



wwPDB X-ray Structure Validation Summary Report ⓘ

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PDB ID : 4GJT / pdb_00004gjt
Title : complex structure of nectin-4 bound to MV-H
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Deposited on : 2012-08-10
Resolution : 3.10 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
Mogul : 2022.3.0, CSD as543be (2022)
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

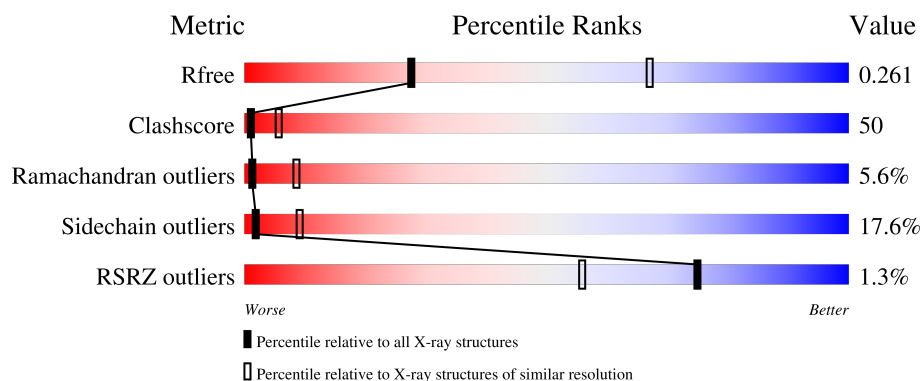
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.10 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	1456 (3.10-3.10)
Clashscore	190562	1539 (3.10-3.10)
Ramachandran outliers	187476	1467 (3.10-3.10)
Sidechain outliers	187428	1467 (3.10-3.10)
RSRZ outliers	180081	1456 (3.10-3.10)

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	A	473	0% 33% 40% 12% • 13%
2	B	123	2% 36% 47% 9% • 7%

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
3	NAG	A	801	-	-	X	-

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 5020 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 Hemagglutinin glycoprotein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	411	Total	C	N	O	S	0	0	0
			3205	2051	540	591	23			

There are 11 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	145	ALA	-	expression tag	UNP Q786F2
A	146	ASP	-	expression tag	UNP Q786F2
A	147	GLY	-	expression tag	UNP Q786F2
A	148	ILE	-	expression tag	UNP Q786F2
A	149	GLN	-	expression tag	UNP Q786F2
A	150	HIS	-	expression tag	UNP Q786F2
A	151	HIS	-	expression tag	UNP Q786F2
A	152	HIS	-	expression tag	UNP Q786F2
A	153	HIS	-	expression tag	UNP Q786F2
A	154	HIS	-	expression tag	UNP Q786F2
A	155	HIS	-	expression tag	UNP Q786F2

- Molecule 2 is a protein called Poliovirus receptor-related protein 4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	114	Total	C	N	O	S	0	0	0
			870	542	157	169	2			
2	C	112	Total	C	N	O	S	0	0	0
			852	531	152	167	2			

There are 16 discrepancies between the modelled and reference sequences:

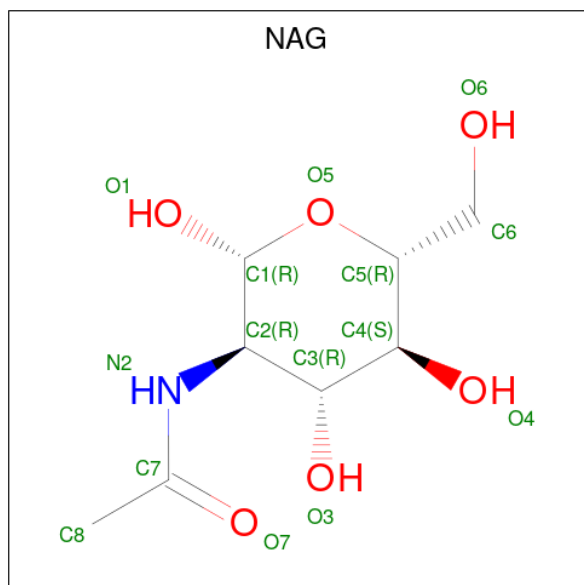
Chain	Residue	Modelled	Actual	Comment	Reference
B	0	MET	-	expression tag	UNP Q96NY8
B	116	GLU	-	expression tag	UNP Q96NY8
B	117	HIS	-	expression tag	UNP Q96NY8

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Chain	Residue	Modelled	Actual	Comment	Reference
B	118	HIS	-	expression tag	UNP Q96NY8
B	119	HIS	-	expression tag	UNP Q96NY8
B	120	HIS	-	expression tag	UNP Q96NY8
B	121	HIS	-	expression tag	UNP Q96NY8
B	122	HIS	-	expression tag	UNP Q96NY8
C	0	MET	-	expression tag	UNP Q96NY8
C	116	GLU	-	expression tag	UNP Q96NY8
C	117	HIS	-	expression tag	UNP Q96NY8
C	118	HIS	-	expression tag	UNP Q96NY8
C	119	HIS	-	expression tag	UNP Q96NY8
C	120	HIS	-	expression tag	UNP Q96NY8
C	121	HIS	-	expression tag	UNP Q96NY8
C	122	HIS	-	expression tag	UNP Q96NY8

- Molecule 3 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 4 is water.

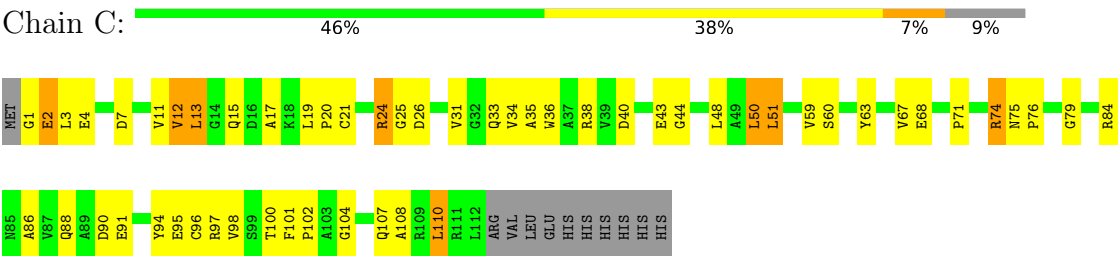
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	63	Total	O	0	0
			63	63		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	6	Total 6	O 6	0	0
4	C	10	Total 10	O 10	0	0

● Molecule 2: Poliovirus receptor-related protein 4



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	82.35Å 171.78Å 117.44Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	37.13 – 3.10 37.13 – 3.10	Depositor EDS
% Data completeness (in resolution range)	99.9 (37.13-3.10) 99.8 (37.13-3.10)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	0.08	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.21 (at 3.12Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7_650)	Depositor
R, R_{free}	0.260 , 0.278 0.256 , 0.261	Depositor DCC
R_{free} test set	774 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	90.8	Xtriage
Anisotropy	0.457	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 66.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	5020	wwPDB-VP
Average B, all atoms (Å ²)	96.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.97% 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 ⓘ

5.1 Standard geometry ⓘ

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

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	0/3285	0.89	10/4465 (0.2%)
2	B	0.37	0/888	0.91	3/1207 (0.2%)
2	C	0.42	0/870	0.84	2/1183 (0.2%)
All	All	0.43	0/5043	0.88	15/6855 (0.2%)

There are no bond length outliers.

The worst 5 of 15 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	165	ALA	N-CA-C	8.72	129.38	110.80
2	B	71	PRO	CA-C-N	7.68	128.30	120.38
2	B	71	PRO	C-N-CA	7.68	128.30	120.38
1	A	162	LEU	N-CA-C	-7.16	103.51	111.82
1	A	553	TYR	CA-C-N	6.56	128.04	119.84

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	3205	0	3153	385	2
2	B	870	0	844	71	2
2	C	852	0	822	45	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	14	0	13	16	0
4	A	63	0	0	62	0
4	B	6	0	0	9	0
4	C	10	0	0	9	0
All	All	5020	0	4832	493	2

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 50.

The worst 5 of 493 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:489:GLU:HB2	4:A:958:HOH:O	1.24	1.33
1:A:464:LEU:CD2	2:B:100:THR:O	1.77	1.30
1:A:588:SER:O	1:A:589:GLU:HG3	1.36	1.22
1:A:376:LEU:N	1:A:376:LEU:HD23	1.55	1.19
1:A:588:SER:C	1:A:589:GLU:HG3	1.69	1.12

All (2) 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:534:VAL:CG2	2:B:24:ARG:CZ[3_455]	1.88	0.32
1:A:534:VAL:CG2	2:B:24:ARG:NE[3_455]	1.97	0.23

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	401/473 (85%)	318 (79%)	56 (14%)	27 (7%)	1 6
2	B	112/123 (91%)	94 (84%)	12 (11%)	6 (5%)	1 9

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	C	110/123 (89%)	100 (91%)	8 (7%)	2 (2%)	6	28
All	All	623/719 (87%)	512 (82%)	76 (12%)	35 (6%)	1	8

5 of 35 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	158	ALA
1	A	160	GLU
1	A	161	GLU
1	A	282	ASN
1	A	375	LYS

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	359/412 (87%)	289 (80%)	70 (20%)	1	6
2	B	91/100 (91%)	77 (85%)	14 (15%)	2	12
2	C	89/100 (89%)	78 (88%)	11 (12%)	4	19
All	All	539/612 (88%)	444 (82%)	95 (18%)	2	9

5 of 95 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	535	GLU
2	B	9	VAL
1	A	547	ARG
1	A	580	ARG
2	B	24	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 18 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	46	GLN
2	C	88	GLN
2	B	69	GLN
1	A	391	GLN
1	A	596	HIS

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](#)

1 ligand is 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	$\# Z > 2$
3	NAG	A	801	1	14,14,15	0.55	0	17,19,21	0.61	0

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
3	NAG	A	801	1	-	3/6/23/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	801	NAG	C4-C5-C6-O6
3	A	801	NAG	O5-C5-C6-O6
3	A	801	NAG	C3-C2-N2-C7

There are no ring outliers.

1 monomer is involved in 16 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	801	NAG	16	0

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	A	411/473 (86%)	-0.11	5 (1%) 76 58	24, 72, 165, 292	0
2	B	114/123 (92%)	0.05	3 (2%) 57 36	51, 119, 200, 234	0
2	C	112/123 (91%)	-0.18	0 100 100	63, 99, 162, 180	0
All	All	637/719 (88%)	-0.09	8 (1%) 75 56	24, 91, 174, 292	0

The worst 5 of 8 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	27	SER	3.9
1	A	390	ASN	3.4
1	A	530	ASP	2.8
2	B	85	ASN	2.5
2	B	30	GLN	2.4

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](#)

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($\text{\AA}^2$)	Q<0.9
3	NAG	A	801	14/15	0.65	0.12	96,111,128,130	0

6.5 Other polymers [i](#)

There are no such residues in this entry.