



wwPDB X-ray Structure Validation Summary Report ⓘ

May 16, 2020 – 04:47 am BST

PDB ID : 1OBP
Title : ODORANT-BINDING PROTEIN FROM BOVINE NASAL MUCOSA
Authors : Tegoni, M.; Cambillau, C.
Deposited on : 1996-01-14
Resolution : 2.00 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 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

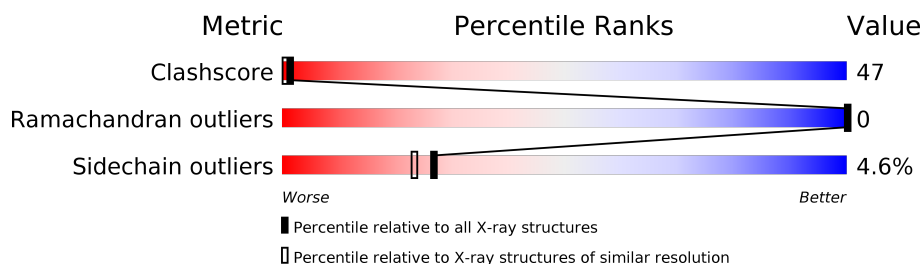
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION



The reported resolution of this entry is 2.00 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))
Clashscore	141614	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)

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 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 $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	A	159	 79% 19% ..
1	B	159	 77% 19% . .

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	UNX	A	161	-	-	X	-
2	UNX	A	162	-	-	X	-
2	UNX	A	163	-	-	X	-
2	UNX	A	164	-	-	X	-
2	UNX	A	165	-	-	X	-

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	UNX	A	166	-	-	X	-
2	UNX	A	167	-	-	X	-
2	UNX	A	169	-	-	X	-
2	UNX	A	171	-	-	X	-
2	UNX	A	173	-	-	X	-
2	UNX	A	174	-	-	X	-
2	UNX	A	175	-	-	X	-
2	UNX	A	176	-	-	X	-
2	UNX	A	177	-	-	X	-
2	UNX	A	178	-	-	X	-
2	UNX	A	179	-	-	X	-
2	UNX	A	180	-	-	X	-
2	UNX	A	182	-	-	X	-
2	UNX	A	183	-	-	X	-
2	UNX	A	184	-	-	X	-
2	UNX	A	185	-	-	X	-
2	UNX	A	186	-	-	X	-
2	UNX	A	187	-	-	X	-
2	UNX	A	188	-	-	X	-
2	UNX	A	189	-	-	X	-
2	UNX	A	190	-	-	X	-
2	UNX	A	191	-	-	X	-
2	UNX	A	192	-	-	X	-
2	UNX	A	193	-	-	X	-
2	UNX	A	194	-	-	X	-
2	UNX	A	195	-	-	X	-
2	UNX	A	196	-	-	X	-
2	UNX	A	197	-	-	X	-
2	UNX	A	198	-	-	X	-
2	UNX	A	199	-	-	X	-
2	UNX	A	200	-	-	X	-
2	UNX	A	201	-	-	X	-
2	UNX	B	161	-	-	X	-
2	UNX	B	162	-	-	X	-
2	UNX	B	163	-	-	X	-
2	UNX	B	164	-	-	X	-
2	UNX	B	165	-	-	X	-
2	UNX	B	166	-	-	X	-
2	UNX	B	167	-	-	X	-
2	UNX	B	168	-	-	X	-
2	UNX	B	170	-	-	X	-
2	UNX	B	171	-	-	X	-

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	UNX	B	172	-	-	X	-
2	UNX	B	173	-	-	X	-
2	UNX	B	174	-	-	X	-
2	UNX	B	175	-	-	X	-
2	UNX	B	176	-	-	X	-
2	UNX	B	177	-	-	X	-
2	UNX	B	178	-	-	X	-
2	UNX	B	179	-	-	X	-
2	UNX	B	180	-	-	X	-
2	UNX	B	181	-	-	X	-
2	UNX	B	182	-	-	X	-
2	UNX	B	183	-	-	X	-
2	UNX	B	184	-	-	X	-
2	UNX	B	185	-	-	X	-
2	UNX	B	186	-	-	X	-
2	UNX	B	188	-	-	X	-
2	UNX	B	189	-	-	X	-
2	UNX	B	190	-	-	X	-
2	UNX	B	191	-	-	X	-
2	UNX	B	192	-	-	X	-
2	UNX	B	193	-	-	X	-
2	UNX	B	194	-	-	X	-
2	UNX	B	196	-	-	X	-
2	UNX	B	197	-	-	X	-
2	UNX	B	199	-	-	X	-
2	UNX	B	201	-	-	X	-

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 4008 atoms, of which 1094 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 ODORANT-BINDING PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	158	Total	C	H	N	O	4	0	0
			1594	821	293	220	260			
1	B	155	Total	C	H	N	O	0	0	0
			1564	806	289	216	253			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	117	GLY	GLU	CONFLICT	UNP P07435
B	117	GLY	GLU	CONFLICT	UNP P07435

- Molecule 2 is UNKNOWN ATOM OR ION (three-letter code: UNX) (formula: X).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	41	Total	X	0	0
			41	41		
2	A	41	Total	X	0	0
			41	41		

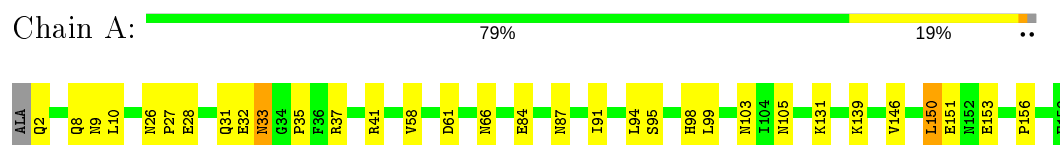
- Molecule 3 is water.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	129	Total	H	O	1	0
			387	258	129		
3	B	127	Total	H	O	0	0
			381	254	127		

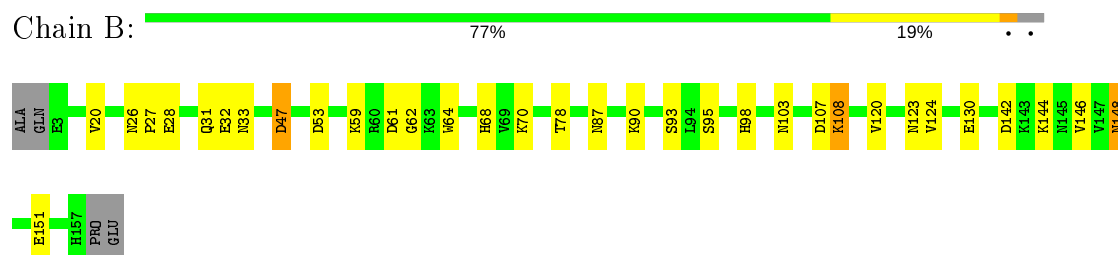
3 Residue-property plots [i](#)

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. 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. 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: ODORANT-BINDING PROTEIN



• Molecule 1: ODORANT-BINDING PROTEIN



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	55.90Å 65.50Å 42.70Å 90.00° 98.80° 90.00°	Depositor
Resolution (Å)	6.00 – 2.00 19.82 – 2.01	Depositor EDS
% Data completeness (in resolution range)	(Not available) (6.00-2.00) 93.9 (19.82-2.01)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.99 (at 2.01Å)	Xtriage
Refinement program	X-PLOR 3.1	Depositor
R, R_{free}	0.164 , 0.247 0.204 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	22.9	Xtriage
Anisotropy	0.276	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.20 , 61.3	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	0.91	EDS
Total number of atoms	4008	wwPDB-VP
Average B, all atoms (Å ²)	21.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.69% 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](#)

Bond lengths and bond angles in the following residue types are not validated in this section: UNX

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	0.54	0/1331	0.73	0/1799
1	B	0.60	0/1304	0.74	0/1763
All	All	0.57	0/2635	0.74	0/3562

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	1301	293	1234	23	1
1	B	1275	289	1213	28	0
2	A	41	0	0	94	0
2	B	41	0	0	98	0
3	A	129	258	0	8	1
3	B	127	254	0	6	3
All	All	2914	1094	2447	241	3

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 47.

The worst 5 of 241 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)
2:B:162:UNX:UNK	2:B:166:UNX:UNK	1.01	0.99
2:A:163:UNX:UNK	2:A:164:UNX:UNK	1.02	0.98
2:B:178:UNX:UNK	2:B:185:UNX:UNK	1.05	0.97
2:B:178:UNX:UNK	2:B:186:UNX:UNK	0.98	0.97
2:B:178:UNX:UNK	2:B:192:UNX:UNK	1.09	0.96

All (3) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:139:LYS:HZ2	3:B:218:HOH:H2[2_656]	1.33	0.27
3:A:214:HOH:O	3:B:321:HOH:H1[2_646]	1.57	0.03
3:B:262:HOH:H1	3:B:284:HOH:O[2_646]	1.60	0.00

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	156/159 (98%)	152 (97%)	4 (3%)	0	100	100
1	B	153/159 (96%)	149 (97%)	4 (3%)	0	100	100
All	All	309/318 (97%)	301 (97%)	8 (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	144/144 (100%)	136 (94%)	8 (6%)	21	17
1	B	141/144 (98%)	136 (96%)	5 (4%)	36	35
All	All	285/288 (99%)	272 (95%)	13 (5%)	27	23

5 of 13 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	131	LYS
1	A	146	VAL
1	B	123	ASN
1	A	58	VAL
1	B	108	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 13 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	98	HIS
1	A	103	ASN
1	B	103	ASN
1	A	87	ASN
1	B	98	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

Of 82 ligands modelled in this entry, 82 are unknown - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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 ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.

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

Unable to reproduce the depositors R factor - this section is therefore empty.

6.3 Carbohydrates ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.

6.4 Ligands ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.

6.5 Other polymers ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.