W O R L D W I D E

wwPDB

P R O T E I N   D A T A   B A N K

wwPDB X-ray Structure Validation Summary Report (i)

Feb 10, 2024 – 10:28 PM EST

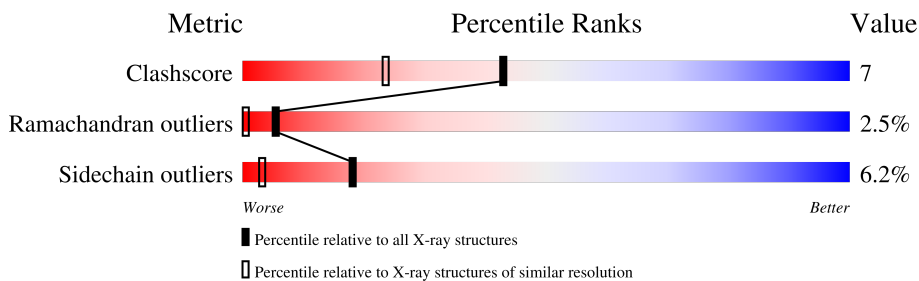|		
PDB ID	:	2RTO
Title	:	STREPTAVIDIN-2-IMINOBIOTIN COMPLEX, PH 2.6, SPACE GROUP I222
Authors	:	Katz, B.A.
Deposited on	:	1997-09-11
Resolution	:	1.58 Å(reported)

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 1.58 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	Percentile Ranks	Value
Clashscore		7
Ramachandran outliers		2.5%
Sidechain outliers		6.2%

Worse   *Better*

▮ Percentile relative to all X-ray structures

▯ Percentile relative to X-ray structures of similar resolution

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	141614	5861 (1.60-1.56)
Ramachandran outliers	138981	5708 (1.60-1.56)
Sidechain outliers	138945	5703 (1.60-1.56)

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%

| Mol	Chain	Length	Quality of chain
1	B	135	66% 19% 5% · 9%
1	D	135	64% 18% 7% · 10%

2 Entry composition ⓘ

There are 3 unique types of molecules in this entry. The entry contains 4198 atoms, of which 2079 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 STREPTAVIDIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	B	123	Total	C	H	N	O	88	13	0
			1943	628	939	171	205			
1	D	121	Total	C	H	N	O	64	12	0
			1891	612	910	167	202			

- Molecule 2 is 2-IMINOBIOTIN (three-letter code: IMI) (formula: $C_{10}H_{17}N_3O_2S$).
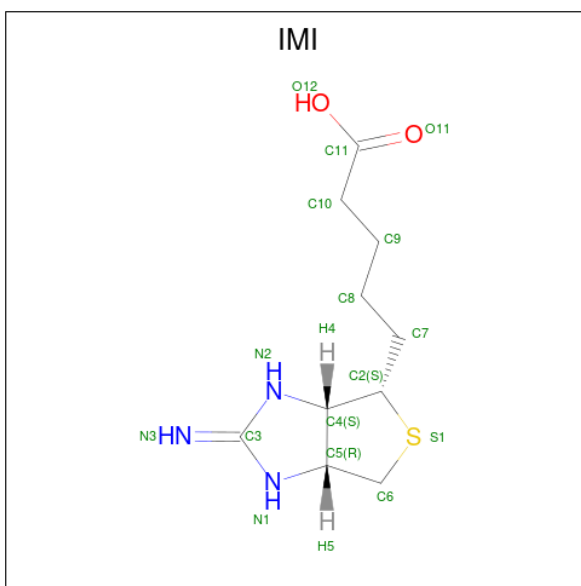
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	B	1	Total	C	H	N	O	S	0	0
			33	10	17	3	2	1		
2	D	1	Total	C	H	N	O	S	0	0
			33	10	17	3	2	1		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	B	45	Total H O 127 82 45			0	9
3	D	57	Total H O 171 114 57			0	5

3 Residue-property plots ⓘ

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. 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.
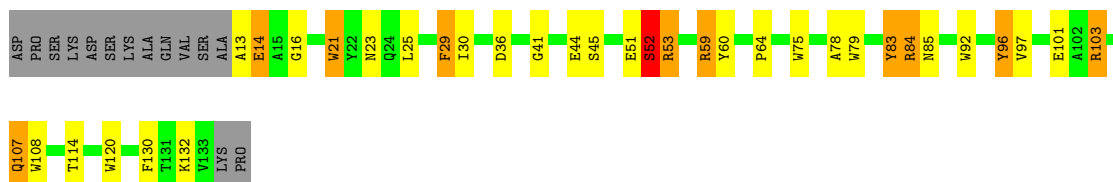
• Molecule 1: STREPTAVIDIN
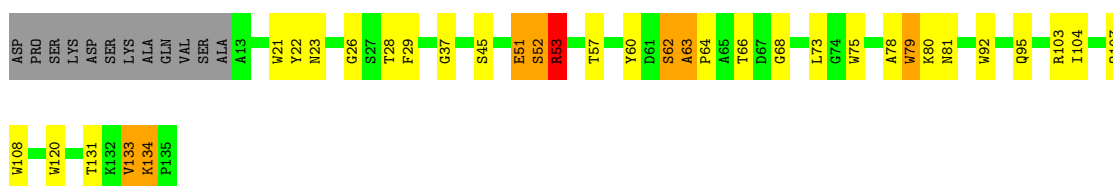
• Molecule 1: STREPTAVIDIN

4 Data and refinement statistics ⓘ

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α, β, γ	95.06Å 105.84Å 48.01Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	7.50 – 1.58 33.30 – 1.30	Depositor EDS
% Data completeness (in resolution range)	71.0 (7.50-1.58) 50.2 (33.30-1.30)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.27 (at 1.30Å)	Xtriage
Refinement program	X-PLOR	Depositor
R, R_{free}	0.208 , 0.253 0.234 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å^2)	10.4	Xtriage
Anisotropy	0.408	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 87.9	EDS
L-test for twinning[2]	$< |L| > = 0.49, < L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	4198	wwPDB-VP
Average B, all atoms (Å^2)	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 12.65% of the height of the origin peak. No significant pseudotranslation is detected.*

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[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 ⓘ

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

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	B	1.42	4/1043 (0.4%)	1.75	31/1428 (2.2%)
1	D	1.39	3/1014 (0.3%)	1.88	38/1389 (2.7%)
All	All	1.41	7/2057 (0.3%)	1.82	69/2817 (2.4%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	B	0	4
1	D	0	2
All	All	0	6

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	45	SER	CA-CB	7.04	1.63	1.52
1	B	45	SER	CA-CB	6.25	1.62	1.52
1	B	21	TRP	CG-CD2	-5.74	1.33	1.43
1	B	108	TRP	CA-CB	5.38	1.65	1.53
1	D	52	SER	CA-CB	5.23	1.60	1.52

The worst 5 of 69 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	21	TRP	CD1-NE1-CE2	10.59	118.53	109.00
1	D	120	TRP	CD1-NE1-CE2	10.42	118.38	109.00
1	B	21	TRP	CD1-NE1-CE2	10.20	118.18	109.00
1	D	75	TRP	CD1-NE1-CE2	9.93	117.94	109.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	D	92	TRP	CD1-NE1-CE2	9.93	117.94	109.00

There are no chirality outliers.

5 of 6 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	103	ARG	Sidechain
1	B	134	LYS	Peptide
1	B	53	ARG	Sidechain
1	B	63[A]	ALA	Peptide
1	D	53	ARG	Sidechain

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	B	1004	939	927	15	6
1	D	981	910	901	13	0
2	B	16	17	15	2	0
2	D	16	17	15	1	0
3	B	45	82	0	0	3
3	D	57	114	0	0	4
All	All	2119	2079	1858	25	8

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 7.

The worst 5 of 25 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:B:22[B]:TYR:CE1	1:B:131:THR:HB	2.12	0.83
1:B:37:GLY:HA2	1:B:60[A]:TYR:CE1	2.36	0.60
1:D:13:ALA:N	1:D:96:TYR:HH	2.01	0.57
1:D:51:GLU:HB3	1:D:84:ARG:HG3	1.90	0.53
1:B:95:GLN:NE2	1:D:114:THR:H	2.07	0.51

The worst 5 of 8 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)
3:B:1491[C]:HOH:O	3:B:1491[C]:HOH:O[3_655]	0.91	1.29
3:B:1464[C]:HOH:O	3:B:1464[C]:HOH:O[3_655]	1.42	0.78
1:B:28:THR:OG1	3:D:952:HOH:H1[6_554]	1.14	0.46
1:B:80:LYS:HZ2	3:B:966:HOH:H2[6_554]	1.23	0.37
1:B:53:ARG:O	3:D:1478:HOH:H1[6_554]	1.25	0.35

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	B	134/135 (99%)	129 (96%)	2 (2%)	3 (2%)	6	1
1	D	131/135 (97%)	122 (93%)	4 (3%)	5 (4%)	3	0
All	All	265/270 (98%)	251 (95%)	6 (2%)	8 (3%)	5	0

5 of 8 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	52	SER
1	D	16	GLY
1	D	52	SER
1	B	64[A]	PRO
1	B	64[B]	PRO

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	B	100/100 (100%)	92 (92%)	8 (8%)	12	1
1	D	97/100 (97%)	90 (93%)	7 (7%)	14	2
All	All	197/200 (98%)	182 (92%)	15 (8%)	18	2

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

Mol	Chain	Res	Type
1	B	133	VAL
1	D	107[A]	GLN
1	D	29[A]	PHE
1	D	107[B]	GLN
1	D	97	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	95	GLN

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 ⓘ

2 ligands are 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	$\#|Z| > 2$
2	IMI	B	300	-	17,17,17	1.66	5 (29%)	20,23,23	3.06	6 (30%)
2	IMI	D	300	-	17,17,17	1.70	5 (29%)	20,23,23	2.90	7 (35%)

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
2	IMI	B	300	-	-	3/7/28/28	0/2/2/2
2	IMI	D	300	-	-	3/7/28/28	0/2/2/2

The worst 5 of 10 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	300	IMI	C3-N1	-2.89	1.30	1.35
2	B	300	IMI	C5-N1	2.88	1.50	1.46
2	D	300	IMI	C3-N2	-2.86	1.30	1.35
2	B	300	IMI	C3-N2	-2.77	1.30	1.35
2	D	300	IMI	C4-N2	2.67	1.50	1.45

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	300	IMI	C5-C6-S1	10.34	115.16	106.31
2	D	300	IMI	C5-C6-S1	8.88	113.92	106.31
2	D	300	IMI	C4-C2-S1	6.16	111.07	105.20
2	B	300	IMI	C4-C2-S1	5.98	110.90	105.20
2	D	300	IMI	N1-C3-N2	3.25	112.53	109.20

There are no chirality outliers.

5 of 6 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	D	300	IMI	C4-C2-C7-C8
2	B	300	IMI	C11-C10-C9-C8
2	D	300	IMI	C9-C10-C11-O12
2	D	300	IMI	C9-C10-C11-O11

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Mol	Chain	Res	Type	Atoms
2	B	300	IMI	C9-C10-C11-O12

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	300	IMI	2	0
2	D	300	IMI	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 ⓘ

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.