



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 09:49 PM UTC

PDB ID : 6XSN / pdb_00006xsn
Title : Crystal structure of NHP VD20.5A4 Fab in complex with 16055 V1V2 1FD6 scaffold
Authors : Aljedani, S.; Pancera, M.
Deposited on : 2020-07-15
Resolution : 2.87 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

<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

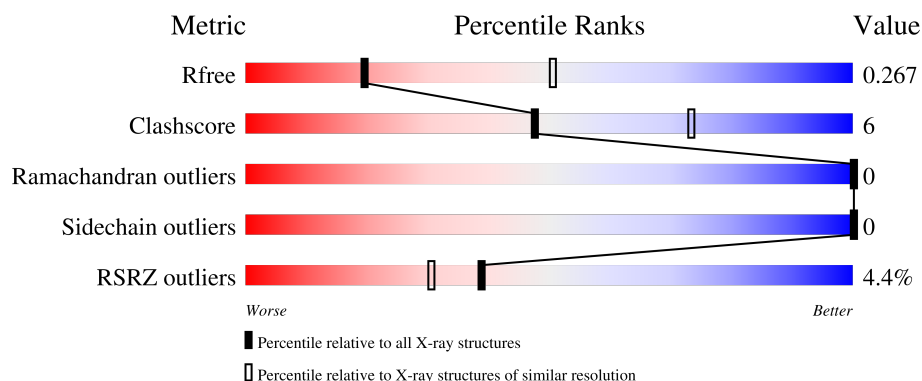
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

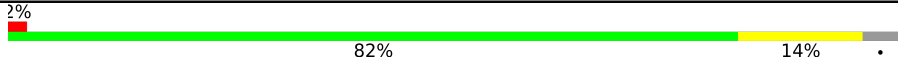
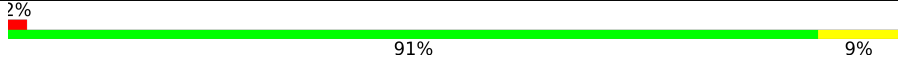
The reported resolution of this entry is 2.87 Å.

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	3557 (2.90-2.86)
Clashscore	190562	3801 (2.90-2.86)
Ramachandran outliers	187476	3699 (2.90-2.86)
Sidechain outliers	187428	3702 (2.90-2.86)
RSRZ outliers	180081	3558 (2.90-2.86)

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	H	224	
2	L	214	
3	C	141	

2 Entry composition [i](#)

There are 8 unique types of molecules in this entry. The entry contains 3644 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 VD20.5A4_heavy_chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	H	214	Total	C	N	O	S	0	0	0
			1583	1010	256	313	4			

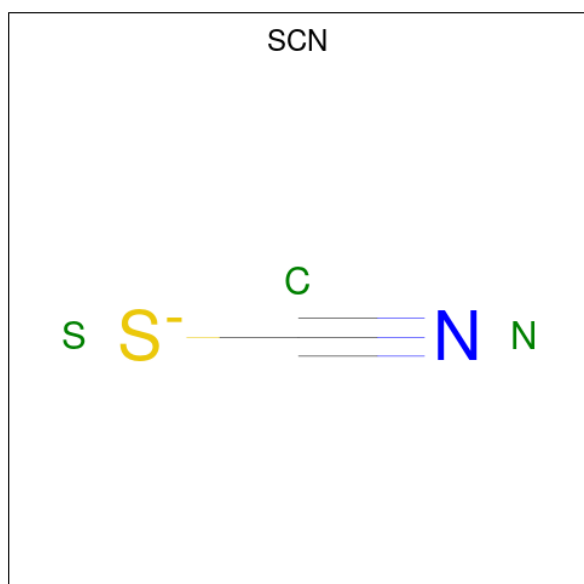
- Molecule 2 is a protein called VD20.5A4_light_chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	L	214	Total	C	N	O	S	0	0	0
			1602	994	264	338	6			

- Molecule 3 is a protein called 16055_V1V2-1FD6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	48	Total	C	N	O	S	0	0	0
			374	231	66	73	4			

- Molecule 4 is THIOCYANATE ION (CCD ID: SCN) (formula: CNS).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	H	1	Total C N S 3 1 1 1	0	0
4	L	1	Total C N S 3 1 1 1	0	0
4	L	1	Total C N S 3 1 1 1	0	0

- Molecule 5 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	H	1	Total C O 4 2 2	0	0
5	L	1	Total C O 4 2 2	0	0
5	L	1	Total C O 4 2 2	0	0
5	L	1	Total C O 4 2 2	0	0

- Molecule 6 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	L	1	Total Na 1 1	0	0

- Molecule 7 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).

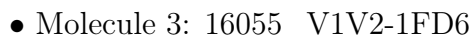
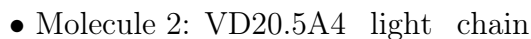


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	C	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	H	17	Total	O	0	0
			17	17		
8	L	28	Total	O	0	0
			28	28		

- Molecule 1: VD20.5A4 heavy chain



4 Data and refinement statistics

Property	Value	Source
Space group	P 41 2 2	Depositor
Cell constants a, b, c, α , β , γ	106.56Å 106.56Å 128.93Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.24 – 2.87 49.24 – 2.87	Depositor EDS
% Data completeness (in resolution range)	93.9 (49.24-2.87) 94.0 (49.24-2.87)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.01 (at 2.86Å)	Xtriage
Refinement program	PHENIX (1.17.1_3660: ???)	Depositor
R, R_{free}	0.221 , 0.267 0.224 , 0.267	Depositor DCC
R_{free} test set	817 reflections (4.62%)	wwPDB-VP
Wilson B-factor (Å ²)	48.8	Xtriage
Anisotropy	0.136	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 38.0	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	3644	wwPDB-VP
Average B, all atoms (Å ²)	50.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.39% 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: SCN, EDO, NA, 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	H	0.17	0/1630	0.41	0/2243
2	L	0.15	0/1634	0.43	0/2227
3	C	0.21	0/377	0.44	0/504
All	All	0.17	0/3641	0.42	0/4974

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	H	1583	0	1488	21	0
2	L	1602	0	1507	12	0
3	C	374	0	331	7	0
4	H	3	0	0	0	0
4	L	6	0	0	0	0
5	H	4	0	6	0	0
5	L	12	0	18	0	0
6	L	1	0	0	0	0
7	C	14	0	13	1	0
8	H	17	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	L	28	0	0	0	0
All	All	3644	0	3363	39	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 (39) 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:H:51:ILE:HG13	1:H:57:THR:HG22	1.75	0.66
2:L:192:TYR:HB2	2:L:209:PHE:CE1	2.31	0.66
1:H:170:LEU:HD12	1:H:176:TYR:CZ	2.31	0.65
1:H:150:VAL:HG22	1:H:200:HIS:HB2	1.79	0.64
3:C:186(B):ARG:HD3	3:C:188:SER:O	2.03	0.59
2:L:132:VAL:HG11	2:L:209:PHE:HE1	1.69	0.57
2:L:193:ALA:HB2	2:L:208:SER:HB3	1.87	0.56
2:L:201:LEU:HD13	2:L:205:VAL:HG12	1.87	0.56
1:H:200:HIS:ND1	1:H:203:SER:HB3	2.21	0.55
1:H:170:LEU:HD21	1:H:174:GLY:HA2	1.91	0.53
2:L:132:VAL:HG11	2:L:209:PHE:CE1	2.43	0.53
2:L:80:PRO:O	2:L:83:VAL:HG23	2.08	0.53
3:C:184:LEU:HD11	3:C:192:ARG:HG3	1.91	0.52
1:H:201:LYS:HG2	1:H:202:PRO:HD3	1.90	0.52
1:H:54:THR:HG21	3:C:185:GLU:OE2	2.11	0.51
2:L:11:LEU:HD11	2:L:19:VAL:HG21	1.94	0.50
1:H:8:GLY:HA3	1:H:20:LEU:HD23	1.93	0.49
2:L:37:GLN:HB2	2:L:47:LEU:HD11	1.95	0.47
1:H:121:VAL:HG11	1:H:198:VAL:HG21	1.96	0.47
1:H:47:TRP:HZ2	1:H:50:ARG:HG2	1.81	0.46
3:C:189:SER:HB2	3:C:191:TYR:CE2	2.50	0.46
2:L:83:VAL:HG11	2:L:166:GLN:HB3	1.98	0.45
3:C:156:ASN:ND2	7:C:301:NAG:O7	2.47	0.45
1:H:119:PRO:HB3	1:H:145:TYR:HB3	1.99	0.44
1:H:47:TRP:CZ2	1:H:49:GLY:HA2	2.53	0.44
2:L:120:PRO:HD3	2:L:132:VAL:HG22	1.99	0.43
3:C:131:CYS:HA	3:C:157:CYS:HA	1.99	0.43
1:H:4:LEU:HD11	1:H:102:VAL:HG23	2.00	0.43
1:H:4:LEU:HB3	1:H:22:CYS:SG	2.59	0.43
1:H:4:LEU:HD21	1:H:34:TRP:HZ3	1.84	0.43
1:H:143:LYS:NZ	1:H:171:GLN:OE1	2.51	0.43
1:H:94:ARG:NH1	1:H:101:ASP:OD2	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:34:TRP:CH2	1:H:94:ARG:HG3	2.54	0.42
2:L:39:LYS:HE2	2:L:81:GLU:O	2.19	0.42
2:L:27:GLN:C	2:L:69:THR:HG22	2.45	0.42
1:H:188:SER:HA	1:H:191:THR:CG2	2.50	0.42
1:H:52:TYR:CD2	1:H:54:THR:HG22	2.55	0.41
1:H:203:SER:O	1:H:203:SER:OG	2.34	0.41
3:C:131:CYS:HB2	3:C:191:TYR:CE2	2.56	0.41

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	H	210/224 (94%)	206 (98%)	4 (2%)	0	100	100
2	L	212/214 (99%)	206 (97%)	6 (3%)	0	100	100
3	C	42/141 (30%)	39 (93%)	3 (7%)	0	100	100
All	All	464/579 (80%)	451 (97%)	13 (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	H	175/193 (91%)	175 (100%)	0	100	100
2	L	179/187 (96%)	179 (100%)	0	100	100
3	C	39/121 (32%)	39 (100%)	0	100	100
All	All	393/501 (78%)	393 (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. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	H	164	HIS
2	L	3	GLN
2	L	138	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 9 ligands modelled in this entry, 1 is monoatomic - leaving 8 for Mogul analysis.

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
5	EDO	L	603	-	3,3,3	0.42	0	2,2,2	0.42	0
4	SCN	H	401	-	1,2,2	0.51	0	0,1,1	-	-
5	EDO	H	402	-	3,3,3	0.42	0	2,2,2	0.42	0
4	SCN	L	604	-	1,2,2	0.45	0	0,1,1	-	-
4	SCN	L	601	-	1,2,2	0.44	0	0,1,1	-	-
5	EDO	L	602	-	3,3,3	0.43	0	2,2,2	0.38	0
5	EDO	L	605	-	3,3,3	0.41	0	2,2,2	0.45	0
7	NAG	C	301	3	14,14,15	2.16	5 (35%)	17,19,21	2.19	4 (23%)

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
5	EDO	L	603	-	-	0/1/1/1	-
5	EDO	H	402	-	-	0/1/1/1	-
5	EDO	L	602	-	-	0/1/1/1	-
5	EDO	L	605	-	-	0/1/1/1	-
7	NAG	C	301	3	-	4/6/23/26	0/1/1/1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	C	301	NAG	O5-C1	4.66	1.51	1.43
7	C	301	NAG	C7-N2	3.88	1.46	1.34
7	C	301	NAG	O5-C5	2.71	1.48	1.43
7	C	301	NAG	C2-N2	2.68	1.50	1.46
7	C	301	NAG	C3-C2	-2.01	1.48	1.52

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	C	301	NAG	C1-O5-C5	6.24	120.55	112.19
7	C	301	NAG	C6-C5-C4	-3.36	104.76	113.02
7	C	301	NAG	O5-C5-C4	3.32	118.90	110.83
7	C	301	NAG	C2-N2-C7	2.14	125.77	122.90

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	C	301	NAG	C1-C2-N2-C7
7	C	301	NAG	O5-C5-C6-O6
7	C	301	NAG	C4-C5-C6-O6
7	C	301	NAG	C3-C2-N2-C7

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	C	301	NAG	1	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	H	214/224 (95%)	-0.04	5 (2%) 61 52	18, 43, 82, 100	0
2	L	214/214 (100%)	-0.02	4 (1%) 66 58	19, 39, 85, 124	0
3	C	48/141 (34%)	1.37	12 (25%) 2 1	45, 89, 123, 135	0
All	All	476/579 (82%)	0.11	21 (4%) 39 30	18, 43, 98, 135	0

All (21) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	C	174	ALA	4.3
2	L	214	CYS	3.9
3	C	135	ASN	3.6
3	C	193	LEU	3.4
3	C	159	PHE	3.4
3	C	171	LYS	3.3
3	C	196	CYS	3.3
3	C	126	CYS	2.9
2	L	209	PHE	2.9
1	H	126	PRO	2.8
3	C	177	TYR	2.8
2	L	170	ASP	2.8
3	C	127	VAL	2.7
3	C	194	ILE	2.6
3	C	173	TYR	2.6
1	H	134	GLY	2.6
3	C	192	ARG	2.6
1	H	31	SER	2.4
2	L	100	GLN	2.4
1	H	77	HIS	2.3
1	H	212	GLU	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 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
7	NAG	C	301	14/15	0.30	0.23	135,147,151,152	0
4	SCN	L	604	3/3	0.64	0.21	51,51,64,75	0
5	EDO	H	402	4/4	0.70	0.30	54,55,60,65	0
4	SCN	L	601	3/3	0.75	0.30	75,75,81,88	0
5	EDO	L	603	4/4	0.80	0.21	53,54,55,56	0
4	SCN	H	401	3/3	0.84	0.12	93,93,94,95	0
5	EDO	L	605	4/4	0.86	0.20	63,65,65,66	0
5	EDO	L	602	4/4	0.89	0.14	27,32,39,43	0
6	NA	L	606	1/1	0.97	0.23	36,36,36,36	0

6.5 Other polymers [i](#)

There are no such residues in this entry.