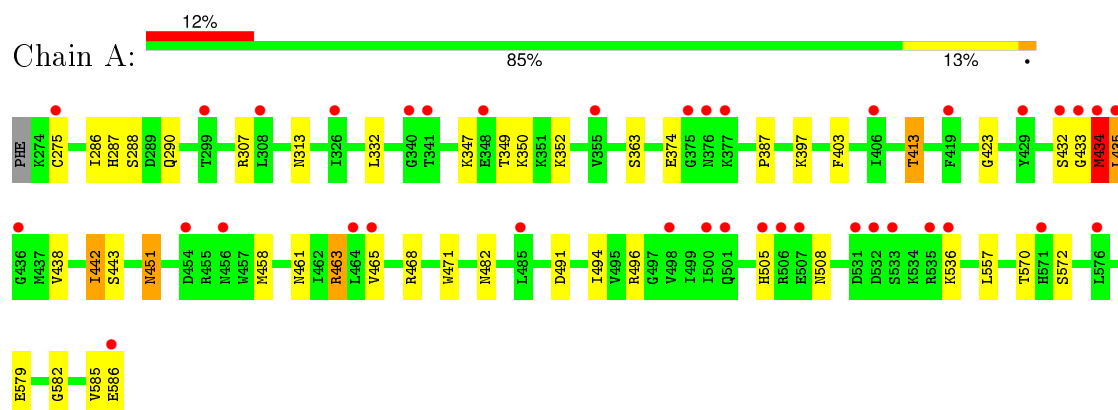
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	255	Total	O	0	0
			255	255		
3	B	6	Total	O	0	0
			6	6		

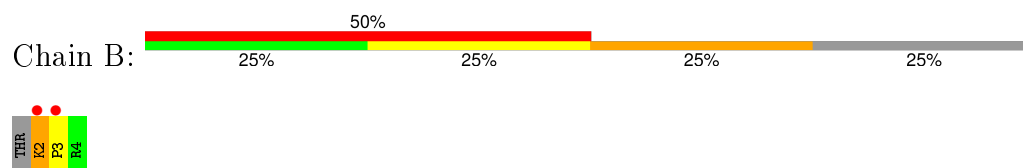
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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 ($\text{RSRZ} > 2$). 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: Neuropilin-1



• Molecule 2: Tuftsin



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	50.95Å 64.65Å 102.31Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	28.34 – 2.15 28.34 – 2.15	Depositor EDS
% Data completeness (in resolution range)	99.2 (28.34-2.15) 99.2 (28.34-2.15)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.84 (at 2.16Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.204 , 0.257 0.201 , 0.247	Depositor DCC
R_{free} test set	955 reflections (5.34%)	DCC
Wilson B-factor (Å ²)	32.5	Xtriage
Anisotropy	0.190	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 38.9	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 18847 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	2802	wwPDB-VP
Average B, all atoms (Å ²)	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.62% 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, 0.375 respectively for untwinned datasets, and 0.333, 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	0.44	0/2578	0.58	0/3483
2	B	0.57	0/28	0.82	0/34
All	All	0.44	0/2606	0.58	0/3517

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	2513	0	2478	27	0
2	B	28	0	32	5	0
3	A	255	0	0	2	0
3	B	6	0	0	0	0
All	All	2802	0	2510	32	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 6.

All (32) 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:443:SER:HB3	1:A:463:ARG:HH22	0.96	1.06

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:443:SER:HB3	1:A:463:ARG:NH2	1.79	0.95
1:A:451:ASN:HD21	1:A:471:TRP:HE1	1.16	0.91
1:A:443:SER:CB	1:A:463:ARG:HH22	1.85	0.85
1:A:458:MET:H	1:A:461:ASN:HD22	1.28	0.82
2:B:2:LYS:HB2	2:B:3:PRO:HD3	1.61	0.82
1:A:275:CYS:HB3	1:A:423:GLY:C	2.05	0.75
1:A:286:ILE:O	1:A:307:ARG:NH2	2.26	0.67
1:A:451:ASN:H	1:A:451:ASN:HD22	1.41	0.67
2:B:2:LYS:CB	2:B:3:PRO:HD3	2.25	0.66
1:A:435:LEU:H	1:A:435:LEU:HD23	1.64	0.61
1:A:570:THR:HG22	1:A:572:SER:H	1.68	0.58
1:A:451:ASN:ND2	1:A:471:TRP:HE1	1.95	0.57
1:A:313:ASN:HD21	1:A:347:LYS:H	1.51	0.57
1:A:585:VAL:O	1:A:586:GLU:HB2	2.03	0.57
1:A:505:HIS:O	1:A:508:ASN:HB2	2.08	0.53
2:B:2:LYS:HB2	2:B:3:PRO:CD	2.38	0.51
1:A:287:HIS:H	1:A:290:GLN:NE2	2.10	0.49
1:A:494:ILE:O	1:A:582:GLY:HA3	2.12	0.49
1:A:349:THR:O	1:A:350:LYS:HB2	2.16	0.46
1:A:491:ASP:HB3	3:A:147:HOH:O	2.15	0.46
2:B:2:LYS:CB	2:B:3:PRO:CD	2.92	0.46
1:A:347:LYS:NZ	3:A:227:HOH:O	2.39	0.45
1:A:585:VAL:O	1:A:586:GLU:CB	2.64	0.45
1:A:352:LYS:HB3	1:A:387:PRO:HG3	1.98	0.44
1:A:413:THR:HG22	1:A:413:THR:O	2.18	0.44
2:B:2:LYS:CG	2:B:3:PRO:HD3	2.49	0.43
1:A:313:ASN:ND2	1:A:347:LYS:H	2.17	0.42
1:A:432:SER:O	1:A:434:MET:N	2.53	0.42
1:A:363:SER:HB3	1:A:403:PHE:HB2	2.03	0.41
1:A:442:ILE:HB	1:A:579:GLU:OE1	2.20	0.41
1:A:397:LYS:HB3	1:A:397:LYS:HE2	1.85	0.41

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	313/314 (100%)	304 (97%)	4 (1%)	5 (2%)	12	5
2	B	1/4 (25%)	1 (100%)	0	0	100	100
All	All	314/318 (99%)	305 (97%)	4 (1%)	5 (2%)	12	5

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	433	GLY
1	A	465	VAL
1	A	413	THR
1	A	434	MET
1	A	435	LEU

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	275/274 (100%)	262 (95%)	13 (5%)	32	28
2	B	3/4 (75%)	2 (67%)	1 (33%)	0	0
All	All	278/278 (100%)	264 (95%)	14 (5%)	29	25

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	288	SER
1	A	332	LEU
1	A	374	GLU
1	A	434	MET
1	A	438	VAL
1	A	442	ILE
1	A	451	ASN
1	A	463	ARG

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Mol	Chain	Res	Type
1	A	468	ARG
1	A	482	ASN
1	A	496	ARG
1	A	536	LYS
1	A	557	LEU
2	B	2	LYS

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

Mol	Chain	Res	Type
1	A	290	GLN
1	A	309	ASN
1	A	313	ASN
1	A	451	ASN
1	A	461	ASN
1	A	478	HIS
1	A	482	ASN
1	A	543	ASN
1	A	544	ASN

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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

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

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	313/314 (99%)	0.74	38 (12%) 6 9	25, 32, 42, 47	0
2	B	3/4 (75%)	2.75	2 (66%) 0 0	52, 52, 56, 57	0
All	All	316/318 (99%)	0.76	40 (12%) 5 8	25, 32, 43, 57	0

All (40) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	433	GLY	13.3
1	A	435	LEU	12.8
1	A	434	MET	12.1
1	A	536	LYS	4.4
1	A	506	ARG	4.1
1	A	376	ASN	4.1
1	A	576	LEU	4.0
1	A	535	ARG	3.9
1	A	464	LEU	3.9
2	B	3	PRO	3.9
1	A	586	GLU	3.4
1	A	375	GLY	3.3
1	A	571	HIS	3.3
2	B	2	LYS	3.2
1	A	436	GLY	3.2
1	A	432	SER	3.2
1	A	507	GLU	3.2
1	A	532	ASP	3.2
1	A	505	HIS	3.0
1	A	348	GLU	2.8
1	A	429	TYR	2.8
1	A	456	ASN	2.8
1	A	419	PHE	2.5
1	A	308	LEU	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	377	LYS	2.4
1	A	406	ILE	2.4
1	A	485	LEU	2.4
1	A	275	CYS	2.3
1	A	454	ASP	2.3
1	A	340	GLY	2.3
1	A	341	THR	2.3
1	A	326	ILE	2.2
1	A	500	ILE	2.2
1	A	498	VAL	2.1
1	A	531	ASP	2.1
1	A	355	VAL	2.1
1	A	501	GLN	2.1
1	A	533	SER	2.1
1	A	465	VAL	2.1
1	A	299	THR	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 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.