



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 03:40 PM GMT

PDB ID : 4CZ2
Title : Complex of human VARP-ANKRD1 with Rab32-GppCp. Selenomet derivative.
Authors : Perez-Dorado, I.; Schaefer, I.B.; McCoy, A.J.; Owen, D.J.; Evans, P.R.
Deposited on : 2014-04-16
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 ⓘ 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

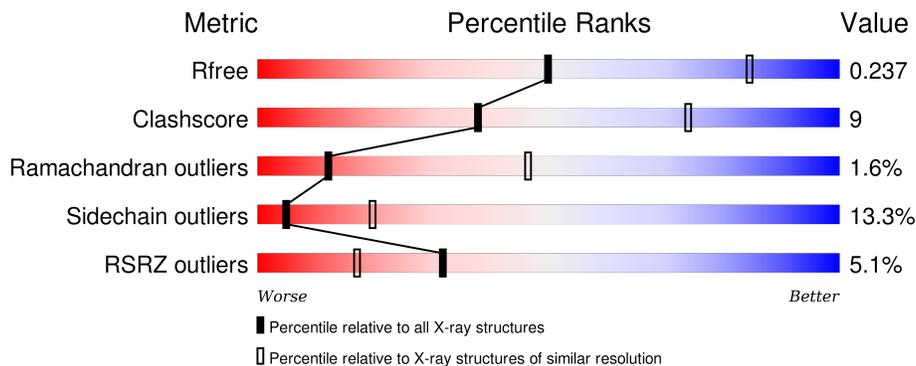
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 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 $\leq 5\%$. 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	230	 55% 16% 25%
1	B	230	 59% 14% 22%
1	C	230	 57% 14% 25%
2	D	203	 63% 16% 17%
2	E	203	 64% 15% 18%

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Mol	Chain	Length	Quality of chain										
2	F	203	 <p>A horizontal bar chart showing the quality distribution of chain F. The bar is divided into four segments: a small red segment (7%), a large green segment (65%), a yellow segment (13%), and a grey segment (19%).</p> <table border="1"><thead><tr><th>Color</th><th>Percentage</th></tr></thead><tbody><tr><td>Red</td><td>7%</td></tr><tr><td>Green</td><td>65%</td></tr><tr><td>Yellow</td><td>13%</td></tr><tr><td>Grey</td><td>19%</td></tr></tbody></table>	Color	Percentage	Red	7%	Green	65%	Yellow	13%	Grey	19%
Color	Percentage												
Red	7%												
Green	65%												
Yellow	13%												
Grey	19%												

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 8249 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 RAS-RELATED PROTEIN RAB-32.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
			Total	C	N	O	S				Se
1	A	172	1388	892	242	247	2	5	0	0	0
1	B	179	1441	924	250	260	2	5	0	0	0
1	C	173	1394	895	243	249	2	5	0	0	0

There are 30 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-4	GLY	-	EXPRESSION TAG	UNP Q13637
A	-3	PRO	-	EXPRESSION TAG	UNP Q13637
A	-2	LEU	-	EXPRESSION TAG	UNP Q13637
A	-1	GLY	-	EXPRESSION TAG	UNP Q13637
A	0	SER	-	EXPRESSION TAG	UNP Q13637
A	85	LEU	GLN	ENGINEERED MUTATION	UNP Q13637
A	100	MSE	VAL	ENGINEERED MUTATION	UNP Q13637
A	153	MSE	GLN	ENGINEERED MUTATION	UNP Q13637
A	158	MSE	VAL	ENGINEERED MUTATION	UNP Q13637
A	192	MSE	ILE	ENGINEERED MUTATION	UNP Q13637
B	-4	GLY	-	EXPRESSION TAG	UNP Q13637
B	-3	PRO	-	EXPRESSION TAG	UNP Q13637
B	-2	LEU	-	EXPRESSION TAG	UNP Q13637
B	-1	GLY	-	EXPRESSION TAG	UNP Q13637
B	0	SER	-	EXPRESSION TAG	UNP Q13637
B	85	LEU	GLN	ENGINEERED MUTATION	UNP Q13637
B	100	MSE	VAL	ENGINEERED MUTATION	UNP Q13637
B	153	MSE	GLN	ENGINEERED MUTATION	UNP Q13637
B	158	MSE	VAL	ENGINEERED MUTATION	UNP Q13637
B	192	MSE	ILE	ENGINEERED MUTATION	UNP Q13637
C	-4	GLY	-	EXPRESSION TAG	UNP Q13637
C	-3	PRO	-	EXPRESSION TAG	UNP Q13637
C	-2	LEU	-	EXPRESSION TAG	UNP Q13637

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-1	GLY	-	EXPRESSION TAG	UNP Q13637
C	0	SER	-	EXPRESSION TAG	UNP Q13637
C	85	LEU	GLN	ENGINEERED MUTATION	UNP Q13637
C	100	MSE	VAL	ENGINEERED MUTATION	UNP Q13637
C	153	MSE	GLN	ENGINEERED MUTATION	UNP Q13637
C	158	MSE	VAL	ENGINEERED MUTATION	UNP Q13637
C	192	MSE	ILE	ENGINEERED MUTATION	UNP Q13637

- Molecule 2 is a protein called ANKYRIN REPEAT DOMAIN-CONTAINING PROTEIN 27.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	D	168	1283	804	225	246	8	0	0	0
2	E	166	1269	795	223	243	8	0	0	0
2	F	165	1262	790	222	242	8	0	0	0

There are 36 discrepancies between the modelled and reference sequences:

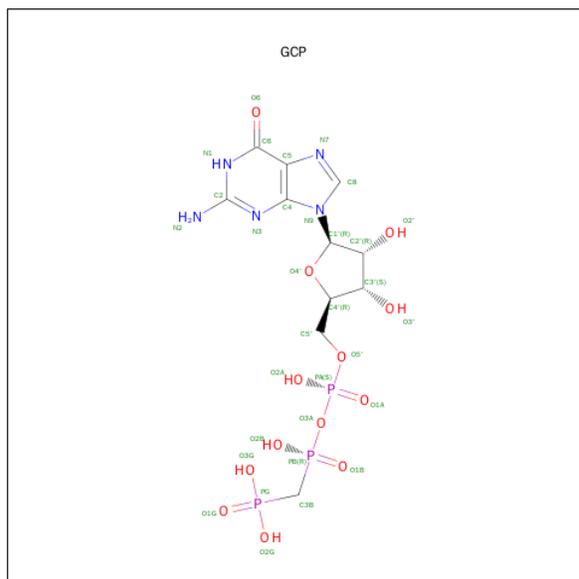
Chain	Residue	Modelled	Actual	Comment	Reference
D	444	GLY	-	EXPRESSION TAG	UNP Q96NW4
D	445	PRO	-	EXPRESSION TAG	UNP Q96NW4
D	446	LEU	-	EXPRESSION TAG	UNP Q96NW4
D	447	GLY	-	EXPRESSION TAG	UNP Q96NW4
D	448	SER	-	EXPRESSION TAG	UNP Q96NW4
D	449	MET	-	EXPRESSION TAG	UNP Q96NW4
D	641	HIS	-	EXPRESSION TAG	UNP Q96NW4
D	642	HIS	-	EXPRESSION TAG	UNP Q96NW4
D	643	HIS	-	EXPRESSION TAG	UNP Q96NW4
D	644	HIS	-	EXPRESSION TAG	UNP Q96NW4
D	645	HIS	-	EXPRESSION TAG	UNP Q96NW4
D	646	HIS	-	EXPRESSION TAG	UNP Q96NW4
E	444	GLY	-	EXPRESSION TAG	UNP Q96NW4
E	445	PRO	-	EXPRESSION TAG	UNP Q96NW4
E	446	LEU	-	EXPRESSION TAG	UNP Q96NW4
E	447	GLY	-	EXPRESSION TAG	UNP Q96NW4
E	448	SER	-	EXPRESSION TAG	UNP Q96NW4
E	449	MET	-	EXPRESSION TAG	UNP Q96NW4
E	641	HIS	-	EXPRESSION TAG	UNP Q96NW4
E	642	HIS	-	EXPRESSION TAG	UNP Q96NW4
E	643	HIS	-	EXPRESSION TAG	UNP Q96NW4

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Chain	Residue	Modelled	Actual	Comment	Reference
E	644	HIS	-	EXPRESSION TAG	UNP Q96NW4
E	645	HIS	-	EXPRESSION TAG	UNP Q96NW4
E	646	HIS	-	EXPRESSION TAG	UNP Q96NW4
F	444	GLY	-	EXPRESSION TAG	UNP Q96NW4
F	445	PRO	-	EXPRESSION TAG	UNP Q96NW4
F	446	LEU	-	EXPRESSION TAG	UNP Q96NW4
F	447	GLY	-	EXPRESSION TAG	UNP Q96NW4
F	448	SER	-	EXPRESSION TAG	UNP Q96NW4
F	449	MET	-	EXPRESSION TAG	UNP Q96NW4
F	641	HIS	-	EXPRESSION TAG	UNP Q96NW4
F	642	HIS	-	EXPRESSION TAG	UNP Q96NW4
F	643	HIS	-	EXPRESSION TAG	UNP Q96NW4
F	644	HIS	-	EXPRESSION TAG	UNP Q96NW4
F	645	HIS	-	EXPRESSION TAG	UNP Q96NW4
F	646	HIS	-	EXPRESSION TAG	UNP Q96NW4

- Molecule 3 is PHOSPHOMETHYLPHOSPHONIC ACID GUANYLATE ESTER (three-letter code: GCP) (formula: C₁₁H₁₈N₅O₁₃P₃).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
3	A	1	Total	C	N	O	P	0	0
			32	11	5	13	3		
3	B	1	Total	C	N	O	P	0	0
			32	11	5	13	3		
3	C	1	Total	C	N	O	P	0	0
			32	11	5	13	3		

- Molecule 4 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	B	1	Total Mg 1 1	0	0
4	A	1	Total Mg 1 1	0	0
4	C	1	Total Mg 1 1	0	0

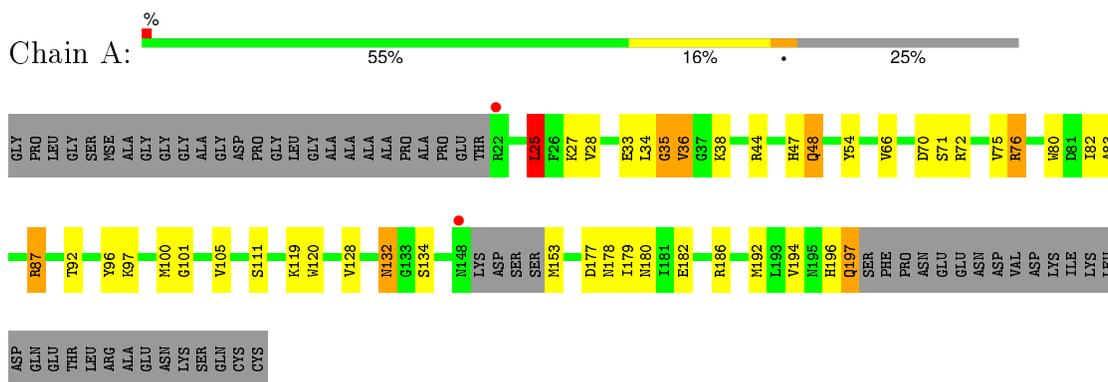
- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	24	Total O 24 24	0	0
5	B	24	Total O 24 24	0	0
5	C	16	Total O 16 16	0	0
5	D	18	Total O 18 18	0	0
5	E	17	Total O 17 17	0	0
5	F	14	Total O 14 14	0	0

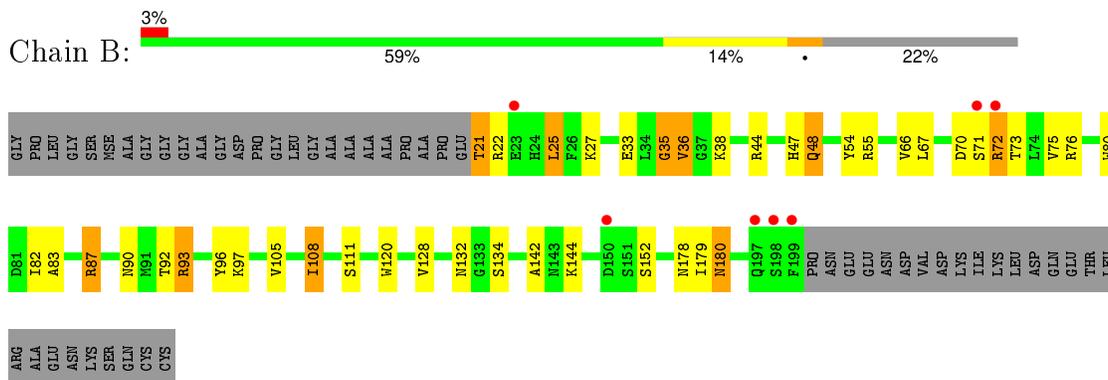
3 Residue-property plots [i](#)

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

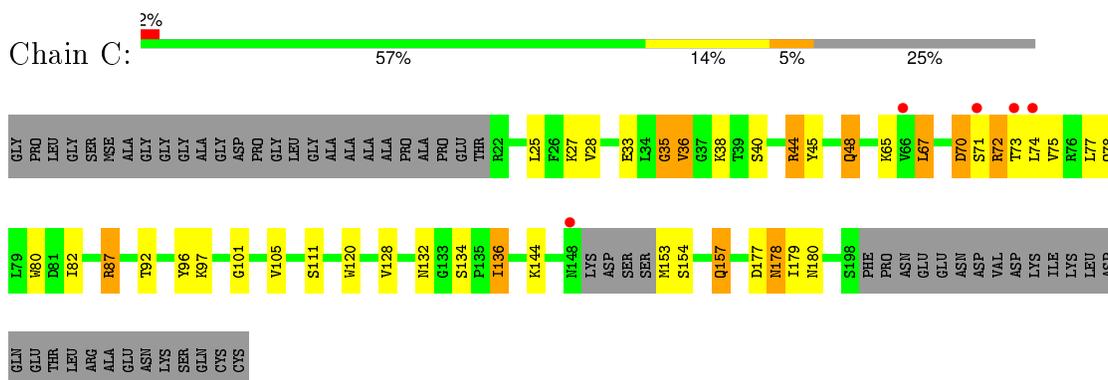
- Molecule 1: RAS-RELATED PROTEIN RAB-32



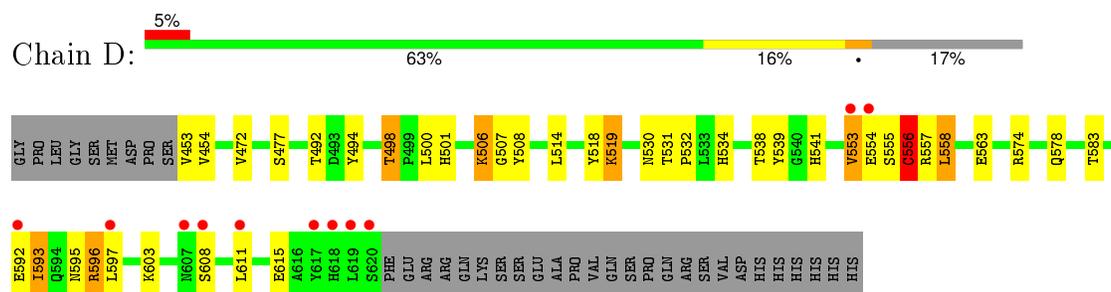
- Molecule 1: RAS-RELATED PROTEIN RAB-32



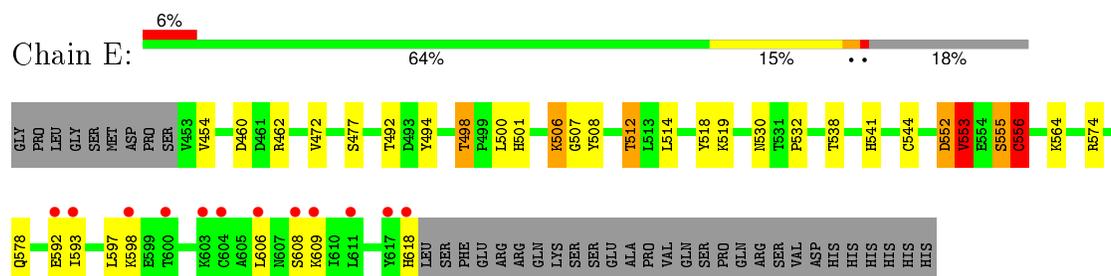
- Molecule 1: RAS-RELATED PROTEIN RAB-32



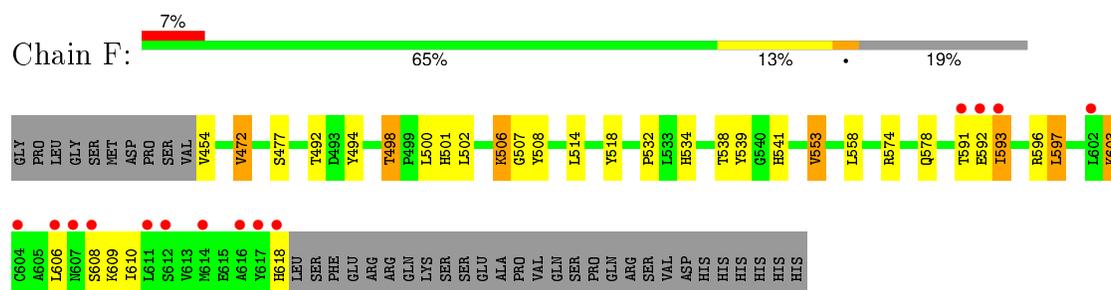
- Molecule 2: ANKYRIN REPEAT DOMAIN-CONTAINING PROTEIN 27



- Molecule 2: ANKYRIN REPEAT DOMAIN-CONTAINING PROTEIN 27



- Molecule 2: ANKYRIN REPEAT DOMAIN-CONTAINING PROTEIN 27



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	113.05Å 122.49Å 131.58Å 90.00° 113.25° 90.00°	Depositor
Resolution (Å)	120.89 – 2.97 57.05 – 2.97	Depositor EDS
% Data completeness (in resolution range)	97.1 (120.89-2.97) 97.1 (57.05-2.97)	Depositor EDS
R_{merge}	0.22	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.86 (at 2.96Å)	Xtriage
Refinement program	REFMAC 5.8.0069	Depositor
R, R_{free}	0.195 , 0.232 0.203 , 0.237	Depositor DCC
R_{free} test set	1679 reflections (5.35%)	DCC
Wilson B-factor (Å ²)	45.7	Xtriage
Anisotropy	0.746	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 54.6	EDS
Estimated twinning fraction	0.036 for h,-k,-h-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.28$	Xtriage
Outliers	0 of 33059 reflections	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	8249	wwPDB-VP
Average B, all atoms (Å ²)	42.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.05% 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, 0.375 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: GCP, MG

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	0.59	0/1415	0.78	1/1901 (0.1%)
1	B	0.57	0/1469	0.76	1/1973 (0.1%)
1	C	0.54	0/1421	0.77	0/1909
2	D	0.57	0/1308	0.77	0/1780
2	E	0.58	0/1294	0.75	0/1761
2	F	0.56	0/1287	0.75	0/1751
All	All	0.57	0/8194	0.76	2/11075 (0.0%)

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	C	0	1
2	D	0	1
2	E	0	1
2	F	0	1
All	All	0	4

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	25	LEU	CB-CG-CD1	5.40	120.18	111.00
1	B	55	ARG	NE-CZ-NH1	5.17	122.89	120.30

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	70	ASP	Peptide
2	D	593	ILE	Peptide
2	E	555	SER	Peptide
2	F	593	ILE	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	1388	0	1382	34	0
1	B	1441	0	1431	27	0
1	C	1394	0	1387	24	0
2	D	1283	0	1268	34	0
2	E	1269	0	1252	28	0
2	F	1262	0	1243	14	0
3	A	32	0	14	3	0
3	B	32	0	14	4	0
3	C	32	0	14	3	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
4	C	1	0	0	0	0
5	A	24	0	0	0	0
5	B	24	0	0	2	0
5	C	16	0	0	0	0
5	D	18	0	0	2	0
5	E	17	0	0	2	0
5	F	14	0	0	1	0
All	All	8249	0	8005	149	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 9.

The worst 5 of 149 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:25:LEU:HG	2:D:553:VAL:HG12	1.28	1.13
1:A:25:LEU:HG	2:D:553:VAL:CG1	1.88	1.04

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:25:LEU:HD13	1:A:76:ARG:HB3	1.42	0.99
1:A:101:GLY:N	1:A:192:MSE:HE2	1.86	0.90
2:D:507:GLY:HA3	2:D:541:HIS:ND1	1.86	0.90

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	168/230 (73%)	163 (97%)	3 (2%)	2 (1%)	16	54
1	B	177/230 (77%)	166 (94%)	8 (4%)	3 (2%)	11	44
1	C	169/230 (74%)	161 (95%)	6 (4%)	2 (1%)	16	54
2	D	166/203 (82%)	153 (92%)	10 (6%)	3 (2%)	11	43
2	E	164/203 (81%)	150 (92%)	10 (6%)	4 (2%)	7	34
2	F	163/203 (80%)	151 (93%)	10 (6%)	2 (1%)	16	54
All	All	1007/1299 (78%)	944 (94%)	47 (5%)	16 (2%)	12	46

5 of 16 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	E	553	VAL
2	D	556	CYS
2	D	593	ILE
2	E	556	CYS
2	E	593	ILE

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	150/186 (81%)	132 (88%)	18 (12%)	6	25
1	B	157/186 (84%)	135 (86%)	22 (14%)	4	18
1	C	151/186 (81%)	133 (88%)	18 (12%)	6	25
2	D	140/172 (81%)	123 (88%)	17 (12%)	6	24
2	E	138/172 (80%)	117 (85%)	21 (15%)	3	15
2	F	137/172 (80%)	117 (85%)	20 (15%)	4	16
All	All	873/1074 (81%)	757 (87%)	116 (13%)	5	20

5 of 116 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	132	ASN
2	D	519	LYS
2	F	592	GLU
1	C	136	ILE
2	D	472	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 16 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	132	ASN
1	C	178	ASN
2	E	464	HIS
1	C	78	GLN
2	E	501	HIS

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](#)

Of 6 ligands modelled in this entry, 3 are monoatomic - leaving 3 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	GCP	A	1198	4	26,34,34	1.29	3 (11%)	34,54,54	1.91	10 (29%)
3	GCP	B	1198	4	26,34,34	1.28	4 (15%)	34,54,54	1.94	8 (23%)
3	GCP	C	1198	4	26,34,34	1.38	5 (19%)	34,54,54	2.03	8 (23%)

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	GCP	A	1198	4	-	0/15/38/38	0/3/3/3
3	GCP	B	1198	4	-	0/15/38/38	0/3/3/3
3	GCP	C	1198	4	-	0/15/38/38	0/3/3/3

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	1198	GCP	C4-N3	-2.11	1.32	1.35
3	C	1198	GCP	C6-C5	2.34	1.45	1.41
3	C	1198	GCP	PG-O3G	2.36	1.60	1.54
3	C	1198	GCP	C5-C4	2.40	1.45	1.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	1198	GCP	C6-C5	2.43	1.46	1.41

The worst 5 of 26 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	1198	GCP	C5-C6-N1	-5.58	115.97	123.59
3	C	1198	GCP	C5-C6-N1	-4.96	116.80	123.59
3	C	1198	GCP	PA-O3A-PB	-4.73	119.44	132.73
3	A	1198	GCP	C5-C6-N1	-4.65	117.23	123.59
3	B	1198	GCP	PA-O3A-PB	-3.74	122.23	132.73

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1198	GCP	3	0
3	B	1198	GCP	4	0
3	C	1198	GCP	3	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	167/230 (72%)	-0.11	2 (1%) 81 61	15, 31, 58, 89	0
1	B	174/230 (75%)	0.12	7 (4%) 42 23	21, 37, 81, 105	0
1	C	168/230 (73%)	0.16	5 (2%) 54 32	25, 49, 75, 86	0
2	D	168/203 (82%)	0.15	11 (6%) 22 11	15, 33, 67, 95	0
2	E	166/203 (81%)	0.24	12 (7%) 18 9	18, 39, 77, 105	0
2	F	165/203 (81%)	0.25	14 (8%) 13 6	21, 36, 74, 91	0
All	All	1008/1299 (77%)	0.14	51 (5%) 32 17	15, 37, 75, 105	0

The worst 5 of 51 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	E	618	HIS	4.9
1	B	199	PHE	4.3
1	B	198	SER	3.7
2	F	592	GLU	3.5
2	E	592	GLU	3.5

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](#)

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(\AA^2)	Q<0.9
3	GCP	A	1198	32/32	0.98	0.15	-0.66	13,16,20,21	0
3	GCP	B	1198	32/32	0.98	0.15	-0.75	15,19,27,29	0
3	GCP	C	1198	32/32	0.98	0.14	-1.01	23,33,42,45	0
4	MG	C	1199	1/1	0.96	0.10	-	26,26,26,26	0
4	MG	B	1199	1/1	0.95	0.08	-	18,18,18,18	0
4	MG	A	1199	1/1	0.97	0.10	-	15,15,15,15	0

6.5 Other polymers [i](#)

There are no such residues in this entry.