



# Full wwPDB X-ray Structure Validation Report ⓘ

May 25, 2020 – 06:52 am BST

PDB ID : 2ORX  
Title : Structural Basis for Ligand Binding and Heparin Mediated Activation of Neuropilin  
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Deposited on : 2007-02-05  
Resolution : 2.40 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](mailto: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.

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

MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.11
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)	:	2.11

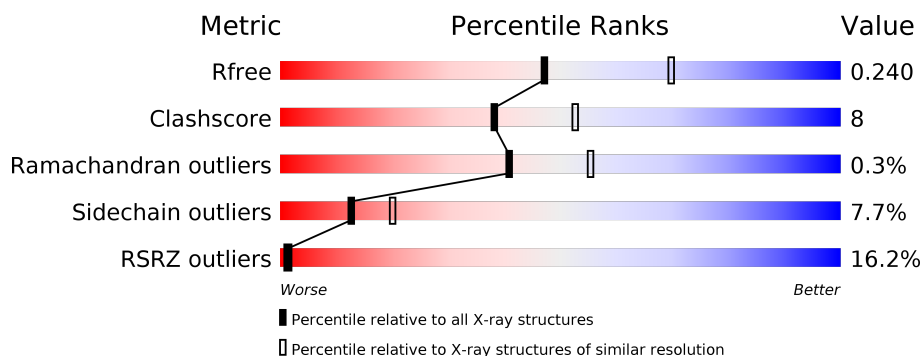
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.40 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))
$R_{free}$	130704	3907 (2.40-2.40)
Clashscore	141614	4398 (2.40-2.40)
Ramachandran outliers	138981	4318 (2.40-2.40)
Sidechain outliers	138945	4319 (2.40-2.40)
RSRZ outliers	127900	3811 (2.40-2.40)

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  $\geq 3$ , 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	314	<div> <div>16%</div> <div>79%</div> <div>19%</div> <div>.</div> </div>

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 2708 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	314	Total	C	N	O	S	0	0	0
			2510	1588	437	471	14			

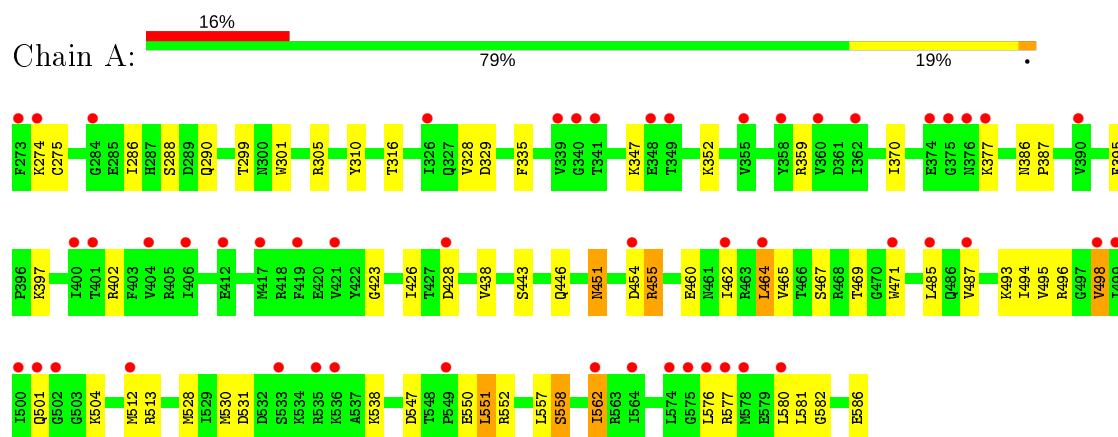
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	198	Total	O	0	0
			198	198		

### 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: Neuropilin-1



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	38.09 Å 92.22 Å 120.11 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.37 – 2.40 29.37 – 2.40	Depositor EDS
% Data completeness (in resolution range)	94.9 (29.37-2.40) 94.9 (29.37-2.40)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.24 (at 2.39 Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, $R_{free}$	0.201 , 0.252 0.194 , 0.240	Depositor DCC
$R_{free}$ test set	823 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	47.6	Xtriage
Anisotropy	0.397	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.30 , 31.1	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.46$ , $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	2708	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	57.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.16% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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	0.56	0/2570	0.69	0/3474

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	2510	0	2463	38	0
2	A	198	0	0	6	0
All	All	2708	0	2463	38	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 8.

All (38) 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:352:LYS:HG2	1:A:387:PRO:HG3	1.51	0.90
1:A:451:ASN:HD21	1:A:471:TRP:HE1	1.16	0.90
1:A:455:ARG:HH11	1:A:455:ARG:HG2	1.49	0.77
1:A:550:GLU:HG2	1:A:552:ARG:NH2	2.04	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:397:LYS:HE2	2:A:174:HOH:O	1.88	0.72
1:A:464:LEU:O	1:A:501:GLN:NE2	2.26	0.67
1:A:451:ASN:H	1:A:451:ASN:HD22	1.50	0.60
1:A:531:ASP:HB2	2:A:71:HOH:O	2.02	0.59
1:A:550:GLU:HG2	1:A:552:ARG:CZ	2.32	0.59
1:A:426:ILE:HD11	2:A:30:HOH:O	2.02	0.59
1:A:531:ASP:HB3	1:A:538:LYS:HG2	1.90	0.53
1:A:586:GLU:HG2	2:A:126:HOH:O	2.09	0.52
1:A:443:SER:H	1:A:446:GLN:NE2	2.08	0.51
1:A:462:ILE:O	1:A:462:ILE:HG22	2.10	0.51
1:A:451:ASN:ND2	1:A:471:TRP:HE1	1.97	0.51
1:A:386:ASN:HB2	1:A:387:PRO:HD2	1.94	0.50
1:A:493:LYS:O	1:A:558:SER:HA	2.11	0.50
1:A:370:ILE:HD13	1:A:547:ASP:HB3	1.92	0.50
1:A:464:LEU:HG	1:A:465:VAL:HG13	1.94	0.49
1:A:286:ILE:HD13	1:A:328:VAL:HG11	1.93	0.49
1:A:498:VAL:HG13	1:A:580:LEU:HD23	1.94	0.49
1:A:495:VAL:HG11	1:A:562:ILE:HD13	1.94	0.49
1:A:494:ILE:O	1:A:582:GLY:HA3	2.14	0.48
1:A:301:TRP:HB3	1:A:316:THR:HB	1.96	0.47
1:A:352:LYS:CG	1:A:387:PRO:HG3	2.36	0.45
1:A:455:ARG:NH1	1:A:455:ARG:HG2	2.24	0.45
1:A:512:MET:HG2	1:A:513:ARG:O	2.19	0.43
1:A:305:ARG:HG2	1:A:310:TYR:CE2	2.54	0.43
1:A:290:GLN:NE2	2:A:112:HOH:O	2.52	0.43
1:A:395:PHE:N	1:A:395:PHE:CD1	2.85	0.42
1:A:274:LYS:HD3	1:A:275:CYS:N	2.34	0.42
1:A:528:MET:O	1:A:530:MET:HE2	2.19	0.42
1:A:501:GLN:HG2	1:A:577:ARG:HB2	2.02	0.41
1:A:551:LEU:HD21	1:A:581:LEU:HD12	2.03	0.41
1:A:377:LYS:HD2	2:A:66:HOH:O	2.20	0.41
1:A:329:ASP:OD1	1:A:402:ARG:NE	2.53	0.41
1:A:494:ILE:HA	1:A:557:LEU:O	2.20	0.41
1:A:335:PHE:O	1:A:423:GLY:HA3	2.22	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	312/314 (99%)	302 (97%)	9 (3%)	1 (0%)	41	55

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	464	LEU

### 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	274/274 (100%)	253 (92%)	21 (8%)	13	20

All (21) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	288	SER
1	A	299	THR
1	A	347	LYS
1	A	359	ARG
1	A	428	ASP
1	A	438	VAL
1	A	451	ASN
1	A	454	ASP
1	A	455	ARG
1	A	460	GLU

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Mol	Chain	Res	Type
1	A	467	SER
1	A	469	THR
1	A	485	LEU
1	A	487	VAL
1	A	496	ARG
1	A	498	VAL
1	A	504	LYS
1	A	551	LEU
1	A	558	SER
1	A	562	ILE
1	A	576	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	290	GLN
1	A	382	GLN
1	A	384	ASN
1	A	446	GLN
1	A	451	ASN
1	A	461	ASN
1	A	501	GLN
1	A	521	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 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	314/314 (100%)	0.88	51 (16%) <b>1</b> <b>1</b>	47, 58, 66, 71	0

All (51) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	576	LEU	5.6
1	A	464	LEU	5.5
1	A	339	VAL	5.3
1	A	578	MET	4.8
1	A	375	GLY	4.6
1	A	564	ILE	4.6
1	A	404	VAL	4.4
1	A	406	ILE	4.2
1	A	341	THR	3.8
1	A	500	ILE	3.8
1	A	574	LEU	3.6
1	A	535	ARG	3.6
1	A	348	GLU	3.5
1	A	454	ASP	3.4
1	A	428	ASP	3.4
1	A	376	ASN	3.4
1	A	358	TYR	3.3
1	A	417	MET	3.2
1	A	580	LEU	3.2
1	A	575	GLY	3.2
1	A	485	LEU	3.2
1	A	498	VAL	3.0
1	A	419	PHE	3.0
1	A	360	VAL	3.0
1	A	421	VAL	2.9
1	A	412	GLU	2.9
1	A	577	ARG	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	536	LYS	2.7
1	A	273	PHE	2.6
1	A	487	VAL	2.6
1	A	340	GLY	2.6
1	A	471	TRP	2.6
1	A	390	VAL	2.5
1	A	326	ILE	2.5
1	A	362	ILE	2.5
1	A	562	ILE	2.5
1	A	377	LYS	2.4
1	A	400	ILE	2.4
1	A	374	GLU	2.4
1	A	462	ILE	2.3
1	A	349	THR	2.3
1	A	284	GLY	2.2
1	A	355	VAL	2.2
1	A	533	SER	2.2
1	A	512	MET	2.2
1	A	501	GLN	2.1
1	A	274	LYS	2.1
1	A	401	THR	2.1
1	A	499	ILE	2.1
1	A	502	GLY	2.1
1	A	549	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.