



wwPDB X-ray Structure Validation Summary Report ⓘ

May 18, 2020 – 07:11 am BST

PDB ID : 4BP9
Title : Oligopeptidase B from Trypanosoma brucei with covalently bound antipain - closed form
Authors : Canning, P.; Rea, D.; Morty, R.; Fulop, V.
Deposited on : 2013-05-23
Resolution : 2.85 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 ⓘ 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

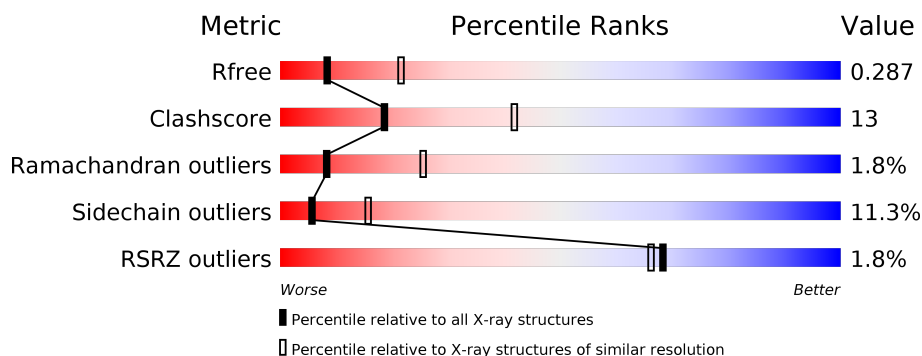
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.85 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	3168 (2.90-2.82)
Clashscore	141614	3438 (2.90-2.82)
Ramachandran outliers	138981	3348 (2.90-2.82)
Sidechain outliers	138945	3351 (2.90-2.82)
RSRZ outliers	127900	3103 (2.90-2.82)

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 $\leq 5\%$. 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	715	<div> <div>66%</div> <div>28%</div> <div>• •</div> </div>
1	B	715	<div> <div>%</div> <div>66%</div> <div>28%</div> <div>• ••</div> </div>
1	C	715	<div> <div>2%</div> <div>66%</div> <div>29%</div> <div>• ••</div> </div>
1	D	715	<div> <div>%</div> <div>68%</div> <div>28%</div> <div>• •</div> </div>
1	E	715	<div> <div>3%</div> <div>66%</div> <div>30%</div> <div>• ••</div> </div>
1	F	715	<div> <div>4%</div> <div>64%</div> <div>30%</div> <div>5% •</div> </div>

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Mol	Chain	Length	Quality of chain
2	G	4	
2	H	4	
2	I	4	
2	J	4	
2	K	4	
2	L	4	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	OAR	G	4	X	-	-	-
2	FC0	H	1	-	-	-	X
2	OAR	H	4	X	-	-	-
2	OAR	I	4	X	-	-	-
2	OAR	J	4	X	-	-	-
2	OAR	K	4	X	-	-	-
2	FC0	L	1	-	-	-	X
2	OAR	L	4	X	-	-	-

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 34406 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 OLIGOPEPTIDASSE B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	710	Total	C	N	O	S	0	0	0
			5634	3568	976	1059	31			
1	B	710	Total	C	N	O	S	0	0	0
			5634	3568	976	1059	31			
1	C	710	Total	C	N	O	S	0	0	0
			5634	3568	976	1059	31			
1	D	710	Total	C	N	O	S	0	0	0
			5634	3568	976	1059	31			
1	E	710	Total	C	N	O	S	0	0	0
			5634	3568	976	1059	31			
1	F	710	Total	C	N	O	S	0	0	0
			5634	3568	976	1059	31			

- Molecule 2 is a protein called ANTIPAIN.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	G	4	Total	C	N	O	0	0	0
			43	27	10	6			
2	H	4	Total	C	N	O	0	0	0
			43	27	10	6			
2	I	4	Total	C	N	O	0	0	0
			43	27	10	6			
2	J	4	Total	C	N	O	0	0	0
			43	27	10	6			
2	K	4	Total	C	N	O	0	0	0
			43	27	10	6			
2	L	4	Total	C	N	O	0	0	0
			43	27	10	6			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	4	OAR	RGL	conflict	NOR NOR00664

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Chain	Residue	Modelled	Actual	Comment	Reference
H	4	OAR	RGL	conflict	NOR NOR00664
I	4	OAR	RGL	conflict	NOR NOR00664
J	4	OAR	RGL	conflict	NOR NOR00664
K	4	OAR	RGL	conflict	NOR NOR00664
L	4	OAR	RGL	conflict	NOR NOR00664

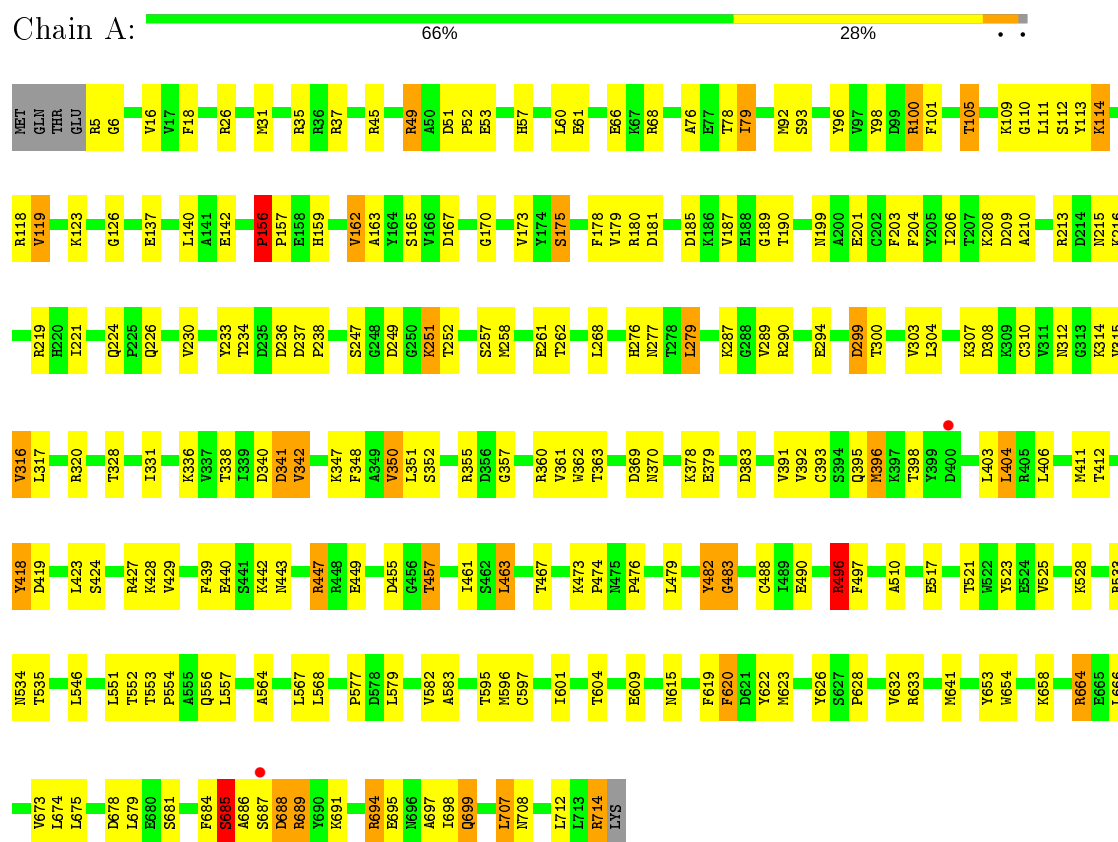
- Molecule 3 is water.

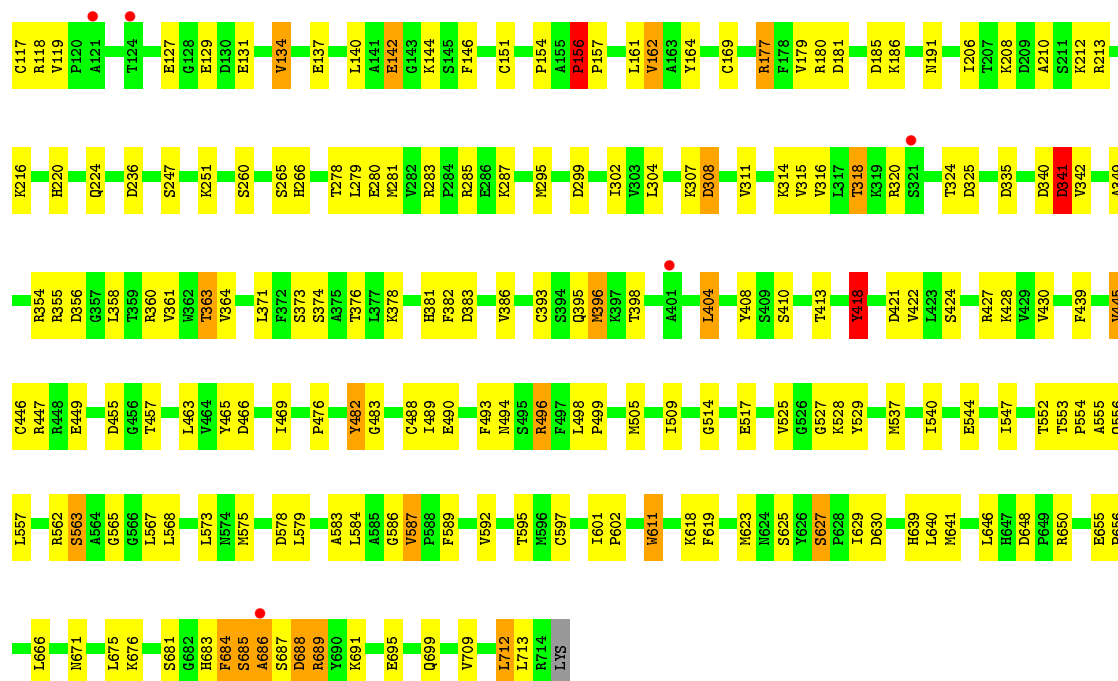
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	109	Total O 109 109	0	0
3	B	75	Total O 75 75	0	0
3	C	36	Total O 36 36	0	0
3	D	39	Total O 39 39	0	0
3	E	37	Total O 37 37	0	0
3	F	48	Total O 48 48	0	0

3 Residue-property plots [i](#)

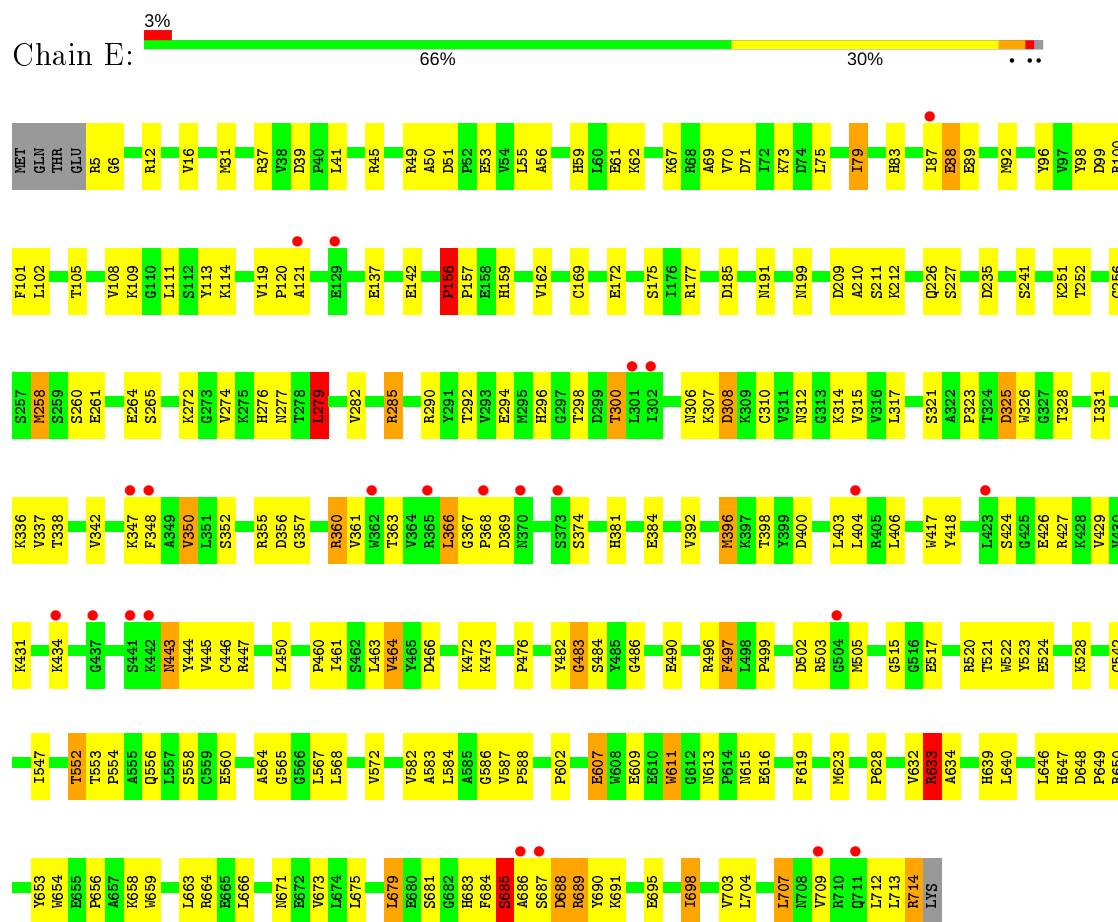
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are 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: OLIGOPEPTIDASSE B

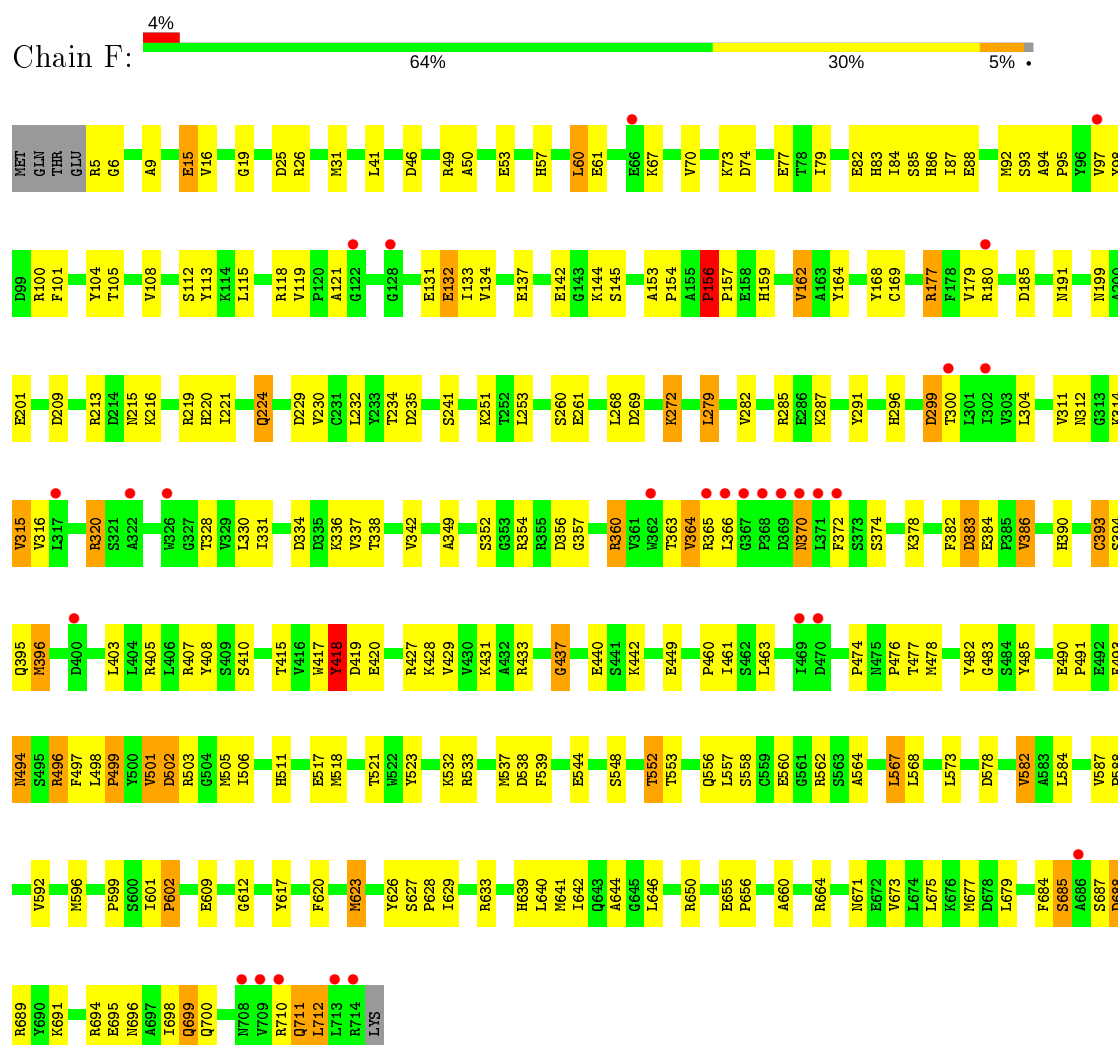




- Molecule 1: OLIGOPEPTIDASSE B



- Molecule 1: OLIGOPEPTIDASSE B



- Molecule 2: ANTIPAIN



- Molecule 2: ANTIPAIN



- Molecule 2: ANTIPAIN



- Molecule 2: ANTIPAIN

Chain J:  50% 25% 25%



● Molecule 2: ANTIPAIN

Chain K:  50% 25% 25%



● Molecule 2: ANTIPAIN

Chain L:  50% 25% 25%



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	71.80 Å 148.80 Å 268.00 Å 90.00° 91.00° 90.00°	Depositor
Resolution (Å)	58.59 – 2.85 58.59 – 2.85	Depositor EDS
% Data completeness (in resolution range)	96.8 (58.59-2.85) 96.7 (58.59-2.85)	Depositor EDS
R_{merge}	0.22	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.23 (at 2.86 Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.213 , 0.281 0.222 , 0.287	Depositor DCC
R_{free} test set	5162 reflections (4.06%)	wwPDB-VP
Wilson B-factor (Å ²)	42.9	Xtriage
Anisotropy	0.703	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 51.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	0.000 for h,-k,-l	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	34406	wwPDB-VP
Average B, all atoms (Å ²)	59.0	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 45.78 % 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 1.2588e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹ Intensities estimated from amplitudes.

² Theoretical 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 ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: FC0, OAR

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	0.76	1/5772 (0.0%)	0.88	8/7832 (0.1%)
1	B	0.75	2/5772 (0.0%)	0.88	10/7832 (0.1%)
1	C	0.65	0/5772	0.79	2/7832 (0.0%)
1	D	0.69	0/5772	0.81	1/7832 (0.0%)
1	E	0.66	0/5772	0.80	3/7832 (0.0%)
1	F	0.69	0/5772	0.83	8/7832 (0.1%)
2	G	1.29	0/17	1.36	0/21
2	H	1.53	0/17	1.88	1/21 (4.8%)
2	I	1.35	0/17	1.72	0/21
2	J	1.33	0/17	1.28	0/21
2	K	1.21	0/17	1.50	0/21
2	L	1.49	0/17	1.73	0/21
All	All	0.70	3/34734 (0.0%)	0.83	33/47118 (0.1%)

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	A	0	2
1	B	0	4
1	C	0	4
1	D	0	4
1	E	0	2
1	F	0	2
2	G	1	2
2	H	1	1
2	I	1	1
2	J	1	1
2	K	1	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
2	L	1	2
All	All	6	26

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	209	ASP	CB-CG	5.88	1.64	1.51
1	A	678	ASP	CB-CG	5.53	1.63	1.51
1	B	560	GLU	CG-CD	5.25	1.59	1.51

The worst 5 of 33 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	533	ARG	NE-CZ-NH2	-8.37	116.12	120.30
1	B	49	ARG	NE-CZ-NH1	7.44	124.02	120.30
1	B	463	LEU	CA-CB-CG	7.20	131.85	115.30
1	B	49	ARG	NE-CZ-NH2	-7.05	116.77	120.30
1	E	279	LEU	CA-CB-CG	6.70	130.72	115.30

5 of 6 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	G	4	OAR	CA
2	H	4	OAR	CA
2	I	4	OAR	CA
2	J	4	OAR	CA
2	K	4	OAR	CA

5 of 26 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	156	PRO	Peptide
1	A	685	SER	Peptide
1	B	156	PRO	Peptide
1	B	482	TYR	Peptide
1	B	685	SER	Peptide

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	5634	0	5522	156	0
1	B	5634	0	5522	139	0
1	C	5634	0	5522	148	0
1	D	5634	0	5522	129	0
1	E	5634	0	5522	147	0
1	F	5634	0	5522	166	0
2	G	43	0	41	1	0
2	H	43	0	40	1	0
2	I	43	0	41	1	0
2	J	43	0	42	4	0
2	K	43	0	42	2	0
2	L	43	0	41	1	0
3	A	109	0	0	12	0
3	B	75	0	0	15	0
3	C	36	0	0	7	0
3	D	39	0	0	6	0
3	E	37	0	0	4	0
3	F	48	0	0	3	0
All	All	34406	0	33379	889	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 13.

The worst 5 of 889 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:C:61:GLU:HG2	1:C:675:LEU:HD23	1.13	1.12
1:E:61:GLU:HG2	1:E:675:LEU:HD23	1.34	1.05
1:A:496:ARG:HH11	1:A:496:ARG:HG2	1.19	1.05
1:D:619:PHE:HB3	1:D:623:MET:HE2	1.38	1.03
1:D:681:SER:HB2	1:D:685:SER:CB	1.87	1.02

There are no symmetry-related clashes.

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	A	708/715 (99%)	651 (92%)	48 (7%)	9 (1%)	12	33
1	B	708/715 (99%)	646 (91%)	51 (7%)	11 (2%)	9	28
1	C	708/715 (99%)	623 (88%)	69 (10%)	16 (2%)	6	20
1	D	708/715 (99%)	645 (91%)	49 (7%)	14 (2%)	7	23
1	E	708/715 (99%)	631 (89%)	63 (9%)	14 (2%)	7	23
1	F	708/715 (99%)	613 (87%)	82 (12%)	13 (2%)	8	25
All	All	4248/4290 (99%)	3809 (90%)	362 (8%)	77 (2%)	8	25

5 of 77 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	156	PRO
1	A	157	PRO
1	A	685	SER
1	B	157	PRO
1	B	274	VAL

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	614/619 (99%)	553 (90%)	61 (10%)	8	21
1	B	614/619 (99%)	537 (88%)	77 (12%)	4	12
1	C	614/619 (99%)	551 (90%)	63 (10%)	7	19

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	D	614/619 (99%)	542 (88%)	72 (12%)	5	14
1	E	614/619 (99%)	543 (88%)	71 (12%)	5	14
1	F	614/619 (99%)	542 (88%)	72 (12%)	5	14
2	G	2/2 (100%)	2 (100%)	0	100	100
2	H	2/2 (100%)	1 (50%)	1 (50%)	0	0
2	I	2/2 (100%)	1 (50%)	1 (50%)	0	0
2	J	2/2 (100%)	2 (100%)	0	100	100
2	K	2/2 (100%)	2 (100%)	0	100	100
2	L	2/2 (100%)	1 (50%)	1 (50%)	0	0
All	All	3696/3726 (99%)	3277 (89%)	419 (11%)	6	16

5 of 419 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	496	ARG
1	D	302	ILE
1	F	384	GLU
1	C	628	PRO
1	D	119	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 38 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	494	ASN
1	D	83	HIS
1	F	700	GLN
1	C	683	HIS
1	D	266	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

12 non-standard protein/DNA/RNA residues 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	OAR	G	4	2	10,10,10	1.62	1 (10%)	9,11,11	1.14	1 (11%)
2	OAR	I	4	2	10,10,10	1.58	1 (10%)	9,11,11	1.14	1 (11%)
2	FC0	L	1	2	11,14,15	0.96	0	11,17,19	0.76	1 (9%)
2	FC0	J	1	2	11,14,15	1.22	0	11,17,19	1.67	1 (9%)
2	OAR	K	4	2	10,10,10	1.47	1 (10%)	9,11,11	1.04	0
2	FC0	H	1	2	11,14,15	0.94	0	11,17,19	1.29	1 (9%)
2	FC0	G	1	2	11,14,15	0.89	0	11,17,19	1.11	1 (9%)
2	OAR	L	4	2	10,10,10	1.51	1 (10%)	9,11,11	0.48	0
2	OAR	J	4	2	10,10,10	1.59	1 (10%)	9,11,11	1.46	3 (33%)
2	FC0	K	1	2	11,14,15	0.94	0	11,17,19	1.16	1 (9%)
2	OAR	H	4	2	10,10,10	1.50	1 (10%)	9,11,11	1.21	1 (11%)
2	FC0	I	1	2	11,14,15	0.74	0	11,17,19	0.95	1 (9%)

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	OAR	G	4	2	1/1/2/3	3/9/9/9	-
2	OAR	I	4	2	1/1/2/3	4/9/9/9	-
2	FC0	L	1	2	-	1/7/11/12	0/1/1/1
2	FC0	J	1	2	-	5/7/11/12	0/1/1/1
2	OAR	K	4	2	1/1/2/3	2/9/9/9	-
2	FC0	H	1	2	-	5/7/11/12	0/1/1/1
2	FC0	G	1	2	-	5/7/11/12	0/1/1/1
2	OAR	L	4	2	1/1/2/3	5/9/9/9	-
2	OAR	J	4	2	1/1/2/3	1/9/9/9	-
2	FC0	K	1	2	-	5/7/11/12	0/1/1/1
2	OAR	H	4	2	1/1/2/3	5/9/9/9	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	FC0	I	1	2	-	4/7/11/12	0/1/1/1

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	G	4	OAR	O-C	-4.59	1.23	1.42
2	I	4	OAR	O-C	-4.38	1.23	1.42
2	L	4	OAR	O-C	-4.35	1.24	1.42
2	H	4	OAR	O-C	-4.14	1.25	1.42
2	J	4	OAR	O-C	-4.09	1.25	1.42

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	J	1	FC0	CG-CB-CA	4.34	120.35	112.97
2	H	1	FC0	CA-N-C1	-3.72	116.82	122.97
2	G	1	FC0	O1-C1-N	-3.00	117.37	125.27
2	H	4	OAR	CB-CA-C	2.99	116.35	112.25
2	K	1	FC0	O1-C1-N	-2.93	117.54	125.27

5 of 6 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	G	4	OAR	CA
2	I	4	OAR	CA
2	K	4	OAR	CA
2	L	4	OAR	CA
2	J	4	OAR	CA

5 of 45 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	G	4	OAR	C-CA-CB-CG
2	I	4	OAR	C-CA-CB-CG
2	L	1	FC0	O1-C1-N-CA
2	J	1	FC0	C-CA-CB-CG
2	J	1	FC0	O1-C1-N-CA

There are no ring outliers.

5 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	J	1	FC0	4	0
2	G	1	FC0	1	0
2	L	4	OAR	1	0
2	K	1	FC0	1	0
2	H	4	OAR	1	0

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	710/715 (99%)	-0.12	2 (0%) 94 94	33, 45, 64, 79	0
1	B	710/715 (99%)	-0.00	5 (0%) 87 87	34, 49, 78, 108	0
1	C	710/715 (99%)	0.14	13 (1%) 68 66	44, 62, 94, 109	0
1	D	710/715 (99%)	-0.05	6 (0%) 86 85	38, 54, 79, 93	0
1	E	710/715 (99%)	0.19	23 (3%) 47 42	37, 63, 106, 130	0
1	F	710/715 (99%)	0.24	28 (3%) 39 34	38, 66, 115, 144	0
2	G	2/4 (50%)	0.11	0 100 100	29, 29, 29, 58	0
2	H	2/4 (50%)	0.11	0 100 100	29, 29, 29, 55	0
2	I	2/4 (50%)	0.06	0 100 100	42, 42, 42, 66	0
2	J	2/4 (50%)	-0.06	0 100 100	38, 38, 38, 60	0
2	K	2/4 (50%)	0.17	0 100 100	33, 33, 33, 65	0
2	L	2/4 (50%)	-0.21	0 100 100	39, 39, 39, 62	0
All	All	4272/4314 (99%)	0.07	77 (1%) 68 66	29, 55, 97, 144	0

The worst 5 of 77 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	686	ALA	4.4
1	F	686	ALA	4.3
1	F	371	LEU	4.2
1	F	469	ILE	3.8
1	E	423	LEU	3.7

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

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum,

median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	FC0	H	1	14/15	0.63	0.44	68,81,87,88	0
2	FC0	J	1	14/15	0.67	0.40	65,83,86,86	0
2	FC0	L	1	14/15	0.68	0.45	74,88,91,91	0
2	FC0	K	1	14/15	0.73	0.37	72,83,84,84	0
2	FC0	G	1	14/15	0.77	0.39	69,77,79,80	0
2	FC0	I	1	14/15	0.81	0.28	70,84,87,88	0
2	OAR	H	4	11/11	0.96	0.15	23,27,32,33	0
2	OAR	J	4	11/11	0.97	0.15	20,23,27,31	0
2	OAR	I	4	11/11	0.97	0.15	19,25,35,37	0
2	OAR	K	4	11/11	0.97	0.17	19,25,30,30	0
2	OAR	L	4	11/11	0.97	0.14	24,26,35,38	0
2	OAR	G	4	11/11	0.98	0.17	16,18,27,28	0

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.