



wwPDB X-ray Structure Validation Summary Report ⓘ

Sep 24, 2017 – 08:53 PM EDT

PDB ID : 5N7X
Title : CRYSTAL STRUCTURE OF STREPTAVIDIN WITH PEPTIDE EWVH-PQFEQKAK
Authors : Lyamichev, V.; Goodrich, L.; Sullivan, E.; Bannen, R.; Benz, J.; Albert, T.; Patel, J.
Deposited on : unknown
Resolution : 1.12 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

<http://wwpdb.org/validation/2016/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
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20029824
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	rb-20029824

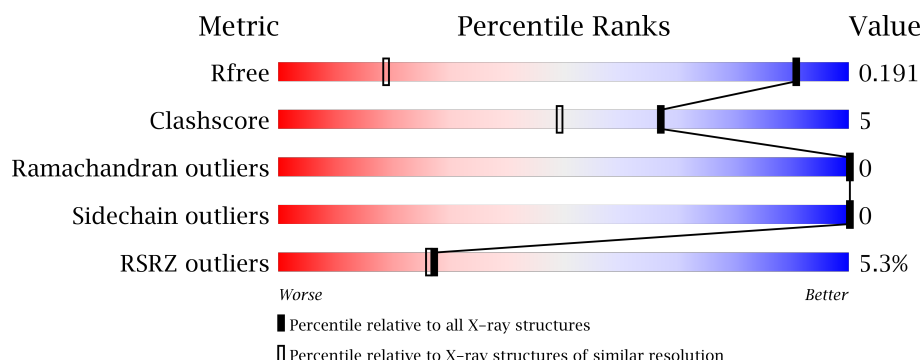
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.12 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.




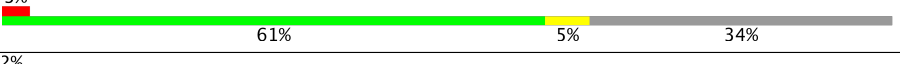





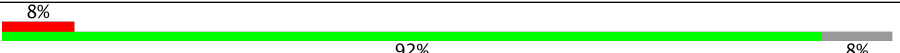
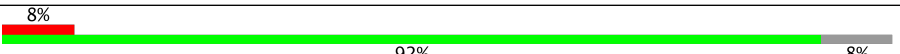
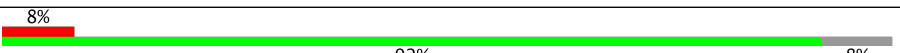
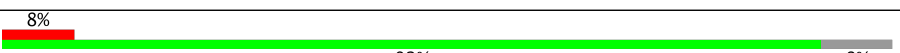
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	100719	1062 (1.16-1.08)
Clashscore	112137	1107 (1.16-1.08)
Ramachandran outliers	110173	1065 (1.16-1.08)
Sidechain outliers	110143	1062 (1.16-1.08)
RSRZ outliers	101464	1067 (1.16-1.08)

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. 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	A	183	
1	B	183	
1	E	183	
1	F	183	
1	H	183	

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Mol	Chain	Length	Quality of chain
1	K	183	
1	M	183	
1	O	183	
2	C	12	
2	D	12	
2	G	12	
2	I	12	
2	J	12	
2	L	12	
2	N	12	
2	P	12	

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 9634 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 Streptavidin.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
1	A	122	Total	C	N	O	0	10	0
			957	602	162	193			
1	B	121	Total	C	N	O	0	9	0
			945	596	160	189			
1	E	122	Total	C	N	O	0	8	0
			945	594	159	192			
1	F	122	Total	C	N	O	0	7	0
			939	590	158	191			
1	H	122	Total	C	N	O	6	9	0
			952	599	162	191			
1	K	122	Total	C	N	O	0	10	0
			951	599	158	194			
1	M	121	Total	C	N	O	0	8	0
			944	595	161	188			
1	O	122	Total	C	N	O	0	7	0
			939	590	158	191			

- Molecule 2 is a protein called GLU-TRP-VAL-HIS-PRO-GLN-PHE-GLU-GLN-LYS-ALA-LYS Peptide.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	11	Total	C	N	O	0	0	0
			99	65	17	17			
2	D	11	Total	C	N	O	0	0	0
			99	65	17	17			
2	G	11	Total	C	N	O	0	0	0
			99	65	17	17			
2	I	11	Total	C	N	O	0	0	0
			99	65	17	17			
2	J	11	Total	C	N	O	0	0	0
			99	65	17	17			
2	L	11	Total	C	N	O	0	0	0
			99	65	17	17			

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	N	11	Total	C	N	O	0	0	0
			99	65	17	17			
2	P	11	Total	C	N	O	0	0	0
			99	65	17	17			

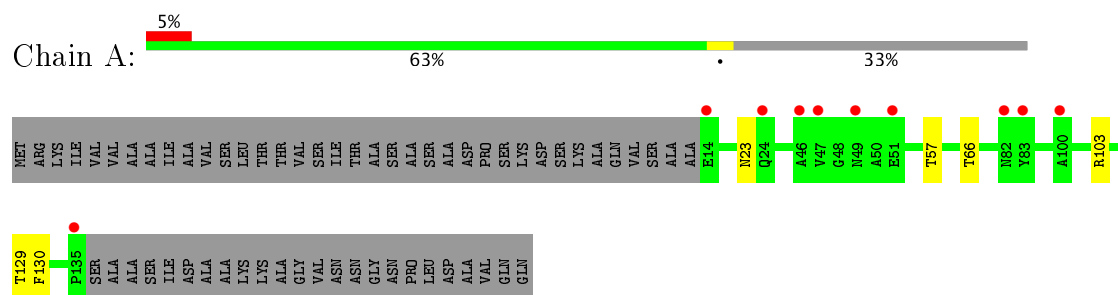
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	129	Total	O	0	0
			129	129		
3	B	153	Total	O	0	0
			153	153		
3	C	11	Total	O	0	0
			11	11		
3	D	9	Total	O	0	0
			9	9		
3	E	150	Total	O	0	0
			150	150		
3	F	140	Total	O	0	0
			140	140		
3	G	10	Total	O	0	0
			10	10		
3	H	148	Total	O	0	0
			148	148		
3	I	10	Total	O	0	0
			10	10		
3	J	24	Total	O	0	0
			24	24		
3	K	147	Total	O	0	0
			147	147		
3	L	14	Total	O	0	0
			14	14		
3	M	158	Total	O	0	0
			158	158		
3	N	11	Total	O	0	0
			11	11		
3	O	136	Total	O	0	0
			136	136		
3	P	20	Total	O	0	0
			20	20		

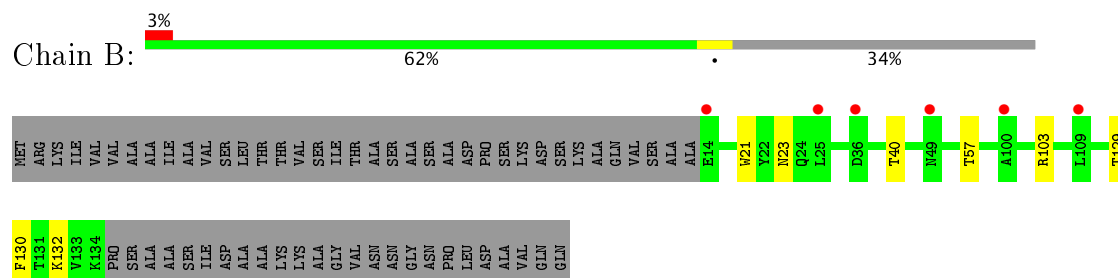
3 Residue-property plots [i](#)

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 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.

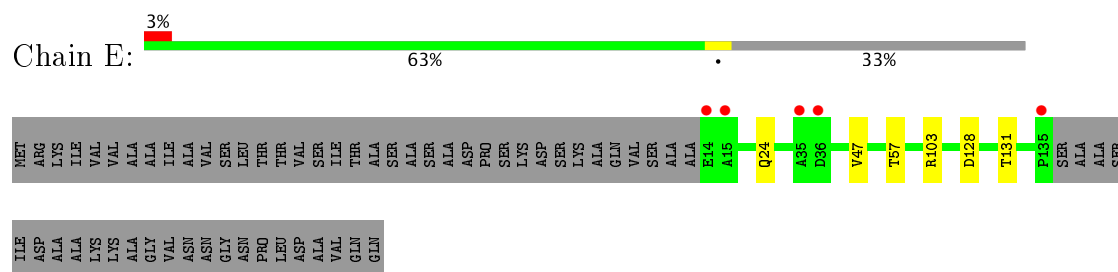
• Molecule 1: Streptavidin



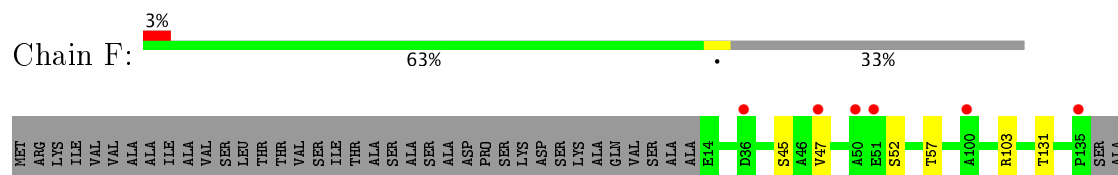
• Molecule 1: Streptavidin



• Molecule 1: Streptavidin



• Molecule 1: Streptavidin



ALA
SER
ILE
ASP
ALA
ALA
LYS
LYS
GLY
VAL
VAL
ASN
ASN
GLY
ASN
PRO
LEU
ASP
ALA
VAL
GLN

- Molecule 1: Streptavidin



MET ARG LYS LYS ILE ILE VAL VAL SER ALA ALA ILE ILE ALA ALA VAL VAL VAL ASN ASN LEU LEU THR THR ALA ALA SER SER SER ASP ASP PRO SER SER LYS LYS ALA ALA VAL VAL SER SER ALA ALA E14 E15 A35 D36 N49 S52 R103 T131 P135 SER ALA ALA SER ILE ASP ALA ALA

LYS LYS LYS ALA GLY VAL ASN ASN GLY ALA ILE ILE ALA ALA VAL VAL VAL ASN ASN LEU LEU THR THR VAL VAL GLN GLN

- Molecule 1: Streptavidin



MET ARG LYS LYS ILE ILE VAL VAL SER ALA ALA ILE ILE ALA ALA VAL VAL VAL ASN ASN LEU LEU THR THR VAL VAL SER SER ILE ILE THR ALA ALA SER SER SER ASP ASP PRO SER SER LYS LYS ALA ALA VAL VAL SER SER ALA ALA E14 N23 Q24 L25 D36 N49 T57 R103 T129 F130 T131 K132 V133 K134 P135 SER ALA

ALA SER ILE ASP ALA ALA LYS LYS ALA ILE ILE ALA ALA VAL VAL VAL ASN ASN GLY GLY ASN PRO LEU LEU ASP ALA VAL GLN GLN

- Molecule 1: Streptavidin



MET ARG LYS LYS ILE ILE VAL VAL SER ALA ALA ILE ILE ALA ALA VAL VAL VAL ASN ASN LEU LEU THR THR VAL VAL SER SER ILE ILE THR ALA ALA SER SER SER ASP ASP PRO SER SER LYS LYS ALA ALA VAL VAL SER SER ALA ALA E14 N23 T42 S45 A46 V47 G48 N49 S52 R53 T57 R84 A100 N105

T129 F130 K134 PRO SER ALA ALA ILE ILE ALA ALA VAL VAL VAL ASN ASN LEU LEU THR THR VAL VAL SER SER ILE ILE THR ALA ALA SER SER SER ASP ASP PRO SER SER LYS LYS ALA ALA VAL VAL VAL ASN ASN GLN GLN

- Molecule 1: Streptavidin



MET ARG LYS LYS ILE ILE VAL VAL SER ALA ALA ILE ILE ALA ALA VAL VAL VAL ASN ASN LEU LEU THR THR VAL VAL SER SER ILE ILE THR ALA ALA SER SER SER ASP ASP PRO SER SER LYS LYS ALA ALA VAL VAL SER SER ALA ALA E14 D36 N49 Y54 R103 L110 T131 P135 SER ALA ALA SER ILE ASP ALA ALA

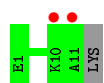
LYS LYS LYS ALA GLY VAL ASN ASN GLY ALA ILE ILE ALA ALA VAL VAL VAL ASN ASN LEU LEU THR THR VAL VAL GLN GLN

- Molecule 2: GLU-TRP-VAL-HIS-PRO-GLN-PHE-GLU-GLN-LYS-ALA-LYS Peptide

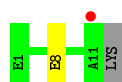
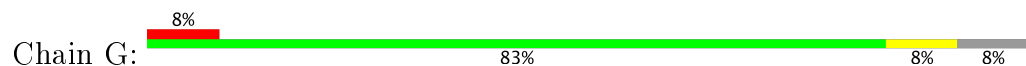


E1 K10 A11 LYS

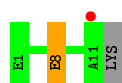
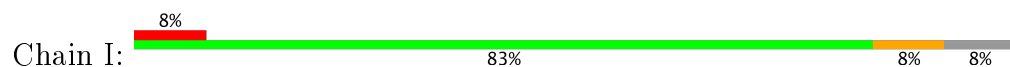
- Molecule 2: GLU-TRP-VAL-HIS-PRO-GLN-PHE-GLU-GLN-LYS-ALA-LYS Peptide



- Molecule 2: GLU-TRP-VAL-HIS-PRO-GLN-PHE-GLU-GLN-LYS-ALA-LYS Peptide



- Molecule 2: GLU-TRP-VAL-HIS-PRO-GLN-PHE-GLU-GLN-LYS-ALA-LYS Peptide



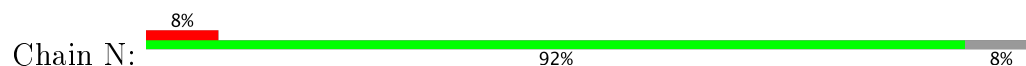
- Molecule 2: GLU-TRP-VAL-HIS-PRO-GLN-PHE-GLU-GLN-LYS-ALA-LYS Peptide



- Molecule 2: GLU-TRP-VAL-HIS-PRO-GLN-PHE-GLU-GLN-LYS-ALA-LYS Peptide



- Molecule 2: GLU-TRP-VAL-HIS-PRO-GLN-PHE-GLU-GLN-LYS-ALA-LYS Peptide



- Molecule 2: GLU-TRP-VAL-HIS-PRO-GLN-PHE-GLU-GLN-LYS-ALA-LYS Peptide



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	57.91Å 64.81Å 81.16Å 96.31° 97.15° 84.09°	Depositor
Resolution (Å)	80.13 – 1.12 47.84 – 1.12	Depositor EDS
% Data completeness (in resolution range)	90.4 (80.13-1.12) 87.5 (47.84-1.12)	Depositor EDS
R_{merge}	0.03	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.59 (at 1.12Å)	Xtriage
Refinement program	REFMAC 5.8.0158	Depositor
R, R_{free}	0.160 , 0.186 0.169 , 0.191	Depositor DCC
R_{free} test set	20178 reflections (5.27%)	DCC
Wilson B-factor (Å ²)	12.5	Xtriage
Anisotropy	0.134	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 47.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	9634	wwPDB-VP
Average B, all atoms (Å ²)	20.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 47.27 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 1.0159e-04.*

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	0.70	0/1008	0.88	0/1379
1	B	0.67	0/992	0.82	0/1357
1	E	0.71	0/990	0.81	0/1355
1	F	0.72	0/981	0.84	0/1343
1	H	0.76	1/1000 (0.1%)	0.84	0/1368
1	K	0.75	0/1002	0.86	0/1373
1	M	0.69	0/988	0.82	1/1351 (0.1%)
1	O	0.72	0/981	0.83	2/1343 (0.1%)
2	C	0.62	0/103	0.60	0/139
2	D	0.59	0/103	0.61	0/139
2	G	0.59	0/103	0.67	0/139
2	I	0.85	1/103 (1.0%)	0.80	0/139
2	J	0.62	0/103	0.61	0/139
2	L	0.64	0/103	0.63	0/139
2	N	0.57	0/103	0.59	0/139
2	P	0.66	0/103	0.64	0/139
All	All	0.71	2/8766 (0.0%)	0.82	3/11981 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	I	8	GLU	CD-OE1	5.40	1.31	1.25
1	H	135	PRO	C-O	-5.34	1.12	1.23

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	O	110	LEU	CB-CG-CD1	6.00	121.20	111.00
1	M	84	ARG	NE-CZ-NH1	-5.78	117.41	120.30
1	O	54	TYR	CB-CG-CD1	5.26	124.15	121.00

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	957	0	916	19	0
1	B	945	0	910	17	0
1	E	945	0	896	13	0
1	F	939	0	888	12	0
1	H	952	0	912	2	0
1	K	951	0	909	13	0
1	M	944	0	906	14	0
1	O	939	0	888	1	0
2	C	99	0	90	0	0
2	D	99	0	90	0	0
2	G	99	0	90	1	0
2	I	99	0	90	1	0
2	J	99	0	90	0	0
2	L	99	0	90	0	0
2	N	99	0	90	0	0
2	P	99	0	90	0	0
3	A	129	0	0	3	0
3	B	153	0	0	3	0
3	C	11	0	0	0	0
3	D	9	0	0	0	0
3	E	150	0	0	1	0
3	F	140	0	0	1	0
3	G	10	0	0	0	0
3	H	148	0	0	0	0
3	I	10	0	0	0	0
3	J	24	0	0	0	0
3	K	147	0	0	5	0
3	L	14	0	0	0	0
3	M	158	0	0	3	0
3	N	11	0	0	0	0
3	O	136	0	0	0	0
3	P	20	0	0	0	0
All	All	9634	0	7945	74	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 5.

The worst 5 of 74 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:M:42[B]:THR:HG21	1:M:53[B]:ARG:HD2	1.42	1.01
1:M:42[B]:THR:CG2	1:M:53[B]:ARG:CG	2.39	1.00
1:M:42[B]:THR:HG21	1:M:53[B]:ARG:CD	1.93	0.96
1:A:103:ARG:HH21	1:A:129[A]:THR:CG2	1.82	0.91
1:K:103:ARG:HH21	1:K:129[A]:THR:CG2	1.82	0.91

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	129/183 (70%)	128 (99%)	1 (1%)	0	100	100
1	B	127/183 (69%)	125 (98%)	2 (2%)	0	100	100
1	E	127/183 (69%)	125 (98%)	2 (2%)	0	100	100
1	F	126/183 (69%)	124 (98%)	2 (2%)	0	100	100
1	H	128/183 (70%)	125 (98%)	3 (2%)	0	100	100
1	K	129/183 (70%)	126 (98%)	3 (2%)	0	100	100
1	M	126/183 (69%)	125 (99%)	1 (1%)	0	100	100
1	O	126/183 (69%)	123 (98%)	3 (2%)	0	100	100
2	C	9/12 (75%)	9 (100%)	0	0	100	100
2	D	9/12 (75%)	9 (100%)	0	0	100	100
2	G	9/12 (75%)	9 (100%)	0	0	100	100
2	I	9/12 (75%)	9 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	J	9/12 (75%)	9 (100%)	0	0	100	100
2	L	9/12 (75%)	9 (100%)	0	0	100	100
2	N	9/12 (75%)	9 (100%)	0	0	100	100
2	P	9/12 (75%)	9 (100%)	0	0	100	100
All	All	1090/1560 (70%)	1073 (98%)	17 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	A	99/134 (74%)	99 (100%)	0	100	100
1	B	97/134 (72%)	97 (100%)	0	100	100
1	E	97/134 (72%)	97 (100%)	0	100	100
1	F	96/134 (72%)	96 (100%)	0	100	100
1	H	98/134 (73%)	98 (100%)	0	100	100
1	K	99/134 (74%)	99 (100%)	0	100	100
1	M	96/134 (72%)	96 (100%)	0	100	100
1	O	96/134 (72%)	96 (100%)	0	100	100
2	C	10/11 (91%)	10 (100%)	0	100	100
2	D	10/11 (91%)	10 (100%)	0	100	100
2	G	10/11 (91%)	10 (100%)	0	100	100
2	I	10/11 (91%)	10 (100%)	0	100	100
2	J	10/11 (91%)	10 (100%)	0	100	100
2	L	10/11 (91%)	10 (100%)	0	100	100
2	N	10/11 (91%)	10 (100%)	0	100	100
2	P	10/11 (91%)	10 (100%)	0	100	100
All	All	858/1160 (74%)	858 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
1	F	82	ASN
1	O	82	ASN
1	K	82	ASN
1	E	82	ASN
1	H	82	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 ⓘ

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	A	122/183 (66%)	0.46	10 (8%) 12 15	11, 16, 35, 50	2 (1%)
1	B	121/183 (66%)	0.33	6 (4%) 30 28	10, 16, 33, 56	2 (1%)
1	E	122/183 (66%)	0.29	5 (4%) 38 34	10, 16, 30, 52	2 (1%)
1	F	122/183 (66%)	0.31	6 (4%) 30 29	9, 15, 29, 49	2 (1%)
1	H	122/183 (66%)	0.36	4 (3%) 47 44	9, 16, 30, 49	2 (1%)
1	K	122/183 (66%)	0.43	6 (4%) 30 29	10, 15, 33, 48	2 (1%)
1	M	121/183 (66%)	0.30	6 (4%) 30 28	9, 15, 31, 51	2 (1%)
1	O	122/183 (66%)	0.24	3 (2%) 58 54	9, 16, 29, 50	2 (1%)
2	C	11/12 (91%)	0.51	2 (18%) 1 3	13, 18, 50, 59	0
2	D	11/12 (91%)	1.21	2 (18%) 1 3	15, 26, 53, 58	0
2	G	11/12 (91%)	1.13	1 (9%) 10 12	12, 19, 39, 64	0
2	I	11/12 (91%)	1.28	1 (9%) 10 12	12, 18, 44, 65	0
2	J	11/12 (91%)	0.23	1 (9%) 10 12	12, 17, 35, 46	0
2	L	11/12 (91%)	0.47	1 (9%) 10 12	16, 23, 45, 50	0
2	N	11/12 (91%)	0.75	1 (9%) 10 12	15, 22, 49, 63	0
2	P	11/12 (91%)	0.39	1 (9%) 10 12	12, 17, 36, 49	0
All	All	1062/1560 (68%)	0.37	56 (5%) 27 26	9, 16, 34, 65	16 (1%)

The worst 5 of 56 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	I	11	ALA	12.4
2	G	11	ALA	10.7
1	K	135	PRO	7.7
2	D	11	ALA	6.1
1	A	49	ASN	5.9

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 carbohydrates 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.