

wwPDB X-ray Structure Validation Summary Report (i)

Aug 6, 2023 – 06:57 PM EDT

PDB ID	:	1KL5
Title	:	an engineered streptavidin with improved affinity for the strep-tag II peptide
		: SAm2-StrepII
Authors	:	Korndoerfer, I.P.; Skerra, A.
Deposited on	:	2001-12-11
Resolution	:	1.80 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 (i) 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 (1)) were used in the production of this report:

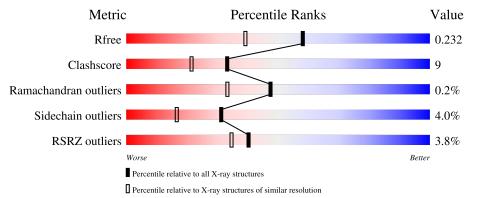
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.35
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)		
Ideal geometry (DNA, RNA)		
Validation Pipeline (wwPDB-VP)	:	2.35

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: $X\text{-}RAY\;DIFFRACTION$

The reported resolution of this entry is 1.80 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	$\begin{array}{c} \textbf{Whole archive} \\ \textbf{(\#Entries)} \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
R_{free}	130704	5950(1.80-1.80)
Clashscore	141614	6793(1.80-1.80)
Ramachandran outliers	138981	6697 (1.80-1.80)
Sidechain outliers	138945	6696 (1.80-1.80)
RSRZ outliers	127900	5850 (1.80-1.80)

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 cl	hain
			2%		
1	А	127		81%	12% • 5%
			2%		
1	В	127		85%	9% • 6%
			2%		
1	С	127		81%	10% • 6%
			6%		
1	D	127		74%	16% • 6%
			22%		
2	Ε	9	11%	44%	44%

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Mol	Chain	Length	Quality of chain			
2	F	9	44%	11%	44%	
2	G	9	44%	22%	33%	
2	Н	9	22%	44%	33%	



2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 3957 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.

Mol	Chain	Residues		Atoms			ZeroOcc	AltConf	Trace		
1	Λ	121	Total	С	Ν	Ο	0	0	0		
1	Л	121	905	566	160	179	0	0	0		
1	В	120	Total	С	Ν	Ο	0	0	0		
	D	120	897	561	159	177	0	0	0		
1	С	120	Total	С	Ν	Ο	0	0	0		
	U	120	897	561	159	177	0	0	U		
1	1 D	D	р	110	Total	С	Ν	Ο	0	0	0
		D 119	892	558	158	176		0	U		

• Molecule 1 is a protein called streptavidin.

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
А	13	MET	-	initiating methionine	UNP P22629
А	44	ILE	GLU	engineered mutation	UNP P22629
А	45	GLY	SER	engineered mutation	UNP P22629
А	47	ARG	VAL	engineered mutation	UNP P22629
В	13	MET	-	initiating methionine	UNP P22629
В	44	ILE	GLU	engineered mutation	UNP P22629
В	45	GLY	SER	engineered mutation	UNP P22629
В	47	ARG	VAL	engineered mutation	UNP P22629
С	13	MET	-	initiating methionine	UNP P22629
С	44	ILE	GLU	engineered mutation	UNP P22629
С	45	GLY	SER	engineered mutation	UNP P22629
С	47	ARG	VAL	engineered mutation	UNP P22629
D	13	MET	-	initiating methionine	UNP P22629
D	44	ILE	GLU	engineered mutation	UNP P22629
D	45	GLY	SER	engineered mutation	UNP P22629
D	47	ARG	VAL	engineered mutation	UNP P22629

• Molecule 2 is a protein called strep-tag II.



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
2	Е	5	Total C N O 43 28 8 7	0	0	0
2	F	5	Total C N O 46 30 8 8	0	0	0
2	G	6	Total C N O 55 36 10 9	0	0	0
2	Н	6	Total C N O 55 36 10 9	0	0	0

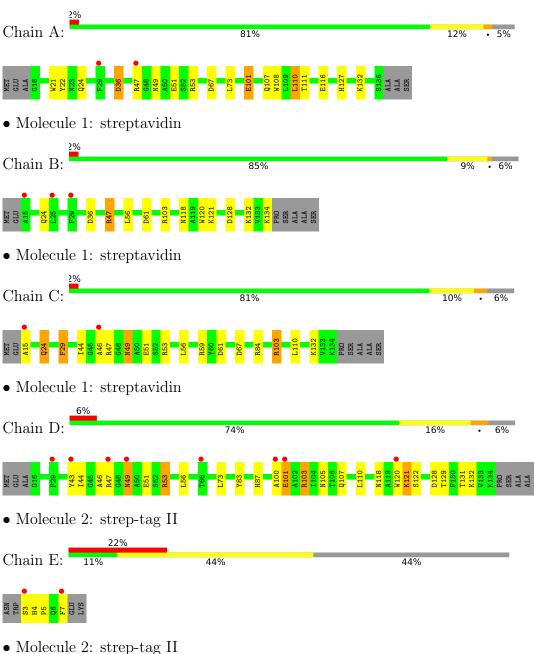
• Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	А	43	Total O 43 43	0	0
3	В	43	Total O 43 43	0	0
3	С	36	$\begin{array}{cc} \text{Total} & \text{O} \\ 36 & 36 \end{array}$	0	0
3	D	41	Total O 41 41	0	0
3	Ε	1	Total O 1 1	0	0
3	F	1	Total O 1 1	0	0
3	Н	2	Total O 2 2	0	0



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.



 \bullet Molecule 1: strept avidin



Chain F:	44%	11%	44%
ASN TRP SER H H E8 LYS			
• Molecule 2	: strep-tag II		
1	1%		
Chain G:	44%	22%	33%
ASN TRP BER H4 F7 K9 K9			
• Molecule 2	: strep-tag II		
Chain H:	1% 22%	44%	33%
ASN TRP SER P5 P5 E8 K9			



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants	58.39Å 86.58Å 47.23Å	Depositor
a, b, c, α , β , γ	90.00° 99.10° 90.00°	Depositor
Resolution (Å)	48.00 - 1.80	Depositor
	47.99 - 1.79	EDS
% Data completeness	94.6 (48.00-1.80)	Depositor
(in resolution range)	94.3 (47.99-1.79)	EDS
R _{merge}	(Not available)	Depositor
R_{sym}	0.04	Depositor
$< I/\sigma(I) > 1$	$2.53 (at 1.79 \text{\AA})$	Xtriage
Refinement program	CNS, REFMAC	Depositor
B B.	0.178 , 0.221	Depositor
R, R_{free}	0.190 , 0.232	DCC
R_{free} test set	2032 reflections $(4.95%)$	wwPDB-VP
Wilson B-factor $(Å^2)$	21.6	Xtriage
Anisotropy	0.253	Xtriage
Bulk solvent $k_{sol}(e/Å^3), B_{sol}(Å^2)$	0.37, 50.8	EDS
L-test for twinning ²	$ \langle L \rangle = 0.50, \langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	3957	wwPDB-VP
Average B, all atoms $(Å^2)$	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 7.14% of the height of the origin peak. No significant pseudotranslation is detected.

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.



¹Intensities estimated from amplitudes.

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		
	Ullalli	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	А	0.86	0/928	1.41	6/1269~(0.5%)	
1	В	0.87	0/919	1.47	2/1256~(0.2%)	
1	С	0.86	0/919	1.47	9/1256~(0.7%)	
1	D	0.78	0/914	1.38	8/1249~(0.6%)	
2	Ε	0.64	0/45	1.04	0/60	
2	F	0.95	0/48	1.27	0/64	
2	G	0.90	0/57	1.69	2/75~(2.7%)	
2	Н	0.74	0/57	0.95	0/75	
All	All	0.84	0/3887	1.43	27/5304~(0.5%)	

There are no bond length outliers.

The worst 5 of 27 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
1	D	128	ASP	CB-CG-OD2	10.39	127.65	118.30
1	А	110	LEU	CB-CG-CD1	-8.65	96.29	111.00
2	G	7	PHE	CB-CG-CD1	-8.25	115.03	120.80
1	С	103	ARG	NE-CZ-NH1	7.67	124.14	120.30
2	G	7	PHE	CB-CG-CD2	7.33	125.93	120.80

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.



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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	А	905	0	855	18	0
1	В	897	0	848	10	0
1	С	897	0	848	13	1
1	D	892	0	843	31	0
2	Е	43	0	35	6	0
2	F	46	0	36	0	0
2	G	55	0	49	1	0
2	Н	55	0	49	2	0
3	А	43	0	0	1	0
3	В	43	0	0	4	1
3	С	36	0	0	3	0
3	D	41	0	0	4	0
3	Е	1	0	0	0	0
3	F	1	0	0	0	0
3	Н	2	0	0	0	0
All	All	3957	0	3563	63	1

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 9.

The worst 5 of 63 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:D:120:TRP:HD1	2:E:7:PHE:CE1	1.49	1.28
1:D:120:TRP:CD1	2:E:7:PHE:CE1	2.28	1.21
1:A:127:HIS:O	1:D:120:TRP:CZ2	2.03	1.12
1:A:127:HIS:O	1:D:120:TRP:CH2	2.07	1.06
1:D:120:TRP:CD1	2:E:7:PHE:HE1	1.69	1.04

All (1) 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 (\AA)	Clash overlap (Å)
1:C:132:LYS:NZ	3:B:176:HOH:O[1_455]	2.13	0.07



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	Percentile	\mathbf{s}
1	А	119/127~(94%)	116 (98%)	3~(2%)	0	100 100	
1	В	118/127~(93%)	115~(98%)	3~(2%)	0	100 100	
1	С	118/127~(93%)	117~(99%)	1 (1%)	0	100 100	
1	D	117/127~(92%)	114 (97%)	2(2%)	1 (1%)	17 6	
2	Ε	3/9~(33%)	3 (100%)	0	0	100 100	
2	F	3/9~(33%)	3~(100%)	0	0	100 100	
2	G	4/9~(44%)	4 (100%)	0	0	100 100	
2	Н	4/9~(44%)	4 (100%)	0	0	100 100	
All	All	486/544 (89%)	476 (98%)	9(2%)	1 (0%)	47 33	

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	101	GLU

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent side chain 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	А	89/92~(97%)	86~(97%)	3~(3%)	37 22
1	В	87/92~(95%)	84 (97%)	3(3%)	37 22
1	С	87/92~(95%)	83~(95%)	4(5%)	27 13
1	D	87/92~(95%)	84 (97%)	3(3%)	37 22

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Mol	Chain	Analysed	Rotameric	Outliers	Percer	ntiles
2	Ε	5/9~(56%)	5~(100%)	0	100	100
2	F	5/9~(56%)	4 (80%)	1 (20%)	1	0
2	G	6/9~(67%)	6 (100%)	0	100	100
2	Н	6/9~(67%)	5~(83%)	1 (17%)	2	0
All	All	372/404~(92%)	357~(96%)	15~(4%)	31	16

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5 of 15 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	С	29	PHE
2	F	8	GLU
1	С	49	ASN
2	Н	9	LYS
1	D	73	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 9 such sidechains are listed below:

Mol	Chain	Res	Type
2	G	6	GLN
2	Н	6	GLN
1	D	87	HIS
1	D	105	ASN
2	Е	6	GLN

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 monosaccharides in this entry.



5.6 Ligand geometry (i)

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 (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, 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	$\langle RSRZ \rangle$	#RSRZ>2	$OWAB(A^2)$	Q<0.9
1	А	121/127~(95%)	0.09	2 (1%) 70 66	13, 22, 42, 56	0
1	В	120/127~(94%)	0.07	3 (2%) 57 52	13, 20, 42, 46	0
1	С	120/127~(94%)	0.07	2 (1%) 70 66	13, 20, 41, 49	0
1	D	119/127~(93%)	0.27	8 (6%) 17 14	14, 23, 47, 56	0
2	Ε	5/9~(55%)	2.36	2 (40%) 0 0	36, 40, 46, 51	0
2	F	5/9~(55%)	0.19	0 100 100	20, 22, 29, 41	0
2	G	6/9~(66%)	0.98	1 (16%) 1 1	22, 27, 46, 50	0
2	Н	6/9~(66%)	0.90	1 (16%) 1 1	24, 29, 51, 59	0
All	All	502/544~(92%)	0.17	19 (3%) 40 35	13, 22, 43, 59	0

The worst 5 of 19 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	120	TRP	9.1
2	Е	3	SER	5.0
1	D	101	GLU	4.7
1	D	29	PHE	4.3
1	А	47	ARG	4.0

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 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.

