wwPDB X-ray Structure Validation Summary Report (i)

Feb 1, 2016 – 05:07 PM GMT

PDB ID	:	4H99
Title	:	Bacterial Photosynthetic Reaction Center from Rhodobacter sphaeroides with ILE M265 replaced with THR
Authors	:	Mattis, A.J.; Wraight, C.A.
Deposited on	:	2012-09-24
Resolution	:	2.97 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 (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

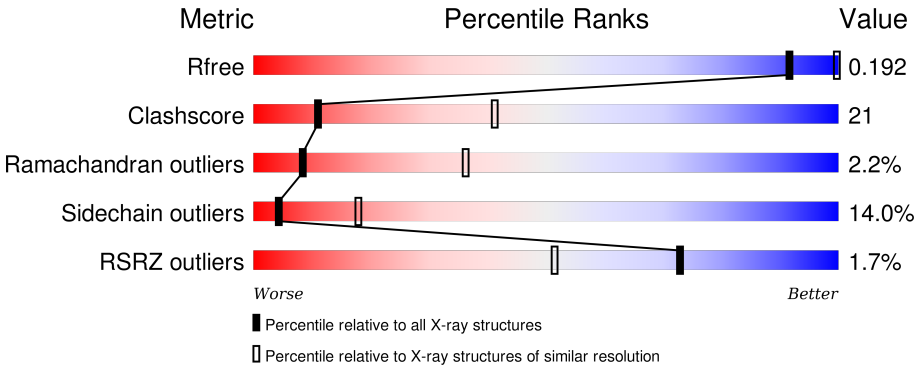
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk26865

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 2.97 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}	91344	1992 (3.00-2.96)
Clashscore	102246	2349 (3.00-2.96)
Ramachandran outliers	100387	2274 (3.00-2.96)
Sidechain outliers	100360	2277 (3.00-2.96)
RSRZ outliers	91569	2007 (3.00-2.96)

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 <=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	L	281	60% 26% 11%
2	M	313	2% 52% 34% 8%
3	H	260	2% 53% 28% 8% 8%

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
5	BPH	L	303	X	-	-	-
6	U10	L	304	-	-	-	X
8	SPO	M	406	-	-	-	X

2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 7005 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 Reaction center protein L chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	L	281	Total	C	N	O	S	0	0	0
			2230	1505	355	362	8			

- Molecule 2 is a protein called Reaction center protein M chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	M	302	Total	C	N	O	S	0	0	0
			2406	1604	394	398	10			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
M	265	THR	ILE	ENGINEERED MUTATION	UNP P0C0Y9
M	303	MET	-	EXPRESSION TAG	UNP P0C0Y9
M	304	ALA	-	EXPRESSION TAG	UNP P0C0Y9
M	305	PRO	-	EXPRESSION TAG	UNP P0C0Y9
M	306	LEU	-	EXPRESSION TAG	UNP P0C0Y9
M	307	ASN	-	EXPRESSION TAG	UNP P0C0Y9
M	308	HIS	-	EXPRESSION TAG	UNP P0C0Y9
M	309	HIS	-	EXPRESSION TAG	UNP P0C0Y9
M	310	HIS	-	EXPRESSION TAG	UNP P0C0Y9
M	311	HIS	-	EXPRESSION TAG	UNP P0C0Y9
M	312	HIS	-	EXPRESSION TAG	UNP P0C0Y9
M	313	HIS	-	EXPRESSION TAG	UNP P0C0Y9

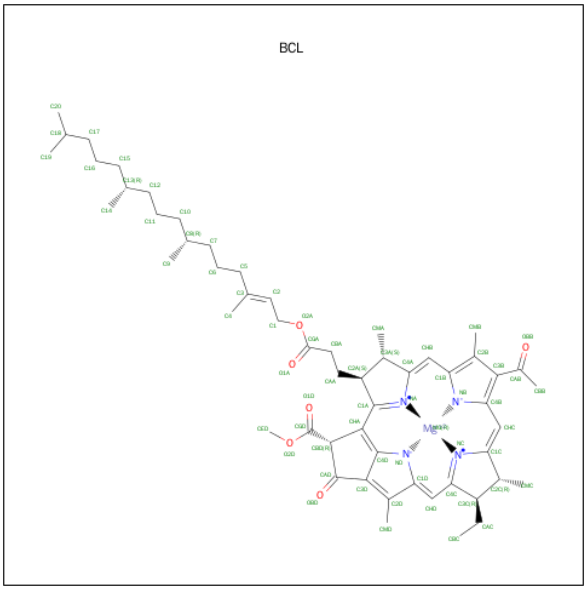
- Molecule 3 is a protein called Reaction center protein H chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	H	240	Total	C	N	O	S	0	0	0
			1829	1169	314	337	9			

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
H	1	MET	-	EXPRESSION TAG	UNP P0C0Y7
H	2	VAL	-	EXPRESSION TAG	UNP P0C0Y7
H	3	GLY	-	EXPRESSION TAG	UNP P0C0Y7
H	4	VAL	-	EXPRESSION TAG	UNP P0C0Y7
H	5	THR	-	EXPRESSION TAG	UNP P0C0Y7
H	6	ALA	-	EXPRESSION TAG	UNP P0C0Y7
H	7	PHE	-	EXPRESSION TAG	UNP P0C0Y7
H	8	GLY	-	EXPRESSION TAG	UNP P0C0Y7
H	9	ASN	-	EXPRESSION TAG	UNP P0C0Y7
H	10	PHE	-	EXPRESSION TAG	UNP P0C0Y7
H	251	VAL	-	EXPRESSION TAG	UNP P0C0Y7
H	252	VAL	-	EXPRESSION TAG	UNP P0C0Y7
H	253	ALA	-	EXPRESSION TAG	UNP P0C0Y7
H	254	ALA	-	EXPRESSION TAG	UNP P0C0Y7
H	255	MET	-	EXPRESSION TAG	UNP P0C0Y7
H	256	LEU	-	EXPRESSION TAG	UNP P0C0Y7
H	257	ALA	-	EXPRESSION TAG	UNP P0C0Y7
H	258	GLU	-	EXPRESSION TAG	UNP P0C0Y7
H	259	TYR	-	EXPRESSION TAG	UNP P0C0Y7
H	260	ALA	-	EXPRESSION TAG	UNP P0C0Y7

- Molecule 4 is BACTERIOCHLOROPHYLL A (three-letter code: BCL) (formula: $C_{55}H_{74}MgN_4O_6$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	L	1	Total	C	Mg	N	O	0	0
			66	55	1	4	6		
4	L	1	Total	C	Mg	N	O	0	0
			66	55	1	4	6		

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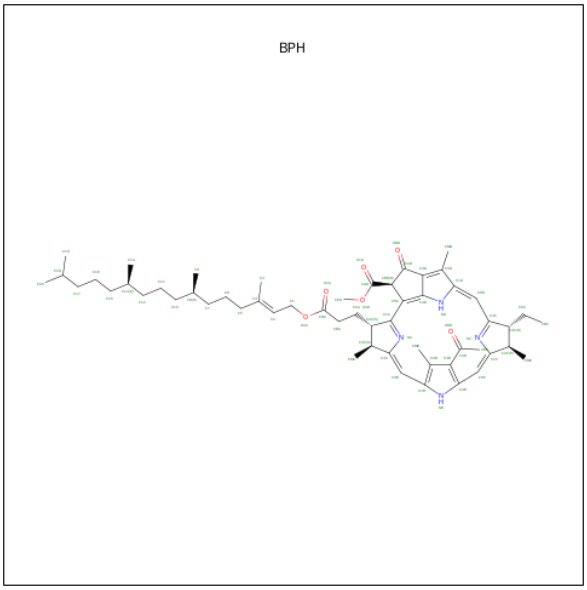
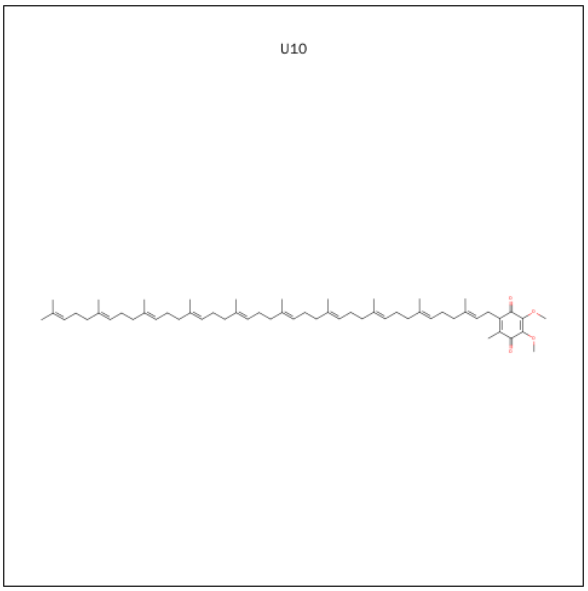
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	M	1	Total	C	Mg	N	O	0	0
			50	39	1	4	6		
4	M	1	Total	C	Mg	N	O	0	0
			66	55	1	4	6		

- Molecule 5 is BACTERIOPHEOPHYTIN A (three-letter code: BPH) (formula: $C_{55}H_{76}N_4O_6$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	L	1	Total	C	N	O	0	0
			65	55	4	6		
5	M	1	Total	C	N	O	0	0
			51	41	4	6		

- Molecule 6 is UBIQUINONE-10 (three-letter code: U10) (formula: $C_{59}H_{90}O_4$).

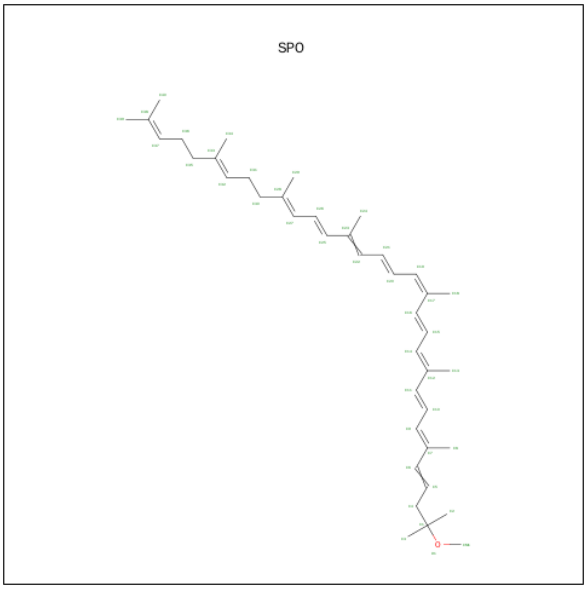


Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	L	1	Total C O 33 29 4	0	0
6	M	1	Total C O 48 44 4	0	0

- Molecule 7 is FE (III) ION (three-letter code: FE) (formula: Fe).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	M	1	Total Fe 1 1	0	0

- Molecule 8 is SPHEROIDENE (three-letter code: SPO) (formula: $C_{41}H_{60}O$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	M	1	Total	C	O	0	0
			42	41	1		

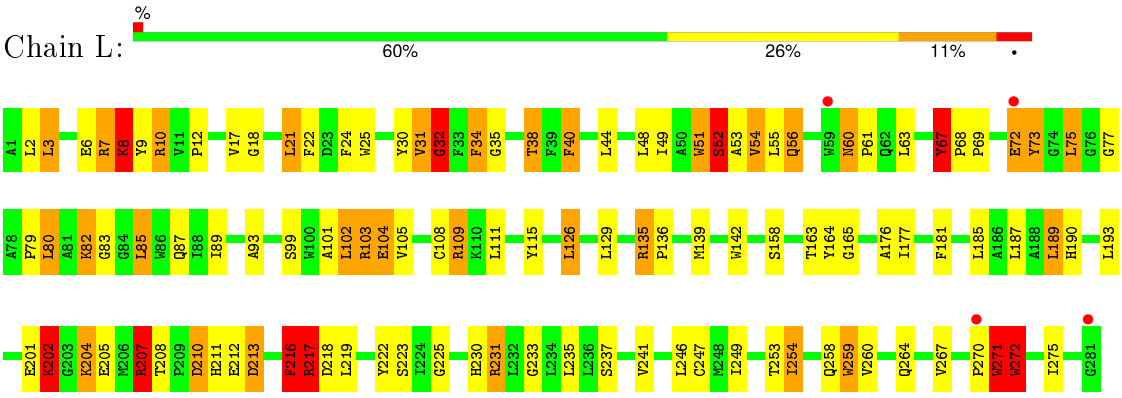
- Molecule 9 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	L	19	Total	O	0	0
			19	19		
9	M	18	Total	O	0	0
			18	18		
9	H	15	Total	O	0	0
			15	15		

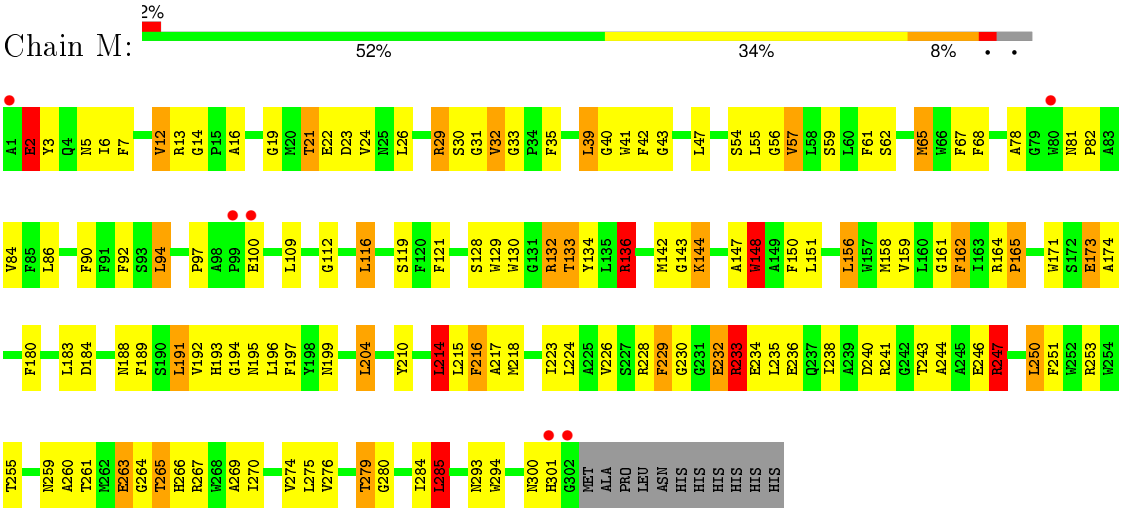
3 Residue-property plots (i)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

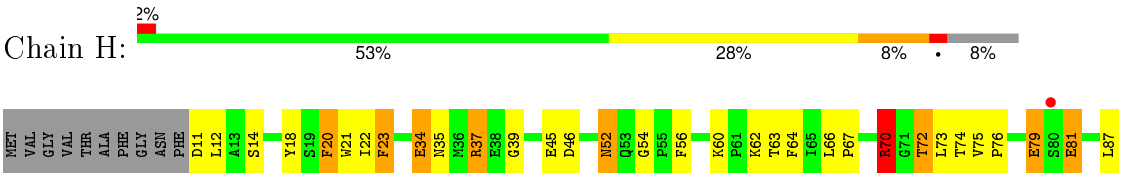
- Molecule 1: Reaction center protein L chain

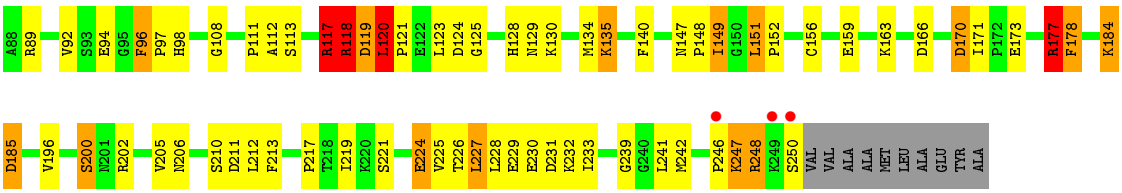


- Molecule 2: Reaction center protein M chain



- Molecule 3: Reaction center protein H chain




A88 B89 V92 S93 E94 G95 F96 P97 H98 G108 P111 A112 S113 R117 R118 D119 L120 P121 E122 L123 D124 G125 H128 N129 K130 M134 K135 F140 N147 P148 I149 G150 L151 P152 C156 E159 K163 D166 D170 I171 P172 E173 R177 F178 K184
D185 V196 S200 N201 R202 V205 N206 S210 D211 L212 F213 P217 T218 I219 K220 S221 E224 V225 T226 L227 L228 E229 E230 D231 K232 I233 G239 G240 L241 M242 P246 K247 R248 K249 S250 VAL VAL ALA ALA MET LEU ALA GLU TYR ALA

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α, β, γ	138.87Å 138.87Å 185.49Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	19.77 – 2.97 19.77 – 2.97	Depositor EDS
% Data completeness (in resolution range)	100.0 (19.77-2.97) 99.6 (19.77-2.97)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.59 (at 2.98Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.174 , 0.194 0.184 , 0.192	Depositor DCC
R_{free} test set	2146 reflections (5.26%)	DCC
Wilson B-factor (Å^2)	65.9	Xtriage
Anisotropy	0.025	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 55.3	EDS
Estimated twinning fraction	0.021 for -h,-k,l	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Outliers	0 of 42919 reflections	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	7005	wwPDB-VP
Average B, all atoms (Å^2)	53.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.74% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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: BCL, BPH, U10, FE, SPO

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	L	1.68	34/2318 (1.5%)	1.44	25/3172 (0.8%)
2	M	1.67	29/2498 (1.2%)	1.39	24/3410 (0.7%)
3	H	1.76	28/1877 (1.5%)	1.54	30/2553 (1.2%)
All	All	1.70	91/6693 (1.4%)	1.45	79/9135 (0.9%)

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	L	0	1
3	H	0	2
All	All	0	3

The worst 5 of 91 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	H	94	GLU	CG-CD	11.30	1.69	1.51
1	L	72	GLU	CG-CD	10.89	1.68	1.51
1	L	82	LYS	CB-CG	10.31	1.80	1.52
1	L	67	TYR	CD2-CE2	10.06	1.54	1.39
3	H	94	GLU	CD-OE1	9.99	1.36	1.25

The worst 5 of 79 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	L	231	ARG	NE-CZ-NH2	-13.09	113.76	120.30
1	L	231	ARG	NE-CZ-NH1	11.94	126.27	120.30
2	M	247	ARG	NE-CZ-NH1	11.91	126.26	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	L	217	ARG	NE-CZ-NH1	11.81	126.21	120.30
2	M	29	ARG	NE-CZ-NH2	-11.35	114.63	120.30

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	H	119	ASP	Peptide
3	H	79	GLU	Peptide
1	L	32	GLY	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	L	2230	0	2178	100	0
2	M	2406	0	2313	107	0
3	H	1829	0	1836	68	0
4	L	132	0	148	9	0
4	M	116	0	115	20	0
5	L	65	0	76	14	0
5	M	51	0	43	9	0
6	L	33	0	39	10	0
6	M	48	0	63	1	0
7	M	1	0	0	0	0
8	M	42	0	60	13	0
9	H	15	0	0	5	0
9	L	19	0	0	3	0
9	M	18	0	0	0	0
All	All	7005	0	6871	289	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 21.

The worst 5 of 289 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:L:82:LYS:CB	1:L:82:LYS:CG	1.80	1.54
4:M:403:BCL:HHC	4:M:403:BCL:HBB3	1.27	1.14
6:L:304:U10:H1M1	6:L:304:U10:C8	1.79	1.12
1:L:38:THR:HG22	1:L:99:SER:HB2	1.20	1.11
1:L:7:ARG:HH11	3:H:98:HIS:CD2	1.69	1.10

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	L	279/281 (99%)	246 (88%)	22 (8%)	11 (4%)	4 20
2	M	300/313 (96%)	260 (87%)	35 (12%)	5 (2%)	11 44
3	H	238/260 (92%)	212 (89%)	24 (10%)	2 (1%)	24 65
All	All	817/854 (96%)	718 (88%)	81 (10%)	18 (2%)	8 36

5 of 18 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	L	52	SER
1	L	55	LEU
1	L	202	LYS
2	M	301	HIS
3	H	185	ASP

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	L	219/220 (100%)	188 (86%)	31 (14%)	4 17
2	M	236/246 (96%)	204 (86%)	32 (14%)	5 19
3	H	195/208 (94%)	167 (86%)	28 (14%)	4 17
All	All	650/674 (96%)	559 (86%)	91 (14%)	4 18

5 of 91 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	M	109	LEU
2	M	214	LEU
3	H	217	PRO
2	M	133	THR
2	M	156	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	L	60	ASN
2	M	193	HIS
3	H	52	ASN
3	H	98	HIS

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 carbohydrates in this entry.

5.6 Ligand geometry

Of 10 ligands modelled in this entry, 1 is monoatomic - leaving 9 for Mogul analysis.

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	$\#\|Z\| > 2$
4	BCL	L	301	-	53,74,74	0.93	3 (5%)	57,115,115	1.56	8 (14%)
4	BCL	L	302	-	53,74,74	0.94	1 (1%)	57,115,115	2.50	21 (36%)
5	BPH	L	303	-	64,70,70	1.65	10 (15%)	73,101,101	2.06	23 (31%)
6	U10	L	304	-	33,33,63	3.93	11 (33%)	40,43,79	3.33	24 (60%)
4	BCL	M	401	-	37,58,74	1.31	3 (8%)	39,95,115	3.28	17 (43%)
4	BCL	M	403	-	53,74,74	0.84	2 (3%)	57,115,115	1.62	9 (15%)
5	BPH	M	404	-	49,55,70	1.75	10 (20%)	56,83,101	2.25	14 (25%)
6	U10	M	405	-	48,48,63	3.25	15 (31%)	58,61,79	2.68	23 (39%)
8	SPO	M	406	-	40,41,41	2.15	10 (25%)	45,50,50	2.90	21 (46%)

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
4	BCL	L	301	-	-	0/37/137/137	0/0/9/9
4	BCL	L	302	-	-	0/37/137/137	0/0/9/9
5	BPH	L	303	-	2/2/18/22	0/54/105/105	0/1/6/6
6	U10	L	304	-	-	0/27/51/87	0/1/1/1
4	BCL	M	401	-	-	0/18/118/137	0/0/9/9
4	BCL	M	403	-	-	0/37/137/137	0/0/9/9
5	BPH	M	404	-	-	0/36/87/105	0/1/6/6
6	U10	M	405	-	-	0/45/69/87	0/1/1/1
8	SPO	M	406	-	-	0/47/47/47	0/0/0/0

The worst 5 of 65 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	M	404	BPH	C4C-NC	-3.40	1.29	1.37
5	M	404	BPH	C1B-C2B	-3.39	1.38	1.45
6	M	405	U10	O3-C3	-3.00	1.29	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	M	405	U10	O4-C4	-2.84	1.29	1.37
5	L	303	BPH	C1A-NA	-2.75	1.31	1.37

The worst 5 of 160 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	M	401	BCL	O1D-CGD-CBD	-8.53	112.40	124.62
6	L	304	U10	O5-C5-C4	-7.72	104.08	120.79
6	M	405	U10	C22-C23-C24	-6.82	112.93	127.76
6	L	304	U10	O2-C2-C3	-6.56	106.59	120.79
4	L	302	BCL	C16-C15-C13	-6.40	94.25	115.49

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
5	L	303	BPH	C8
5	L	303	BPH	C13

There are no torsion outliers.

There are no ring outliers.

9 monomers are involved in 70 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	L	301	BCL	3	0
4	L	302	BCL	6	0
5	L	303	BPH	14	0
6	L	304	U10	10	0
4	M	401	BCL	7	0
4	M	403	BCL	15	0
5	M	404	BPH	9	0
6	M	405	U10	1	0
8	M	406	SPO	13	0

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

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, 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	<RSRZ>	#RSRZ>2			OWAB(Å^2)	Q<0.9
1	L	281/281 (100%)	-0.66	4 (1%)	78	57	35, 48, 83, 98	0
2	M	302/313 (96%)	-0.68	6 (1%)	68	46	34, 52, 82, 108	0
3	H	240/260 (92%)	-0.49	4 (1%)	73	51	38, 52, 69, 96	0
All	All	823/854 (96%)	-0.62	14 (1%)	73	51	34, 50, 81, 108	0

The worst 5 of 14 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	M	1	ALA	6.0
3	H	250	SER	4.5
2	M	302	GLY	3.3
3	H	80	SER	3.0
2	M	301	HIS	2.9

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

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates

There are no carbohydrates in this entry.

6.4 Ligands

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95^{th} 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	LLDF	B-factors(Å^2)	Q<0.9
6	U10	L	304	33/63	0.74	0.35	11.69	64,85,99,101	0
8	SPO	M	406	42/42	0.87	0.28	3.08	64,87,114,116	0
4	BCL	M	403	66/66	0.96	0.15	1.32	30,51,61,77	0
6	U10	M	405	48/63	0.94	0.15	0.96	31,50,76,82	0
4	BCL	L	301	66/66	0.97	0.16	0.92	34,48,55,58	0
5	BPH	L	303	65/65	0.98	0.12	0.00	27,38,50,54	0
5	BPH	M	404	51/65	0.98	0.11	-0.17	36,54,66,101	0
4	BCL	L	302	66/66	0.98	0.09	-0.61	24,34,54,64	0
4	BCL	M	401	50/66	0.98	0.10	-0.70	35,43,80,100	0
7	FE	M	402	1/1	1.00	0.07	-2.18	41,41,41,41	0

6.5 Other polymers (i)

There are no such residues in this entry.