



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 11:31 PM GMT

PDB ID : 1XMZ
Title : Crystal structure of the dark state of kindling fluorescent protein kfp from anemonia sulcata
Authors : Quillin, M.L.; Anstrom, D.M.; Shu, X.; O'Leary, S.; Kallio, K.; Chudakov, D.M.; Remington, S.J.
Deposited on : 2004-10-04
Resolution : 1.38 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
<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
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

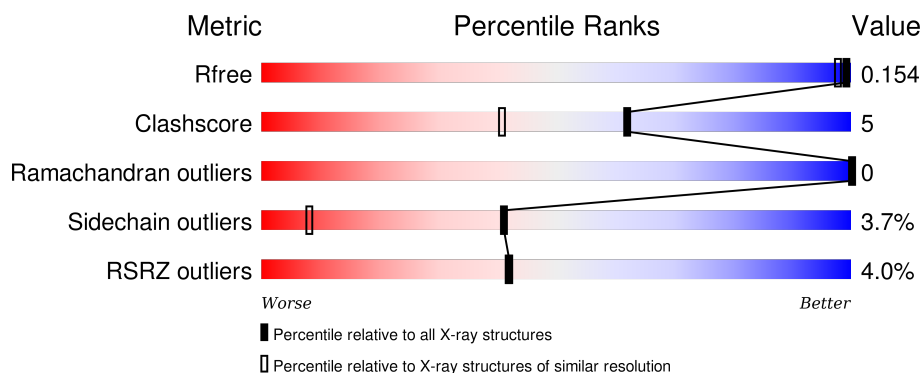
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.38 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	1918 (1.40-1.36)
Clashscore	102246	2042 (1.40-1.36)
Ramachandran outliers	100387	1993 (1.40-1.36)
Sidechain outliers	100360	1992 (1.40-1.36)
RSRZ outliers	91569	1917 (1.40-1.36)

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	241	
1	B	241	

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	NH2	A	240	-	-	-	X
2	NH2	B	240	-	-	-	X
3	BME	A	252	-	-	-	X

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 4295 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 GFP-like chromoprotein FP595.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	225	Total	C	N	O	S	0	22	0
			1884	1210	310	349	15			
1	B	232	Total	C	N	O	S	0	19	0
			1918	1227	321	355	15			

There are 32 discrepancies between the modelled and reference sequences:

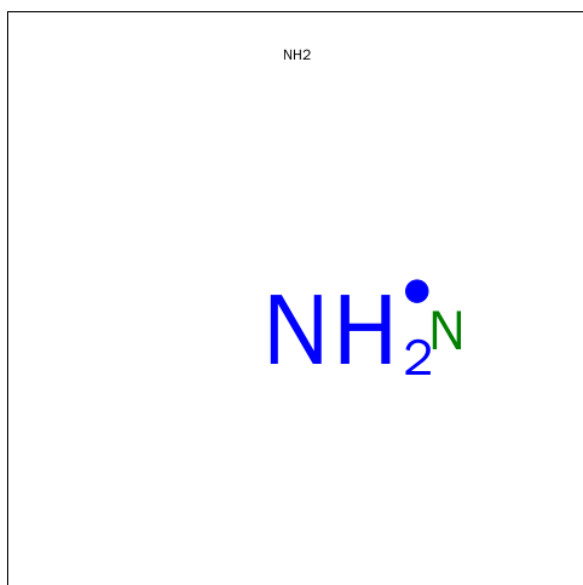
Chain	Residue	Modelled	Actual	Comment	Reference
A	-10	MET	-	EXPRESSION TAG	GB 9937258
A	-9	ARG	-	EXPRESSION TAG	GB 9937258
A	-8	GLY	-	EXPRESSION TAG	GB 9937258
A	-7	SER	-	EXPRESSION TAG	GB 9937258
A	-6	HIS	-	EXPRESSION TAG	GB 9937258
A	-5	HIS	-	EXPRESSION TAG	GB 9937258
A	-4	HIS	-	EXPRESSION TAG	GB 9937258
A	-3	HIS	-	EXPRESSION TAG	GB 9937258
A	-2	HIS	-	EXPRESSION TAG	GB 9937258
A	-1	HIS	-	EXPRESSION TAG	GB 9937258
A	0	GLY	-	EXPRESSION TAG	GB 9937258
A	1	SER	MET	EXPRESSION TAG	GB 9937258
A	65	CRK	MET	CHROMOPHORE	GB 9937258
A	65	CRK	TYR	CHROMOPHORE	GB 9937258
A	65	CRK	GLY	CHROMOPHORE	GB 9937258
A	48	GLY	ALA	ENGINEERED	GB 9937258
B	-10	MET	-	EXPRESSION TAG	GB 9937258
B	-9	ARG	-	EXPRESSION TAG	GB 9937258
B	-8	GLY	-	EXPRESSION TAG	GB 9937258
B	-7	SER	-	EXPRESSION TAG	GB 9937258
B	-6	HIS	-	EXPRESSION TAG	GB 9937258
B	-5	HIS	-	EXPRESSION TAG	GB 9937258
B	-4	HIS	-	EXPRESSION TAG	GB 9937258
B	-3	HIS	-	EXPRESSION TAG	GB 9937258
B	-2	HIS	-	EXPRESSION TAG	GB 9937258

Continued on next page...

Continued from previous page...

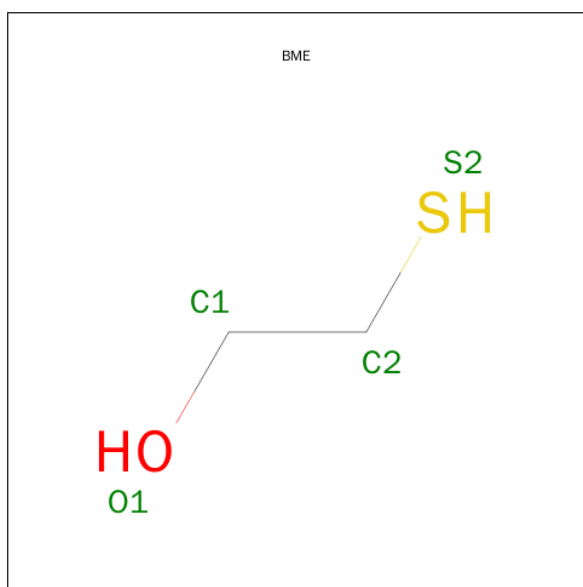
Chain	Residue	Modelled	Actual	Comment	Reference
B	-1	HIS	-	EXPRESSION TAG	GB 9937258
B	0	GLY	-	EXPRESSION TAG	GB 9937258
B	1	SER	MET	EXPRESSION TAG	GB 9937258
B	65	CRK	MET	CHROMOPHORE	GB 9937258
B	65	CRK	TYR	CHROMOPHORE	GB 9937258
B	65	CRK	GLY	CHROMOPHORE	GB 9937258
B	48	GLY	ALA	ENGINEERED	GB 9937258

- Molecule 2 is AMINO GROUP (three-letter code: NH2) (formula: H₂N).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total N 1 1	0	0
2	B	1	Total N 1 1	0	0

- Molecule 3 is BETA-MERCAPTOETHANOL (three-letter code: BME) (formula: C₂H₆OS).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	O	S	0	0
			4	2	1	1		
3	A	1	Total	C	O	S	0	0
			4	2	1	1		
3	A	1	Total	C	O	S	0	0
			4	2	1	1		
3	A	1	Total	C	O	S	0	0
			4	2	1	1		
3	B	1	Total	C	O	S	0	0
			4	2	1	1		
3	B	1	Total	C	O	S	0	0
			4	2	1	1		
3	B	1	Total	C	O	S	0	0
			4	2	1	1		

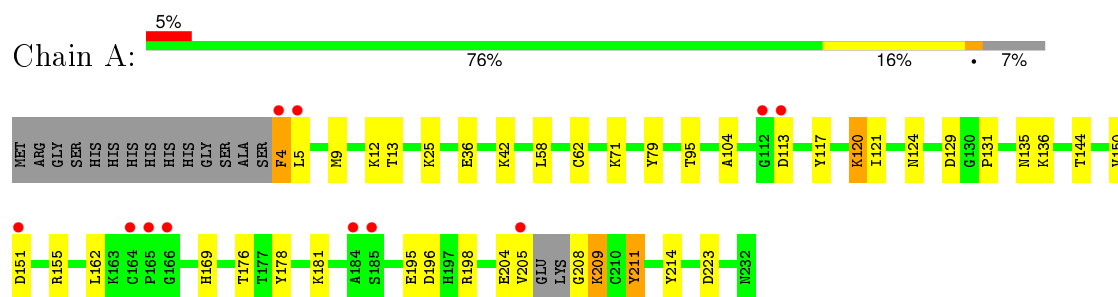
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	230	Total	O	0	2
			230	230		
4	B	233	Total	O	0	3
			233	233		

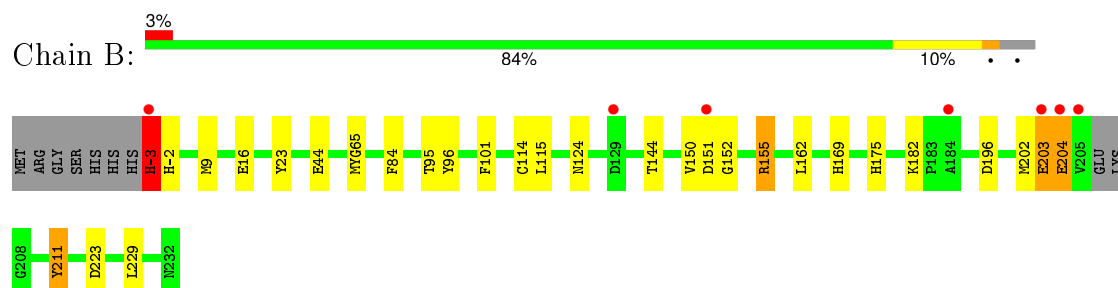
3 Residue-property plots [i](#)

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 ($\text{RSRZ} > 2$). 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: GFP-like chromoprotein FP595



- Molecule 1: GFP-like chromoprotein FP595



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	76.52Å 125.40Å 92.75Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 1.38 18.74 – 1.38	Depositor EDS
% Data completeness (in resolution range)	96.5 (50.00-1.38) 95.5 (18.74-1.38)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	6.63 (at 1.38Å)	Xtriage
Refinement program	SHELXL-97	Depositor
R, R_{free}	0.139 , 0.191 0.147 , 0.154	Depositor DCC
R_{free} test set	4307 reflections (5.17%)	DCC
Wilson B-factor (Å ²)	13.5	Xtriage
Anisotropy	0.285	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 60.7	EDS
Estimated twinning fraction	0.006 for 1/2*h-1/2*k,-3/2*h-1/2*k,-l 0.011 for 1/2*h+1/2*k,3/2*h-1/2*k,-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Outliers	1 of 89407 reflections (0.001%)	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	4295	wwPDB-VP
Average B, all atoms (Å ²)	22.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.74% of the height of the origin peak. No significant pseudotranslation is detected.*

¹ Intensities estimated from amplitudes.

² Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ 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: CRK, NH2, BME

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	0.60	0/2001	1.31	16/2691 (0.6%)
1	B	0.62	0/2027	1.30	13/2729 (0.5%)
All	All	0.61	0/4028	1.31	29/5420 (0.5%)

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	1

There are no bond length outliers.

All (29) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	-3	HIS	C-N-CA	15.81	161.24	121.70
1	A	155[A]	ARG	NE-CZ-NH1	8.96	124.78	120.30
1	A	155[B]	ARG	NE-CZ-NH1	8.96	124.78	120.30
1	A	223	ASP	CB-CG-OD2	8.13	125.61	118.30
1	A	214	TYR	CB-CG-CD2	8.07	125.84	121.00
1	A	150	VAL	C-N-CA	7.25	139.84	121.70
1	B	211[A]	TYR	CB-CG-CD2	7.11	125.27	121.00
1	B	211[B]	TYR	CB-CG-CD2	7.11	125.27	121.00
1	A	214	TYR	CB-CG-CD1	-6.77	116.94	121.00
1	B	211[A]	TYR	CB-CG-CD1	-6.40	117.16	121.00
1	B	211[B]	TYR	CB-CG-CD1	-6.40	117.16	121.00
1	A	151	ASP	C-N-CA	6.12	135.14	122.30
1	B	151	ASP	CA-CB-CG	6.09	126.81	113.40
1	A	129	ASP	CB-CG-OD1	6.01	123.71	118.30

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	96	TYR	CB-CG-CD2	-5.96	117.42	121.00
1	B	155[A]	ARG	CD-NE-CZ	5.89	131.84	123.60
1	B	155[B]	ARG	CD-NE-CZ	5.89	131.84	123.60
1	B	151	ASP	CB-CG-OD2	5.68	123.42	118.30
1	A	117	TYR	CG-CD1-CE1	-5.58	116.83	121.30
1	B	-3	HIS	CA-CB-CG	5.36	122.72	113.60
1	A	79	TYR	CB-CG-CD1	5.34	124.20	121.00
1	B	223[A]	ASP	CB-CG-OD1	5.33	123.10	118.30
1	B	223[B]	ASP	CB-CG-OD1	5.33	123.10	118.30
1	A	195[A]	GLU	OE1-CD-OE2	-5.33	116.91	123.30
1	A	195[B]	GLU	OE1-CD-OE2	-5.33	116.91	123.30
1	A	211[A]	TYR	CB-CG-CD1	-5.20	117.88	121.00
1	A	211[B]	TYR	CB-CG-CD1	-5.20	117.88	121.00
1	A	4	PHE	O-C-N	-5.03	114.65	122.70
1	A	198	ARG	NE-CZ-NH1	5.03	122.81	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	-3	HIS	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	1884	0	1823	21	0
1	B	1918	0	1839	19	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	16	0	20	4	0
3	B	12	0	15	2	0
4	A	230	0	0	6	0
4	B	233	0	0	6	0
All	All	4295	0	3697	41	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.

All (41) 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:A:131:PRO:HG3	3:A:252:BME:H22	1.52	0.91
1:B:95[A]:THR:HG21	4:B:335:HOH:O	1.85	0.76
1:B:114:CYS:HB2	3:B:251:BME:H12	1.71	0.72
1:A:144[A]:THR:HG22	1:A:196:ASP:OD1	1.93	0.68
1:B:144[A]:THR:HG22	1:B:196:ASP:OD1	1.92	0.67
3:A:252:BME:H12	4:A:407:HOH:O	1.96	0.66
1:B:204:GLU:HB3	1:B:211[A]:TYR:CE2	2.32	0.64
1:B:44[B]:GLU:HG2	4:B:377:HOH:O	2.00	0.60
1:A:5:LEU:HA	1:A:9[A]:MET:CE	2.38	0.54
1:A:208:GLY:HA2	1:A:211[B]:TYR:OH	2.09	0.53
1:A:95[A]:THR:HG21	4:A:335:HOH:O	2.08	0.53
1:A:25[A]:LYS:HE3	4:A:457:HOH:O	2.11	0.49
1:A:13[A]:THR:HG21	1:A:62:CYS:O	2.13	0.49
1:A:5:LEU:HD22	1:A:9[A]:MET:SD	2.53	0.48
1:A:5:LEU:HA	1:A:9[A]:MET:HE3	1.96	0.48
1:A:204:GLU:HG3	1:A:211[A]:TYR:CE2	2.48	0.48
1:A:162:LEU:O	1:A:169:HIS:HA	2.14	0.48
1:B:175:HIS:HE1	4:B:316:HOH:O	1.97	0.47
1:A:205:VAL:O	1:A:209:LYS:NZ	2.49	0.46
1:B:150[B]:VAL:HG11	1:B:155[B]:ARG:HG3	1.98	0.45
1:B:114:CYS:CB	3:B:251:BME:H12	2.43	0.45
1:A:42[B]:LYS:NZ	3:A:253:BME:O1	2.49	0.45
1:A:12:LYS:NZ	4:A:475:HOH:O	2.50	0.45
1:A:36[B]:GLU:HG3	4:A:386:HOH:O	2.16	0.45
1:A:131:PRO:CG	3:A:252:BME:H22	2.35	0.45
1:B:9[B]:MET:SD	1:B:115:LEU:HD11	2.56	0.44
1:B:155[A]:ARG:NH1	4:B:471:HOH:O	2.50	0.44
1:B:16[B]:GLU:OE1	1:B:23:TYR:OH	2.35	0.44
1:B:152:GLY:N	4:B:485:HOH:O	2.48	0.44
1:A:104:ALA:HB2	1:A:121[B]:ILE:HD13	2.00	0.43
1:A:58:LEU:HD22	1:A:121[A]:ILE:CD1	2.50	0.42
1:A:120[A]:LYS:HE3	4:B:370:HOH:O	2.18	0.42
1:A:71[A]:LYS:NZ	4:A:405:HOH:O	2.50	0.42
1:B:150[B]:VAL:CG1	1:B:155[B]:ARG:HG3	2.50	0.42
1:B:95[A]:THR:HG22	1:B:101:PHE:CE2	2.55	0.41
1:B:203:GLU:HG3	1:B:204:GLU:N	2.35	0.41
1:B:162:LEU:O	1:B:169:HIS:HA	2.20	0.41
1:A:176:THR:HG21	1:A:178:TYR:CZ	2.56	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:84:PHE:O	1:B:182:LYS:NZ	2.54	0.41
1:B:65:CRK:O2	1:B:65:CRK:HD2	2.21	0.41
1:B:-3:HIS:ND1	1:B:-2:HIS:N	2.68	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	240/241 (100%)	234 (98%)	6 (2%)	0	100	100
1	B	244/241 (101%)	240 (98%)	4 (2%)	0	100	100
All	All	484/482 (100%)	474 (98%)	10 (2%)	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	210/201 (104%)	200 (95%)	10 (5%)	31	4
1	B	212/201 (106%)	206 (97%)	6 (3%)	51	14
All	All	422/402 (105%)	406 (96%)	16 (4%)	41	7

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	4	PHE
1	A	113	ASP
1	A	120[A]	LYS
1	A	120[B]	LYS
1	A	124	ASN
1	A	135	ASN
1	A	136	LYS
1	A	181[A]	LYS
1	A	181[B]	LYS
1	A	209	LYS
1	B	-3	HIS
1	B	124	ASN
1	B	202	MET
1	B	203	GLU
1	B	204	GLU
1	B	229	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	124	ASN
1	B	124	ASN
1	B	157	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

2 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
1	CRK	A	65	1	23,24,24	1.71	5 (21%)	24,32,32	3.93	8 (33%)
1	CRK	B	65	1	23,24,24	1.70	7 (30%)	24,32,32	3.52	7 (29%)

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
1	CRK	A	65	1	-	0/12/31/31	0/2/2/2
1	CRK	B	65	1	-	0/12/31/31	0/2/2/2

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	65	CRK	CG2-CB2	-4.68	1.37	1.46
1	B	65	CRK	CG2-CB2	-3.46	1.39	1.46
1	B	65	CRK	CA3-N3	-3.22	1.41	1.47
1	A	65	CRK	CA3-N3	-2.52	1.43	1.47
1	B	65	CRK	CB2-CA2	2.15	1.37	1.35
1	A	65	CRK	CE2-CZ	2.20	1.45	1.41
1	B	65	CRK	C1-N3	2.21	1.43	1.38
1	B	65	CRK	CD2-CG2	2.44	1.44	1.39
1	B	65	CRK	CD1-CG2	2.52	1.44	1.39
1	A	65	CRK	CE1-CZ	2.56	1.46	1.41
1	B	65	CRK	CE1-CZ	2.81	1.47	1.41
1	A	65	CRK	CD2-CG2	3.14	1.45	1.39

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	65	CRK	CB2-CA2-N2	-8.68	113.15	128.67
1	B	65	CRK	CB2-CA2-N2	-7.34	115.55	128.67
1	A	65	CRK	CA3-N3-C2	-3.92	117.60	123.99
1	A	65	CRK	CA2-C2-N3	-3.83	101.48	103.40
1	B	65	CRK	O2-C2-N3	-2.40	119.33	124.50
1	B	65	CRK	CA3-N3-C2	-2.27	120.29	123.99
1	B	65	CRK	CG2-CB2-CA2	2.87	133.94	130.22
1	A	65	CRK	N3-C1-N2	3.13	116.81	113.26
1	B	65	CRK	C2-CA2-N2	4.00	112.11	108.91
1	A	65	CRK	C2-CA2-N2	6.13	113.80	108.91
1	B	65	CRK	CB2-CA2-C2	6.52	131.91	122.36

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	65	CRK	CB2-CA2-C2	6.95	132.54	122.36
1	A	65	CRK	CG2-CB2-CA2	8.48	141.23	130.22
1	A	65	CRK	O2-C2-CA2	9.26	135.95	130.95
1	B	65	CRK	O2-C2-CA2	12.46	137.68	130.95

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	B	65	CRK	1	0

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 9 ligands modelled in this entry, 2 are modelled with single atom - leaving 7 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	$\# Z > 2$
3	BME	A	250	1	3,3,3	0.27	0	2,2,2	0.36	0
3	BME	A	251	1	3,3,3	0.53	0	2,2,2	0.11	0
3	BME	A	252	1	3,3,3	0.35	0	2,2,2	0.48	0
3	BME	A	253	1	3,3,3	0.35	0	2,2,2	0.78	0
3	BME	B	250	1	3,3,3	0.47	0	2,2,2	0.49	0
3	BME	B	251	1	3,3,3	0.51	0	2,2,2	0.59	0
3	BME	B	252	1	3,3,3	0.58	0	2,2,2	1.49	1 (50%)

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
3	BME	A	250	1	-	0/1/1/1	0/0/0/0
3	BME	A	251	1	-	0/1/1/1	0/0/0/0
3	BME	A	252	1	-	0/1/1/1	0/0/0/0
3	BME	A	253	1	-	0/1/1/1	0/0/0/0
3	BME	B	250	1	-	0/1/1/1	0/0/0/0
3	BME	B	251	1	-	0/1/1/1	0/0/0/0
3	BME	B	252	1	-	0/1/1/1	0/0/0/0

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	252	BME	O1-C1-C2	-2.10	101.64	110.83

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	252	BME	3	0
3	A	253	BME	1	0
3	B	251	BME	2	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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	224/241 (92%)	0.32	11 (4%) 33 32	10, 22, 35, 51	0
1	B	231/241 (95%)	0.18	7 (3%) 54 54	10, 17, 31, 65	0
All	All	455/482 (94%)	0.25	18 (3%) 42 42	10, 19, 35, 65	0

All (18) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	-3	HIS	8.7
1	A	4	PHE	8.2
1	B	205	VAL	6.4
1	A	151	ASP	5.5
1	B	151	ASP	4.7
1	A	205	VAL	4.5
1	A	166	GLY	4.3
1	A	113	ASP	4.0
1	A	184	ALA	3.9
1	A	165	PRO	3.5
1	B	204	GLU	3.3
1	A	5	LEU	2.8
1	B	203	GLU	2.8
1	A	112	GLY	2.5
1	A	185	SER	2.5
1	A	164	CYS	2.3
1	B	129	ASP	2.1
1	B	184	ALA	2.1

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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, 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	LLDF	B-factors(Å ²)	Q<0.9
1	CRK	A	65	23/23	0.97	0.06	-	13,16,20,24	0
1	CRK	B	65	23/23	0.98	0.05	-	12,15,17,22	0

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

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, 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	LLDF	B-factors(Å ²)	Q<0.9
2	NH2	B	240	1/1	0.96	0.11	4.58	22,22,22,22	0
2	NH2	A	240	1/1	0.97	0.13	4.00	31,31,31,31	0
3	BME	A	252	4/4	0.94	0.22	2.83	60,92,92,93	0
3	BME	A	253	4/4	0.96	0.19	1.08	41,54,57,57	0
3	BME	B	252	4/4	0.91	0.12	0.72	23,28,32,39	0
3	BME	A	250	4/4	0.99	0.09	0.37	18,18,20,33	0
3	BME	B	250	4/4	0.98	0.09	0.15	14,15,18,24	0
3	BME	A	251	4/4	0.98	0.11	-0.21	29,47,47,54	0
3	BME	B	251	4/4	0.98	0.12	-	22,34,36,45	0

6.5 Other polymers [i](#)

There are no such residues in this entry.