



Full wwPDB X-ray Structure Validation Report ⓘ

May 16, 2020 – 11:29 am BST

PDB ID : 3LT6
Title : A transition from strong right-handed to canonical left-handed supercoiling in a conserved coiled coil segment of trimeric autotransporter adhesins - the Mutant 4 structure
Authors : Zeth, K.; Hernandez-Alvarez, B.; Lupas, A.N.
Deposited on : 2010-02-15
Resolution : 1.80 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.11
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) : 2.11

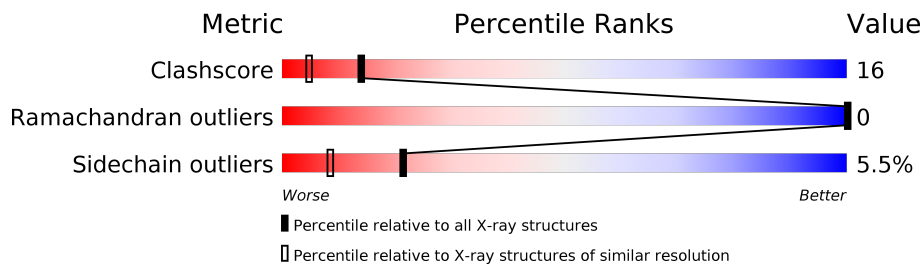
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.80 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	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	141614	6793 (1.80-1.80)
Ramachandran outliers	138981	6697 (1.80-1.80)
Sidechain outliers	138945	6696 (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 on 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 $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	A	64	58% 22% 5% 16%
1	B	64	66% 28% 5%
1	C	64	61% 27% 5% 8%
1	D	64	73% 23% .
1	E	64	69% 16% 5% 11%
1	F	64	70% 23% 5% .

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 2921 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 Adhesin yadA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	Se			
1	A	54	442	272	83	86	1	0	0	0
1	B	61	483	297	90	95	1	0	0	0
1	C	59	469	288	88	92	1	0	0	0
1	D	62	495	304	91	98	2	0	2	0
1	E	57	465	285	87	92	1	0	1	0
1	F	63	502	307	93	101	1	0	1	0

There are 48 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	28	MSE	PHE	CONFLICT	UNP P31489
A	29	HIS	ARG	CONFLICT	UNP P31489
A	32	GLU	ASP	CONFLICT	UNP P31489
A	39	GLU	ASP	CONFLICT	UNP P31489
A	40	LYS	THR	CONFLICT	UNP P31489
A	42	LEU	VAL	CONFLICT	UNP P31489
A	43	LEU	ASP	CONFLICT	UNP P31489
A	45	LEU	GLY	CONFLICT	UNP P31489
B	28	MSE	PHE	CONFLICT	UNP P31489
B	29	HIS	ARG	CONFLICT	UNP P31489
B	32	GLU	ASP	CONFLICT	UNP P31489
B	39	GLU	ASP	CONFLICT	UNP P31489
B	40	LYS	THR	CONFLICT	UNP P31489
B	42	LEU	VAL	CONFLICT	UNP P31489
B	43	LEU	ASP	CONFLICT	UNP P31489
B	45	LEU	GLY	CONFLICT	UNP P31489
C	28	MSE	PHE	CONFLICT	UNP P31489

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Chain	Residue	Modelled	Actual	Comment	Reference
C	29	HIS	ARG	CONFLICT	UNP P31489
C	32	GLU	ASP	CONFLICT	UNP P31489
C	39	GLU	ASP	CONFLICT	UNP P31489
C	40	LYS	THR	CONFLICT	UNP P31489
C	42	LEU	VAL	CONFLICT	UNP P31489
C	43	LEU	ASP	CONFLICT	UNP P31489
C	45	LEU	GLY	CONFLICT	UNP P31489
D	28	MSE	PHE	CONFLICT	UNP P31489
D	29	HIS	ARG	CONFLICT	UNP P31489
D	32	GLU	ASP	CONFLICT	UNP P31489
D	39	GLU	ASP	CONFLICT	UNP P31489
D	40	LYS	THR	CONFLICT	UNP P31489
D	42	LEU	VAL	CONFLICT	UNP P31489
D	43	LEU	ASP	CONFLICT	UNP P31489
D	45	LEU	GLY	CONFLICT	UNP P31489
E	28	MSE	PHE	CONFLICT	UNP P31489
E	29	HIS	ARG	CONFLICT	UNP P31489
E	32	GLU	ASP	CONFLICT	UNP P31489
E	39	GLU	ASP	CONFLICT	UNP P31489
E	40	LYS	THR	CONFLICT	UNP P31489
E	42	LEU	VAL	CONFLICT	UNP P31489
E	43	LEU	ASP	CONFLICT	UNP P31489
E	45	LEU	GLY	CONFLICT	UNP P31489
F	28	MSE	PHE	CONFLICT	UNP P31489
F	29	HIS	ARG	CONFLICT	UNP P31489
F	32	GLU	ASP	CONFLICT	UNP P31489
F	39	GLU	ASP	CONFLICT	UNP P31489
F	40	LYS	THR	CONFLICT	UNP P31489
F	42	LEU	VAL	CONFLICT	UNP P31489
F	43	LEU	ASP	CONFLICT	UNP P31489
F	45	LEU	GLY	CONFLICT	UNP P31489

- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	20	Total O 20 20	0	0
2	B	22	Total O 22 22	0	0
2	C	11	Total O 11 11	0	0
2	D	4	Total O 4 4	0	0

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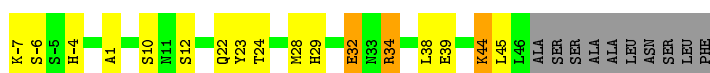
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	E	5	Total	O	0	0
			5	5		
2	F	3	Total	O	0	0
			3	3		

3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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: Adhesin yadA

Chain A: 



- Molecule 1: Adhesin yadA

Chain B: 



- Molecule 1: Adhesin yadA

Chain C: 



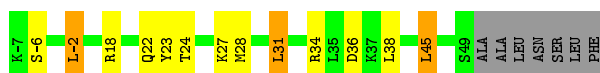
- Molecule 1: Adhesin yadA

Chain D: 



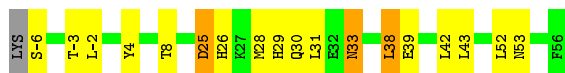
- Molecule 1: Adhesin yadA

Chain E: 



- Molecule 1: Adhesin yadA

Chain F: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	40.00Å 115.76Å 48.08Å 90.00° 89.93° 90.00°	Depositor
Resolution (Å)	19.30 – 1.80 19.29 – 1.80	Depositor EDS
% Data completeness (in resolution range)	98.4 (19.30-1.80) 91.9 (19.29-1.80)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.00 (at 1.80Å)	Xtriage
Refinement program	REFMAC 5.5.0063	Depositor
R, R_{free}	0.227 , 0.266 0.281 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	24.0	Xtriage
Anisotropy	0.130	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 51.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.58$, $\langle L^2 \rangle = 0.43$	Xtriage
Estimated twinning fraction	0.039 for h,-k,-l	Xtriage
Reported twinning fraction	0.760 for H, K, L 0.240 for h,-k,-l	Depositor
Outliers	0 of 37255 reflections	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	2921	wwPDB-VP
Average B, all atoms (Å ²)	20.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 9.83% 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](#)

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	1.11	2/445 (0.4%)	1.03	0/593
1	B	0.91	0/486	1.04	1/651 (0.2%)
1	C	0.97	0/472	1.06	3/632 (0.5%)
1	D	0.99	0/504	0.98	0/675
1	E	1.07	0/471	1.11	3/628 (0.5%)
1	F	0.93	0/505	0.95	1/677 (0.1%)
All	All	1.00	2/2883 (0.1%)	1.03	8/3856 (0.2%)

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	F	0	1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	32	GLU	CG-CD	-5.92	1.43	1.51
1	A	23	TYR	CD1-CE1	-5.24	1.31	1.39

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	B	34	ARG	NE-CZ-NH1	5.46	123.03	120.30
1	E	36	ASP	CB-CG-OD1	5.39	123.15	118.30
1	E	34	ARG	NE-CZ-NH2	-5.27	117.66	120.30
1	F	25	ASP	CB-CG-OD1	5.22	123.00	118.30
1	C	24	THR	CA-CB-CG2	-5.17	105.16	112.40
1	C	34	ARG	NE-CZ-NH2	-5.09	117.76	120.30
1	E	-2	LEU	CB-CG-CD2	-5.06	102.39	111.00
1	C	18	ARG	NE-CZ-NH2	-5.04	117.78	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	F	-6	SER	Peptide

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	A	442	0	462	19	0
1	B	483	0	499	24	0
1	C	469	0	486	21	0
1	D	495	0	511	33	0
1	E	465	0	485	16	0
1	F	502	0	515	28	0
2	A	20	0	0	5	0
2	B	22	0	0	4	0
2	C	11	0	0	0	0
2	D	4	0	0	0	0
2	E	5	0	0	1	0
2	F	3	0	0	1	0
All	All	2921	0	2958	91	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 16.

All (91) 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:46:LEU:HD11	2:E:60:HOH:O	1.40	1.21
1:A:44:LYS:HE3	2:A:76:HOH:O	1.54	1.06
1:D:28[A]:MSE:CE	1:E:31:LEU:HD22	1.94	0.96
1:D:28[A]:MSE:HE1	1:E:31:LEU:HD22	1.47	0.95
1:D:-3:THR:O	1:D:0:THR:HG22	1.77	0.85
1:F:4:TYR:O	1:F:8[B]:THR:HG22	1.75	0.85
1:D:38:LEU:HD23	1:E:38:LEU:HD13	1.60	0.83
1:D:0:THR:HG23	1:F:-2:LEU:HD13	1.62	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:29:HIS:CD2	2:B:57:HOH:O	2.33	0.80
1:A:-7:LYS:N	1:A:-6:SER:HA	1.94	0.79
1:D:31:LEU:HD12	1:F:28:MSE:CE	2.13	0.79
1:D:0:THR:CG2	1:F:-2:LEU:HD13	2.13	0.79
1:B:18:ARG:O	1:B:22:GLN:HG3	1.83	0.78
1:E:-6:SER:HB2	1:F:-3:THR:OG1	1.84	0.78
1:D:24:THR:O	1:D:28[A]:MSE:HG2	1.85	0.77
1:B:36:ASP:OD1	1:C:34:ARG:NH2	2.18	0.73
1:D:23:TYR:CZ	1:D:27:LYS:HE3	2.26	0.71
1:D:28[A]:MSE:SE	1:E:31:LEU:HD22	2.42	0.70
1:D:31:LEU:HD12	1:F:28:MSE:SE	2.42	0.69
1:A:38:LEU:HD13	1:C:38:LEU:HD23	1.73	0.68
1:A:34:ARG:NH1	1:C:32:GLU:OE1	2.27	0.66
1:B:56:PHE:O	2:B:70:HOH:O	2.14	0.65
1:C:53:ASN:HA	1:C:54:SER:C	2.17	0.65
1:A:39:GLU:OE2	1:B:34:ARG:NH2	2.30	0.65
1:D:38:LEU:HD11	1:F:42:LEU:HD12	1.79	0.64
1:A:1:ALA:HB3	2:A:79:HOH:O	1.97	0.64
1:A:-7:LYS:H3	1:A:-6:SER:HA	1.62	0.62
1:A:-6:SER:HB2	1:B:-3:THR:OG1	2.00	0.61
1:A:24:THR:O	1:A:28:MSE:HG2	2.01	0.61
1:C:36:ASP:OD2	1:E:18:ARG:NH1	2.32	0.61
1:D:31:LEU:HD13	1:F:31:LEU:HD23	1.82	0.60
1:B:28:MSE:SE	1:C:31:LEU:HD12	2.52	0.60
1:B:52:LEU:HB3	1:C:52:LEU:HD21	1.85	0.58
1:D:5:THR:O	1:D:9:VAL:HG23	2.02	0.58
1:E:24:THR:O	1:E:28:MSE:HG2	2.04	0.57
1:D:0:THR:HG23	1:F:-2:LEU:CD1	2.34	0.57
1:D:31:LEU:CD1	1:F:28:MSE:CE	2.81	0.57
1:B:56:PHE:CB	2:B:58:HOH:O	2.53	0.56
1:D:28[A]:MSE:CE	1:E:31:LEU:CD2	2.78	0.55
1:D:27:LYS:HB3	1:F:28:MSE:HE2	1.87	0.55
1:F:4:TYR:O	1:F:8[A]:THR:HG23	2.08	0.54
1:D:28[A]:MSE:SE	1:E:31:LEU:CD2	3.06	0.54
1:A:22:GLN:HG3	2:A:74:HOH:O	2.08	0.54
1:A:29:HIS:CE1	2:A:64:HOH:O	2.61	0.53
1:D:27:LYS:O	1:F:28:MSE:CE	2.57	0.53
1:B:40:LYS:HG2	1:B:44:LYS:HE2	1.91	0.53
1:A:39:GLU:HG2	1:B:38:LEU:HD11	1.90	0.53
1:A:-7:LYS:H2	1:A:-6:SER:HA	1.74	0.52
1:C:10:SER:O	1:C:14:LYS:HG3	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:-4:HIS:HB3	2:A:75:HOH:O	2.09	0.52
1:D:28[A]:MSE:SE	1:E:27:LYS:HB3	2.60	0.51
1:A:39:GLU:HG2	1:B:38:LEU:CD1	2.40	0.51
1:D:38:LEU:CD1	1:F:42:LEU:HD12	2.40	0.51
1:B:28:MSE:SE	1:C:31:LEU:CD1	3.08	0.51
1:F:26:HIS:CE1	1:F:30:GLN:NE2	2.79	0.51
1:A:32:GLU:HG3	1:B:31:LEU:HD13	1.93	0.50
1:C:3:SER:O	1:C:7:VAL:HG23	2.12	0.49
1:D:0:THR:HG21	1:F:-2:LEU:HD13	1.93	0.49
1:B:42:LEU:HD12	1:C:38:LEU:HD12	1.94	0.49
1:B:39:GLU:O	1:B:43:LEU:HD13	2.12	0.49
1:C:49:SER:O	1:C:53:ASN:ND2	2.47	0.48
1:D:27:LYS:O	1:F:28:MSE:HE2	2.14	0.47
1:A:45:LEU:HD23	1:A:45:LEU:C	2.35	0.47
1:D:31:LEU:HD12	1:F:28:MSE:HE1	1.94	0.47
1:D:38:LEU:HD11	1:F:38:LEU:HG	1.98	0.46
1:C:29:HIS:ND1	1:E:22[A]:GLN:HG2	2.30	0.46
1:B:31:LEU:HD23	1:C:31:LEU:HD22	1.97	0.46
1:E:31:LEU:HB3	1:F:31:LEU:CD2	2.46	0.46
1:B:26:HIS:N	1:B:26:HIS:CD2	2.84	0.46
1:B:31:LEU:HD23	1:C:31:LEU:HD13	1.98	0.46
1:C:29:HIS:ND1	1:E:22[A]:GLN:CG	2.79	0.46
1:B:42:LEU:HD12	1:C:38:LEU:CD1	2.46	0.45
1:A:45:LEU:HD12	1:C:46:LEU:HG	1.97	0.45
1:F:33:ASN:HB2	2:F:57:HOH:O	2.16	0.45
1:D:28[A]:MSE:HB3	1:D:28[A]:MSE:HE3	1.74	0.45
1:F:25:ASP:O	1:F:29:HIS:HB2	2.17	0.45
1:F:43:LEU:HA	1:F:43:LEU:HD23	1.81	0.44
1:D:27:LYS:O	1:F:28:MSE:HE1	2.18	0.44
1:D:31:LEU:CD1	1:F:28:MSE:HE3	2.48	0.44
1:B:9:VAL:HG13	1:C:12:SER:HB2	2.00	0.42
1:B:40:LYS:HB2	1:B:40:LYS:HE3	1.94	0.42
1:D:41:ARG:CZ	1:F:43:LEU:HD21	2.49	0.42
1:D:52:LEU:HD21	1:F:52:LEU:HB3	2.00	0.42
1:A:-7:LYS:N	1:A:-6:SER:CA	2.77	0.41
1:E:45:LEU:O	1:E:45:LEU:HD22	2.20	0.41
1:B:26:HIS:CD2	2:B:71:HOH:O	2.73	0.41
1:B:22:GLN:O	1:B:26:HIS:CD2	2.74	0.41
1:C:29:HIS:ND1	1:E:22[A]:GLN:CD	2.74	0.41
1:C:53:ASN:ND2	1:C:53:ASN:N	2.68	0.41
1:D:-3:THR:HG23	1:F:-2:LEU:HB2	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:23:TYR:CZ	1:E:27:LYS:HE2	2.56	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	52/64 (81%)	51 (98%)	1 (2%)	0	100	100
1	B	59/64 (92%)	59 (100%)	0	0	100	100
1	C	57/64 (89%)	56 (98%)	1 (2%)	0	100	100
1	D	62/64 (97%)	62 (100%)	0	0	100	100
1	E	56/64 (88%)	55 (98%)	1 (2%)	0	100	100
1	F	62/64 (97%)	62 (100%)	0	0	100	100
All	All	348/384 (91%)	345 (99%)	3 (1%)	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	A	52/58 (90%)	48 (92%)	4 (8%)	13	4
1	B	55/58 (95%)	54 (98%)	1 (2%)	59	48

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	C	54/58 (93%)	50 (93%)	4 (7%)	13	4
1	D	57/58 (98%)	55 (96%)	2 (4%)	36	21
1	E	55/58 (95%)	52 (94%)	3 (6%)	21	8
1	F	58/58 (100%)	54 (93%)	4 (7%)	15	5
All	All	331/348 (95%)	313 (95%)	18 (5%)	21	9

All (18) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	10	SER
1	A	12	SER
1	A	34	ARG
1	A	44	LYS
1	B	55	LEU
1	C	-2	LEU
1	C	27	LYS
1	C	52	LEU
1	C	53	ASN
1	D	-2	LEU
1	D	3	SER
1	E	-2	LEU
1	E	31	LEU
1	E	45	LEU
1	F	33	ASN
1	F	38	LEU
1	F	39	GLU
1	F	53	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	29	HIS
1	B	2	ASN
1	B	26	HIS
1	B	29	HIS
1	C	22	GLN
1	C	53	ASN
1	D	26	HIS
1	E	-4	HIS
1	E	2	ASN

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Mol	Chain	Res	Type
1	F	26	HIS
1	F	30	GLN
1	F	33	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 carbohydrates 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

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.