Full wwPDB X-ray Structure Validation Report ⓘ

Oct 27, 2023 – 04:16 AM EDT

PDB ID	:	3HS9
Title	:	Intersectin 1-peptide-AP2 beta ear complex
Authors	:	Vahedi-Faridi, A.; Pechstein, A.; Schaefer, J.G.; Saenger, W.; Haucke, V.
Deposited on	:	2009-06-10
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
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:

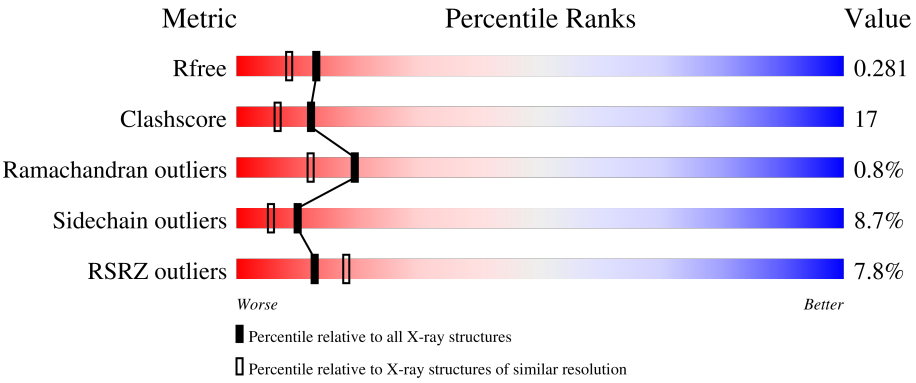
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

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}	130704	1479 (2.16-2.16)
Clashscore	141614	1585 (2.16-2.16)
Ramachandran outliers	138981	1560 (2.16-2.16)
Sidechain outliers	138945	1559 (2.16-2.16)
RSRZ outliers	127900	1456 (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 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 <=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	260	6% 59% 27% · 10%
2	P	12	33% 58% 25% 8% 8%

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 2085 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 AP-2 complex subunit beta-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	233	1858	1194	312	341	11	0	0	0

There are 23 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	678	MET	-	expression tag	UNP P62944
A	679	GLY	-	expression tag	UNP P62944
A	680	SER	-	expression tag	UNP P62944
A	681	SER	-	expression tag	UNP P62944
A	682	HIS	-	expression tag	UNP P62944
A	683	HIS	-	expression tag	UNP P62944
A	684	HIS	-	expression tag	UNP P62944
A	685	HIS	-	expression tag	UNP P62944
A	686	HIS	-	expression tag	UNP P62944
A	687	HIS	-	expression tag	UNP P62944
A	688	SER	-	expression tag	UNP P62944
A	689	SER	-	expression tag	UNP P62944
A	690	GLY	-	expression tag	UNP P62944
A	691	LEU	-	expression tag	UNP P62944
A	692	VAL	-	expression tag	UNP P62944
A	693	PRO	-	expression tag	UNP P62944
A	694	ARG	-	expression tag	UNP P62944
A	695	GLY	-	expression tag	UNP P62944
A	696	SER	-	expression tag	UNP P62944
A	697	HIS	-	expression tag	UNP P62944
A	698	MET	-	expression tag	UNP P62944
A	699	ALA	-	expression tag	UNP P62944
A	700	SER	-	expression tag	UNP P62944

- Molecule 2 is a protein called peptide from Intersectin-1, residues 841-851.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	P	11	Total	C	N	O	0	0	0
			94	61	15	18			

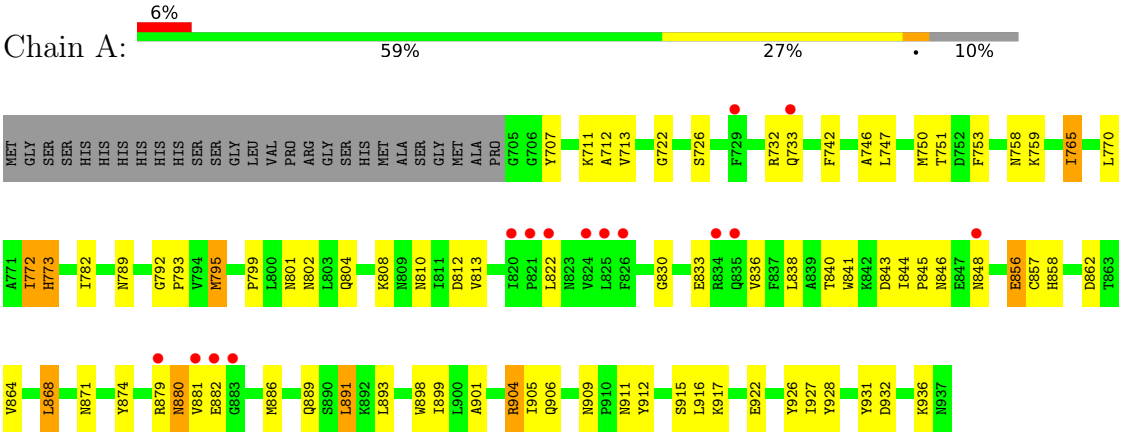
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	133	Total	O	0	0
			133	133		

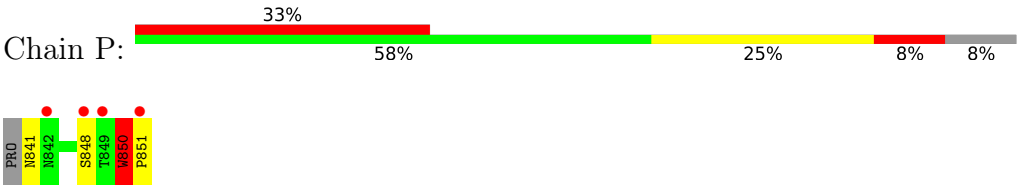
3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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: AP-2 complex subunit beta-1



• Molecule 2: peptide from Intersectin-1, residues 841-851



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	122.09Å 47.10Å 58.95Å 90.00° 97.66° 90.00°	Depositor
Resolution (Å)	50.00 – 2.15 27.79 – 1.95	Depositor EDS
% Data completeness (in resolution range)	95.7 (50.00-2.15) 95.8 (27.79-1.95)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	0.04	Depositor
$< I/\sigma(I) >$ [1]	2.22 (at 1.95Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.249 , 0.283 0.253 , 0.281	Depositor DCC
R_{free} test set	982 reflections (4.19%)	wwPDB-VP
Wilson B-factor (Å^2)	37.9	Xtriage
Anisotropy	0.852	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.36 , 54.6	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	2085	wwPDB-VP
Average B, all atoms (Å^2)	53.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 9.59% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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

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	0.60	0/1901	0.73	0/2583
2	P	0.92	1/99 (1.0%)	0.82	0/137
All	All	0.62	1/2000 (0.1%)	0.73	0/2720

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	P	850	TRP	CB-CG	-5.24	1.40	1.50

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	1858	0	1868	54	0
2	P	94	0	73	12	0
3	A	133	0	0	4	0
All	All	2085	0	1941	66	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 17.

All (66) 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:707:TYR:H	1:A:871:ASN:HD21	1.04	0.95
2:P:850:TRP:H	2:P:851:PRO:CD	1.80	0.92
1:A:751:THR:H	1:A:810:ASN:ND2	1.69	0.90
2:P:850:TRP:N	2:P:850:TRP:CD1	2.46	0.80
2:P:850:TRP:N	2:P:851:PRO:CD	2.47	0.74
2:P:850:TRP:N	2:P:851:PRO:HD2	2.03	0.72
2:P:850:TRP:H	2:P:851:PRO:HD3	1.54	0.72
2:P:850:TRP:N	2:P:850:TRP:HD1	1.85	0.72
2:P:850:TRP:H	2:P:851:PRO:HD2	1.54	0.70
1:A:751:THR:H	1:A:810:ASN:HD22	1.39	0.70
1:A:782:ILE:HG22	3:A:97:HOH:O	1.92	0.69
1:A:707:TYR:N	1:A:871:ASN:HD21	1.86	0.69
1:A:750:MET:HA	1:A:810:ASN:HD21	1.58	0.68
1:A:886:MET:SD	1:A:904:ARG:HG3	2.35	0.67
2:P:850:TRP:H	2:P:850:TRP:HD1	1.43	0.66
1:A:772:ILE:HG13	1:A:782:ILE:HD11	1.78	0.64
1:A:879:ARG:HD3	3:A:118:HOH:O	1.99	0.62
1:A:893:LEU:HD22	3:A:106:HOH:O	2.00	0.61
1:A:880:ASN:C	1:A:880:ASN:HD22	2.06	0.59
1:A:753:PHE:HB3	1:A:770:LEU:HD23	1.84	0.58
1:A:759:LYS:CG	1:A:793:PRO:HB2	2.33	0.58
1:A:833:GLU:HB3	1:A:836:VAL:HG23	1.85	0.58
1:A:874:TYR:O	1:A:889:GLN:HA	2.05	0.57
1:A:759:LYS:HG3	1:A:793:PRO:HB2	1.88	0.55
1:A:909:ASN:HD21	1:A:911:ASN:HB2	1.72	0.54
2:P:850:TRP:CD1	2:P:851:PRO:HD3	2.43	0.53
1:A:864:VAL:O	1:A:868:LEU:HB2	2.08	0.53
1:A:891:LEU:HD11	1:A:927:ILE:HD12	1.90	0.53
1:A:905:ILE:HG23	1:A:912:TYR:CE1	2.43	0.53
1:A:841:TRP:O	1:A:917:LYS:HE2	2.08	0.53
1:A:844:ILE:HB	1:A:917:LYS:HE3	1.91	0.53
1:A:857:CYS:HG	1:A:912:TYR:HE2	1.56	0.52
1:A:830:GLY:O	1:A:898:TRP:HZ3	1.94	0.51
1:A:808:LYS:HG3	1:A:813:VAL:HG22	1.93	0.51
1:A:765:ILE:HG22	1:A:789:ASN:OD1	2.11	0.50
1:A:845:PRO:O	1:A:848:ASN:HB2	2.12	0.50
1:A:881:VAL:O	1:A:882:GLU:HB2	2.11	0.49
2:P:850:TRP:HD1	2:P:851:PRO:HD3	1.78	0.49
1:A:711:LYS:HE3	3:A:25:HOH:O	2.13	0.48
1:A:840:THR:O	1:A:844:ILE:HD12	2.14	0.48
1:A:759:LYS:HB3	1:A:795:MET:HB3	1.96	0.47
1:A:773:HIS:CD2	1:A:773:HIS:H	2.33	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:801:ASN:HB3	1:A:822:LEU:HD11	1.96	0.47
1:A:901:ALA:HB2	1:A:916:LEU:HD23	1.97	0.47
1:A:856:GLU:OE2	1:A:858:HIS:HE1	1.98	0.46
1:A:891:LEU:HG	1:A:899:ILE:HB	1.97	0.46
1:A:810:ASN:HD22	1:A:810:ASN:H	1.63	0.46
2:P:841:ASN:HD22	2:P:841:ASN:N	2.15	0.45
1:A:758:ASN:ND2	1:A:804:GLN:OE1	2.42	0.45
1:A:712:ALA:O	1:A:713:VAL:C	2.54	0.45
1:A:765:ILE:HD12	1:A:792:GLY:HA3	1.99	0.45
1:A:799:PRO:HD2	1:A:802:ASN:HB2	1.97	0.45
1:A:822:LEU:HD22	1:A:926:TYR:CB	2.48	0.43
1:A:868:LEU:HD21	1:A:931:TYR:CE1	2.54	0.43
2:P:850:TRP:CD1	2:P:851:PRO:CD	3.01	0.43
1:A:772:ILE:CG1	1:A:782:ILE:HD11	2.48	0.42
1:A:880:ASN:C	1:A:880:ASN:ND2	2.73	0.42
1:A:932:ASP:O	1:A:936:LYS:HB2	2.20	0.42
1:A:765:ILE:HD12	1:A:792:GLY:CA	2.50	0.42
1:A:901:ALA:HA	1:A:915:SER:O	2.20	0.42
1:A:732:ARG:HD2	1:A:733:GLN:HE22	1.86	0.41
1:A:722:GLY:HA3	1:A:746:ALA:HB2	2.01	0.41
1:A:812:ASP:OD1	1:A:813:VAL:N	2.44	0.40
1:A:833:GLU:HB3	1:A:836:VAL:CG2	2.52	0.40
1:A:846:ASN:HA	1:A:917:LYS:NZ	2.36	0.40
1:A:901:ALA:HB2	1:A:916:LEU:CD2	2.52	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	231/260 (89%)	216 (94%)	14 (6%)	1 (0%)	34 29

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
2	P	9/12 (75%)	5 (56%)	3 (33%)	1 (11%)	0 0
All	All	240/272 (88%)	221 (92%)	17 (7%)	2 (1%)	19 12

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	P	850	TRP
1	A	856	GLU

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	209/230 (91%)	192 (92%)	17 (8%)	11 7
2	P	10/11 (91%)	8 (80%)	2 (20%)	1 0
All	All	219/241 (91%)	200 (91%)	19 (9%)	10 6

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	726	SER
1	A	742	PHE
1	A	747	LEU
1	A	765	ILE
1	A	772	ILE
1	A	773	HIS
1	A	795	MET
1	A	838	LEU
1	A	843	ASP
1	A	862	ASP
1	A	868	LEU
1	A	880	ASN
1	A	891	LEU
1	A	904	ARG

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Mol	Chain	Res	Type
1	A	906	GLN
1	A	922	GLU
1	A	928	TYR
2	P	848	SER
2	P	850	TRP

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

Mol	Chain	Res	Type
1	A	733	GLN
1	A	749	HIS
1	A	773	HIS
1	A	810	ASN
1	A	858	HIS
1	A	871	ASN
1	A	880	ASN
1	A	911	ASN
1	A	937	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 monosaccharides in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

5.7 Other polymers

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^{th} 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	233/260 (89%)	0.26	15 (6%)	19	26	35, 50, 77, 85	0
2	P	11/12 (91%)	2.65	4 (36%)	0	0	20, 70, 72, 73	0
All	All	244/272 (89%)	0.37	19 (7%)	13	18	20, 51, 76, 85	0

All (19) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	P	851	PRO	8.0
2	P	849	THR	4.2
2	P	848	SER	3.8
1	A	881	VAL	3.3
1	A	826	PHE	3.3
1	A	733	GLN	3.2
1	A	848	ASN	3.0
1	A	825	LEU	2.9
1	A	824	VAL	2.8
1	A	879	ARG	2.8
2	P	842	ASN	2.7
1	A	821	PRO	2.6
1	A	820	ILE	2.6
1	A	834	ARG	2.5
1	A	883	GLY	2.4
1	A	822	LEU	2.4
1	A	729	PHE	2.1
1	A	882	GLU	2.0
1	A	835	GLN	2.0

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

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates (i)

There are no monosaccharides 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.