



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 18, 2026 – 01:13 AM UTC

PDB ID : 5ZHX / pdb_00005zhx
Title : Crystal structure of SmgGDS-558 and farnesylated RhoA complex
Authors : Shimizu, H.; Toma-Fukai, S.; Shimizu, T.
Deposited on : 2018-03-13
Resolution : 3.50 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 types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

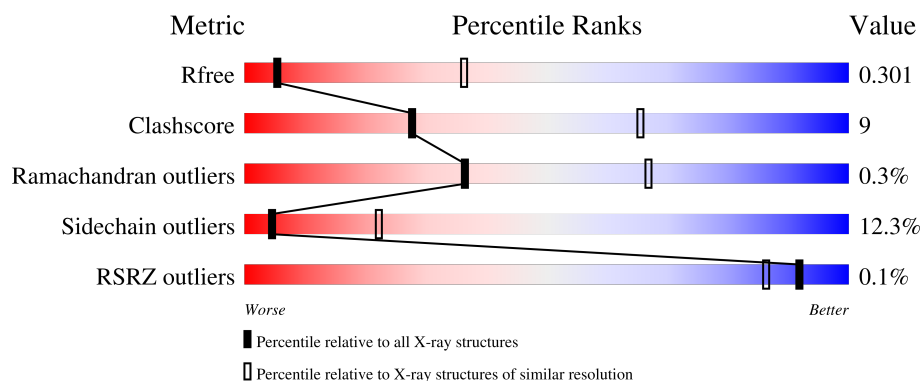
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.50 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}	180053	1085 (3.54-3.46)
Clashscore	190562	1140 (3.54-3.46)
Ramachandran outliers	187476	1113 (3.54-3.46)
Sidechain outliers	187428	1114 (3.54-3.46)
RSRZ outliers	180081	1084 (3.54-3.46)

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 of 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	487	
1	B	487	
1	C	487	
1	D	487	
2	e	198	

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Mol	Chain	Length	Quality of chain
2	f	198	62%15%••21%
2	g	198	62%15%•21%
2	h	198	% 60%18%5%18%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 18720 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 Rap1 GTPase-GDP dissociation stimulator 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	469	Total	C	N	O	S	0	0	0
			3411	2145	595	652	19			
1	B	469	Total	C	N	O	S	0	0	0
			3411	2145	595	652	19			
1	C	469	Total	C	N	O	S	0	0	0
			3411	2145	595	652	19			
1	D	469	Total	C	N	O	S	0	0	0
			3411	2145	595	652	19			

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	72	GLY	-	expression tag	UNP P52306
A	73	PRO	-	expression tag	UNP P52306
A	74	LEU	-	expression tag	UNP P52306
A	75	GLY	-	expression tag	UNP P52306
A	76	SER	-	expression tag	UNP P52306
B	72	GLY	-	expression tag	UNP P52306
B	73	PRO	-	expression tag	UNP P52306
B	74	LEU	-	expression tag	UNP P52306
B	75	GLY	-	expression tag	UNP P52306
B	76	SER	-	expression tag	UNP P52306
C	72	GLY	-	expression tag	UNP P52306
C	73	PRO	-	expression tag	UNP P52306
C	74	LEU	-	expression tag	UNP P52306
C	75	GLY	-	expression tag	UNP P52306
C	76	SER	-	expression tag	UNP P52306
D	72	GLY	-	expression tag	UNP P52306
D	73	PRO	-	expression tag	UNP P52306
D	74	LEU	-	expression tag	UNP P52306
D	75	GLY	-	expression tag	UNP P52306
D	76	SER	-	expression tag	UNP P52306

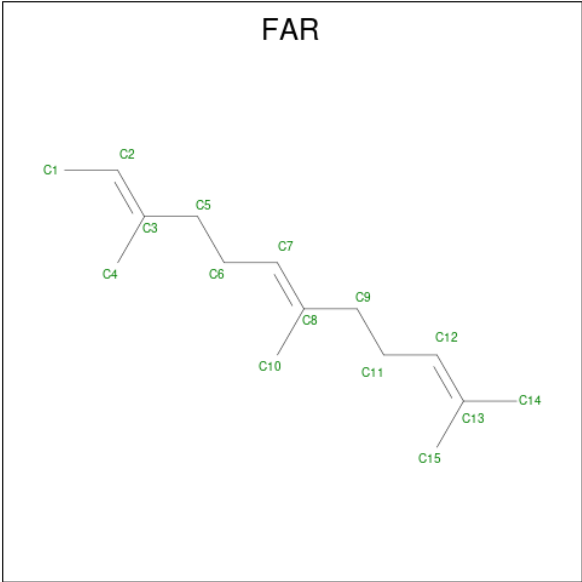
- Molecule 2 is a protein called Transforming protein RhoA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	e	163	Total	C	N	O	S	0	0	0
			1288	813	222	242	11			
2	f	156	Total	C	N	O	S	0	0	0
			1220	767	213	231	9			
2	g	156	Total	C	N	O	S	0	0	0
			1220	767	213	231	9			
2	h	163	Total	C	N	O	S	0	0	0
			1288	813	222	242	11			

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
e	-4	GLY	-	expression tag	UNP P61586
e	-3	PRO	-	expression tag	UNP P61586
e	-2	LEU	-	expression tag	UNP P61586
e	-1	GLY	-	expression tag	UNP P61586
e	0	SER	-	expression tag	UNP P61586
e	193	ALA	LEU	engineered mutation	UNP P61586
f	-4	GLY	-	expression tag	UNP P61586
f	-3	PRO	-	expression tag	UNP P61586
f	-2	LEU	-	expression tag	UNP P61586
f	-1	GLY	-	expression tag	UNP P61586
f	0	SER	-	expression tag	UNP P61586
f	193	ALA	LEU	engineered mutation	UNP P61586
g	-4	GLY	-	expression tag	UNP P61586
g	-3	PRO	-	expression tag	UNP P61586
g	-2	LEU	-	expression tag	UNP P61586
g	-1	GLY	-	expression tag	UNP P61586
g	0	SER	-	expression tag	UNP P61586
g	193	ALA	LEU	engineered mutation	UNP P61586
h	-4	GLY	-	expression tag	UNP P61586
h	-3	PRO	-	expression tag	UNP P61586
h	-2	LEU	-	expression tag	UNP P61586
h	-1	GLY	-	expression tag	UNP P61586
h	0	SER	-	expression tag	UNP P61586
h	193	ALA	LEU	engineered mutation	UNP P61586

- Molecule 3 is FARNESYL (CCD ID: FAR) (formula: C₁₅H₂₆).

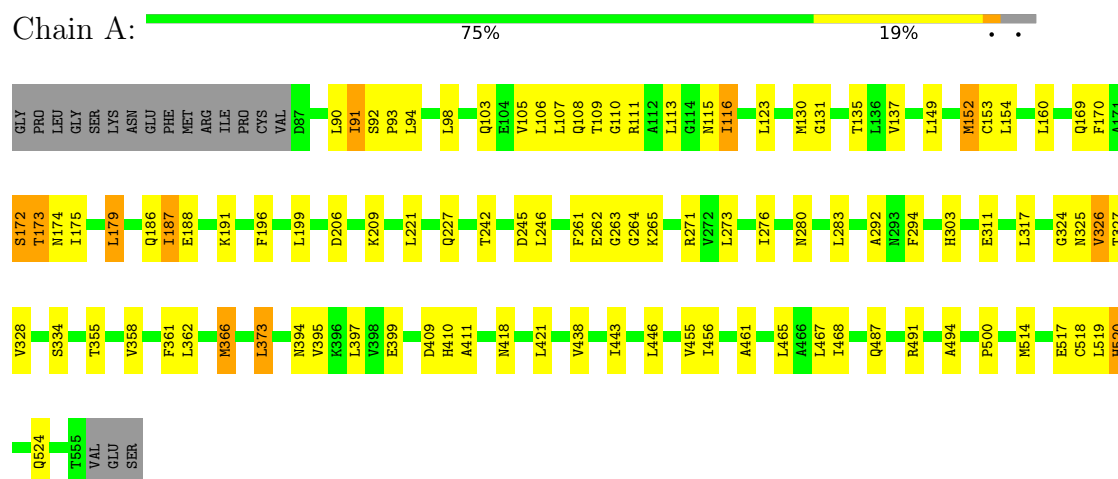


Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	e	1	Total C 15 15	0	0
3	f	1	Total C 15 15	0	0
3	g	1	Total C 15 15	0	0
3	h	1	Total C 15 15	0	0

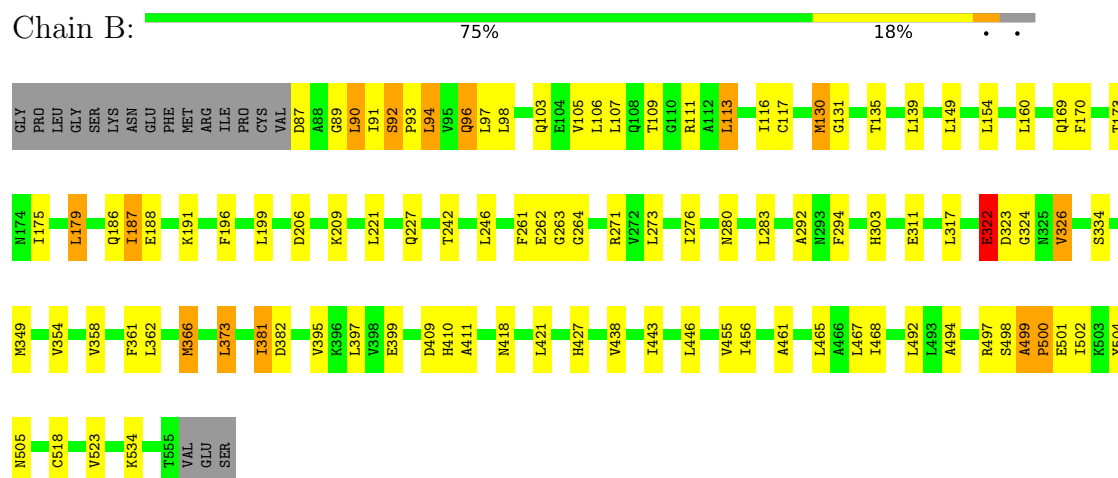
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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: Rap1 GTPase-GDP dissociation stimulator 1

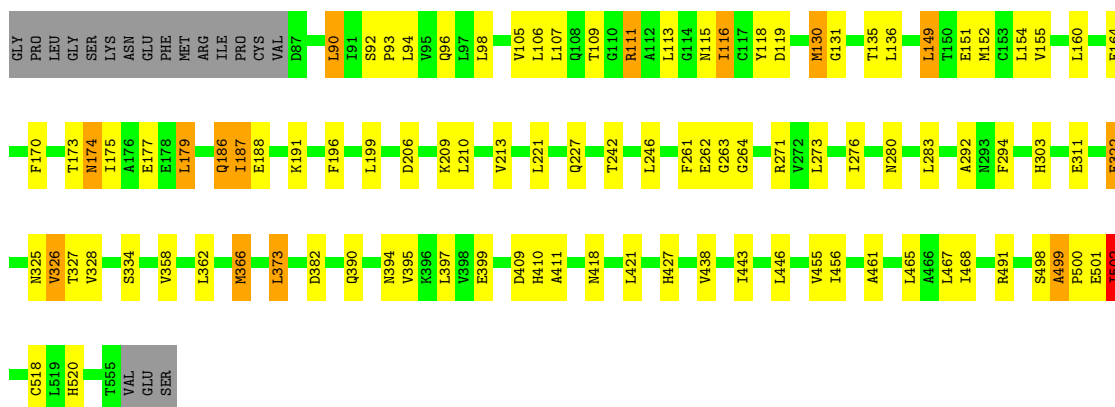


- Molecule 1: Rap1 GTPase-GDP dissociation stimulator 1



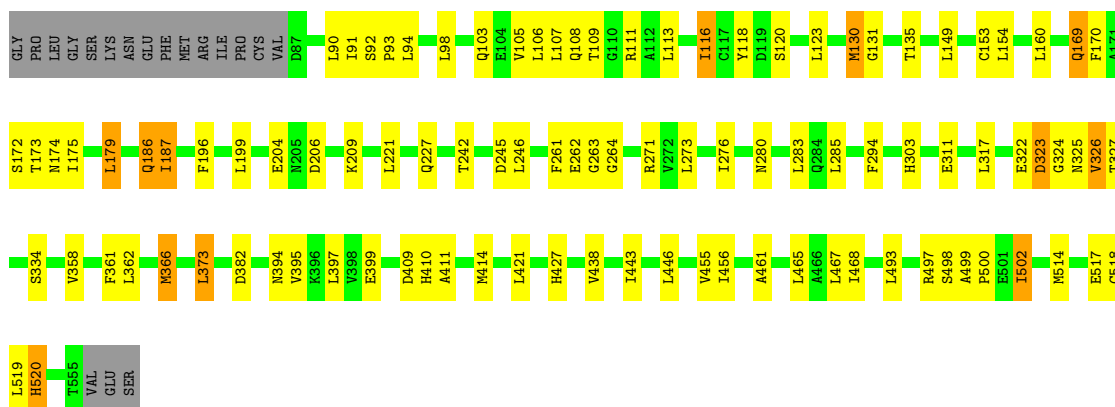
- Molecule 1: Rap1 GTPase-GDP dissociation stimulator 1





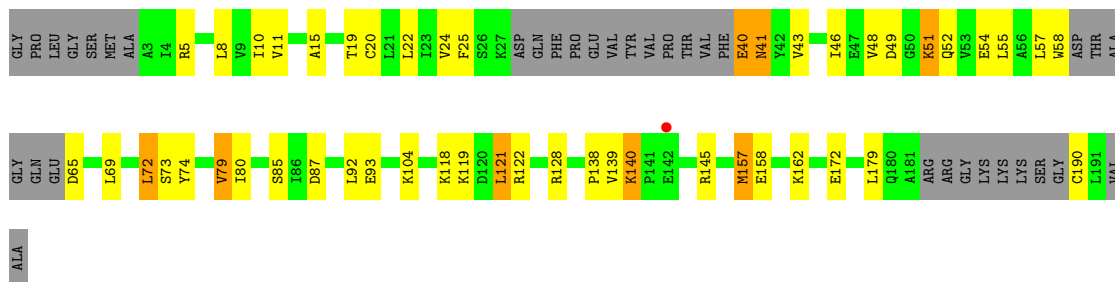
- Molecule 1: Rap1 GTPase-GDP dissociation stimulator 1

Chain D: 76% 18% . .



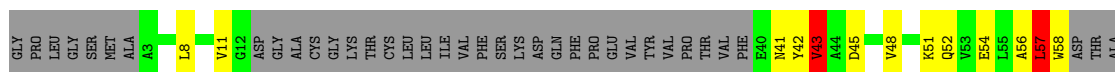
- Molecule 2: Transforming protein RhoA

Chain e: % 58% 21% . 18%



- Molecule 2: Transforming protein RhoA

Chain f: 62% 15% . . 21%



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	93.32Å 181.77Å 205.31Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	136.10 – 3.50 136.10 – 3.50	Depositor EDS
% Data completeness (in resolution range)	99.6 (136.10-3.50) 99.6 (136.10-3.50)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.09 (at 3.46Å)	Xtriage
Refinement program	REFMAC 5.8.0049	Depositor
R, R_{free}	0.250 , 0.306 0.248 , 0.301	Depositor DCC
R_{free} test set	2213 reflections (4.93%)	wwPDB-VP
Wilson B-factor (Å ²)	113.5	Xtriage
Anisotropy	0.055	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 89.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.26$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	18720	wwPDB-VP
Average B, all atoms (Å ²)	133.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.31% 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, 0.333 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: FAR

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	0.64	0/3443	0.99	4/4664 (0.1%)
1	B	0.65	1/3443 (0.0%)	1.03	8/4664 (0.2%)
1	C	0.63	1/3443 (0.0%)	0.99	5/4664 (0.1%)
1	D	0.66	1/3443 (0.0%)	1.01	6/4664 (0.1%)
2	e	0.74	0/1308	1.00	1/1760 (0.1%)
2	f	0.77	0/1240	1.01	4/1672 (0.2%)
2	g	0.75	0/1240	1.00	6/1672 (0.4%)
2	h	0.78	0/1308	1.01	5/1760 (0.3%)
All	All	0.68	3/18868 (0.0%)	1.01	39/25520 (0.2%)

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	2
1	C	0	3
1	D	0	3
2	e	0	1
2	f	0	4
2	g	0	1
All	All	0	16

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	502	ILE	CA-C	5.58	1.59	1.52
1	C	502	ILE	CA-C	5.58	1.59	1.52
1	B	322	GLU	N-CA	5.09	1.52	1.46

The worst 5 of 39 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	h	46	ILE	N-CA-C	10.24	125.40	113.42
2	e	46	ILE	N-CA-C	9.78	124.86	113.42
1	B	324	GLY	N-CA-C	8.78	124.74	113.24
1	B	117	CYS	N-CA-C	8.75	122.93	108.49
1	C	262	GLU	N-CA-C	8.41	123.11	113.02

There are no chirality outliers.

5 of 16 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	116	ILE	Peptide
1	A	494	ALA	Peptide
1	B	322	GLU	Peptide
1	B	499	ALA	Peptide
1	C	116	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	3411	0	3358	57	0
1	B	3411	0	3358	88	0
1	C	3411	0	3358	75	0
1	D	3411	0	3358	59	0
2	e	1288	0	1296	20	0
2	f	1220	0	1201	18	0
2	g	1220	0	1201	25	0
2	h	1288	0	1296	23	0
3	e	15	0	25	2	0
3	f	15	0	25	1	0
3	g	15	0	25	4	0
3	h	15	0	24	0	0
All	All	18720	0	18525	334	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 334 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:325:ASN:CG	1:C:327:THR:HG22	1.37	1.43
1:C:325:ASN:ND2	1:C:327:THR:HG22	1.32	1.39
1:B:186:GLN:OE1	1:B:191:LYS:CG	1.72	1.36
1:A:170:PHE:O	1:A:173:THR:HG22	1.24	1.29
1:C:325:ASN:ND2	1:C:327:THR:CG2	1.96	1.29

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	467/487 (96%)	437 (94%)	28 (6%)	2 (0%)	30	62
1	B	467/487 (96%)	438 (94%)	27 (6%)	2 (0%)	30	62
1	C	467/487 (96%)	436 (93%)	29 (6%)	2 (0%)	30	62
1	D	467/487 (96%)	437 (94%)	28 (6%)	2 (0%)	30	62
2	e	155/198 (78%)	146 (94%)	9 (6%)	0	100	100
2	f	150/198 (76%)	140 (93%)	10 (7%)	0	100	100
2	g	150/198 (76%)	139 (93%)	11 (7%)	0	100	100
2	h	155/198 (78%)	146 (94%)	9 (6%)	0	100	100
All	All	2478/2740 (90%)	2319 (94%)	151 (6%)	8 (0%)	36	67

5 of 8 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	394	ASN
1	B	505	ASN
1	D	394	ASN

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Mol	Chain	Res	Type
1	C	394	ASN
1	C	499	ALA

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	340/414 (82%)	302 (89%)	38 (11%)	6	25
1	B	340/414 (82%)	305 (90%)	35 (10%)	7	28
1	C	340/414 (82%)	306 (90%)	34 (10%)	7	28
1	D	340/414 (82%)	307 (90%)	33 (10%)	8	30
2	e	142/169 (84%)	110 (78%)	32 (22%)	1	5
2	f	130/169 (77%)	112 (86%)	18 (14%)	3	19
2	g	130/169 (77%)	115 (88%)	15 (12%)	5	24
2	h	142/169 (84%)	113 (80%)	29 (20%)	1	7
All	All	1904/2332 (82%)	1670 (88%)	234 (12%)	4	22

5 of 234 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	153	CYS
2	h	79	VAL
2	e	20	CYS
2	h	57	LEU
2	g	121	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 36 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	330	HIS
2	h	117	ASN
1	D	345	ASN

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Mol	Chain	Res	Type
1	D	459	ASN
1	B	427	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 oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

4 ligands 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	$\# Z > 2$
3	FAR	g	201	2	14,14,14	2.71	2 (14%)	15,16,16	1.04	2 (13%)
3	FAR	f	201	2	14,14,14	2.68	2 (14%)	15,16,16	1.21	2 (13%)
3	FAR	h	201	2	14,14,14	2.60	2 (14%)	15,16,16	1.08	1 (6%)
3	FAR	e	201	2	14,14,14	2.64	2 (14%)	15,16,16	1.15	2 (13%)

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	FAR	g	201	2	-	4/14/14/14	-
3	FAR	f	201	2	-	4/14/14/14	-
3	FAR	h	201	2	-	6/14/14/14	-
3	FAR	e	201	2	-	5/14/14/14	-

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	e	201	FAR	C10-C8	-7.10	1.33	1.50
3	f	201	FAR	C10-C8	-7.05	1.33	1.50
3	g	201	FAR	C10-C8	-7.02	1.33	1.50
3	g	201	FAR	C15-C13	-7.01	1.31	1.50
3	h	201	FAR	C10-C8	-6.84	1.34	1.50

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	e	201	FAR	C1-C2-C3	-2.58	120.58	126.44
3	h	201	FAR	C10-C8-C9	2.16	118.97	115.23
3	f	201	FAR	C6-C7-C8	-2.08	122.86	127.62
3	g	201	FAR	C6-C7-C8	-2.06	122.92	127.62
3	f	201	FAR	C10-C8-C9	2.05	118.78	115.23

There are no chirality outliers.

5 of 19 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	f	201	FAR	C3-C5-C6-C7
3	f	201	FAR	C9-C11-C12-C13
3	g	201	FAR	C3-C5-C6-C7
3	h	201	FAR	C12-C11-C9-C8
3	e	201	FAR	C12-C11-C9-C8

There are no ring outliers.

3 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	g	201	FAR	4	0
3	f	201	FAR	1	0
3	e	201	FAR	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	469/487 (96%)	-0.43	0 100 100	79, 124, 170, 232	0
1	B	469/487 (96%)	-0.36	0 100 100	66, 136, 219, 273	0
1	C	469/487 (96%)	-0.46	0 100 100	73, 119, 165, 199	0
1	D	469/487 (96%)	-0.50	0 100 100	64, 106, 151, 195	0
2	e	163/198 (82%)	-0.11	1 (0%) 85 65	86, 179, 263, 305	0
2	f	156/198 (78%)	-0.20	0 100 100	93, 162, 213, 242	0
2	g	156/198 (78%)	-0.32	0 100 100	72, 130, 204, 256	0
2	h	163/198 (82%)	-0.18	2 (1%) 76 52	73, 154, 213, 318	0
All	All	2514/2740 (91%)	-0.38	3 (0%) 92 86	64, 126, 211, 318	0

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	h	54	GLU	3.0
2	h	142	GLU	2.7
2	e	142	GLU	2.1

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 oligosaccharides 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. 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
3	FAR	e	201	15/15	0.90	0.21	117,126,149,153	0
3	FAR	g	201	15/15	0.94	0.20	112,120,149,150	0
3	FAR	h	201	15/15	0.94	0.16	84,96,128,139	0
3	FAR	f	201	15/15	0.96	0.14	79,85,100,102	0

6.5 Other polymers [i](#)

There are no such residues in this entry.