



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 09:09 PM UTC

PDB ID : 1FOE / pdb_00001foe
Title : CRYSTAL STRUCTURE OF RAC1 IN COMPLEX WITH THE GUANINE NUCLEOTIDE EXCHANGE REGION OF TIAM1
Authors : Worthylake, D.K.; Rossman, K.L.; Sondek, J.
Deposited on : 2000-08-27
Resolution : 2.80 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

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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)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

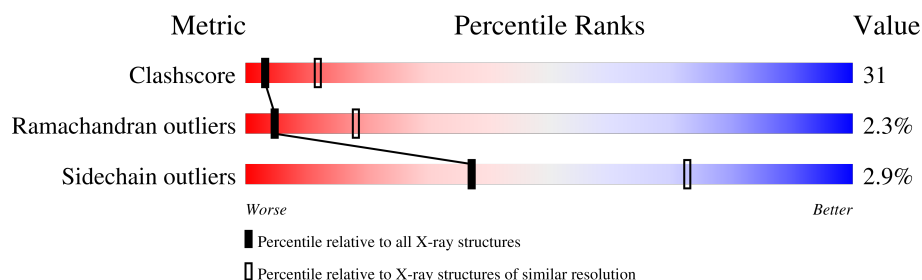
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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))
Clashscore	190562	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)

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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	377	52% 41% . .
1	C	377	54% 38% 5% .
1	E	377	53% 39% 5% .
1	G	377	52% 40% 5% .
2	B	177	53% 42% 5%
2	D	177	53% 43% 5%
2	F	177	53% 44% .
2	H	177	51% 44% 5%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 17570 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 T-LYMPHOMA INVASION AND METASTASIS INDUCING PROTEIN 1.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	368	Total	C	N	O	S	Se	369	0	0
			2989	1918	509	550	6	6			
1	C	366	Total	C	N	O	S	Se	309	0	0
			2972	1907	506	547	6	6			
1	E	367	Total	C	N	O	S	Se	369	0	0
			2980	1913	507	548	6	6			
1	G	367	Total	C	N	O	S	Se	307	0	0
			2980	1913	507	548	6	6			

There are 32 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1031	MSE	THR	modified residue	UNP Q60610
A	1032	GLY	THR	cloning artifact	UNP Q60610
A	1063	MSE	MET	modified residue	UNP Q60610
A	1091	MSE	MET	modified residue	UNP Q60610
A	1224	MSE	MET	modified residue	UNP Q60610
A	1234	MSE	MET	modified residue	UNP Q60610
A	1264	MSE	MET	modified residue	UNP Q60610
A	1334	MSE	MET	modified residue	UNP Q60610
C	1031	MSE	THR	modified residue	UNP Q60610
C	1032	GLY	THR	cloning artifact	UNP Q60610
C	1063	MSE	MET	modified residue	UNP Q60610
C	1091	MSE	MET	modified residue	UNP Q60610
C	1224	MSE	MET	modified residue	UNP Q60610
C	1234	MSE	MET	modified residue	UNP Q60610
C	1264	MSE	MET	modified residue	UNP Q60610
C	1334	MSE	MET	modified residue	UNP Q60610
E	1031	MSE	THR	modified residue	UNP Q60610
E	1032	GLY	THR	cloning artifact	UNP Q60610
E	1063	MSE	MET	modified residue	UNP Q60610
E	1091	MSE	MET	modified residue	UNP Q60610

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Chain	Residue	Modelled	Actual	Comment	Reference
E	1224	MSE	MET	modified residue	UNP Q60610
E	1234	MSE	MET	modified residue	UNP Q60610
E	1264	MSE	MET	modified residue	UNP Q60610
E	1334	MSE	MET	modified residue	UNP Q60610
G	1031	MSE	THR	modified residue	UNP Q60610
G	1032	GLY	THR	cloning artifact	UNP Q60610
G	1063	MSE	MET	modified residue	UNP Q60610
G	1091	MSE	MET	modified residue	UNP Q60610
G	1224	MSE	MET	modified residue	UNP Q60610
G	1234	MSE	MET	modified residue	UNP Q60610
G	1264	MSE	MET	modified residue	UNP Q60610
G	1334	MSE	MET	modified residue	UNP Q60610

- Molecule 2 is a protein called RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	177	Total	C	N	O	S	14	0	0
			1384	889	228	259	8			
2	D	177	Total	C	N	O	S	14	0	0
			1384	889	228	259	8			
2	F	177	Total	C	N	O	S	14	0	0
			1384	889	228	259	8			
2	H	177	Total	C	N	O	S	14	0	0
			1384	889	228	259	8			

- Molecule 3 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	1	Total O S 5 4 1	0	0
3	D	1	Total O S 5 4 1	0	0
3	F	1	Total O S 5 4 1	0	0
3	H	1	Total O S 5 4 1	0	0

- Molecule 4 is water.

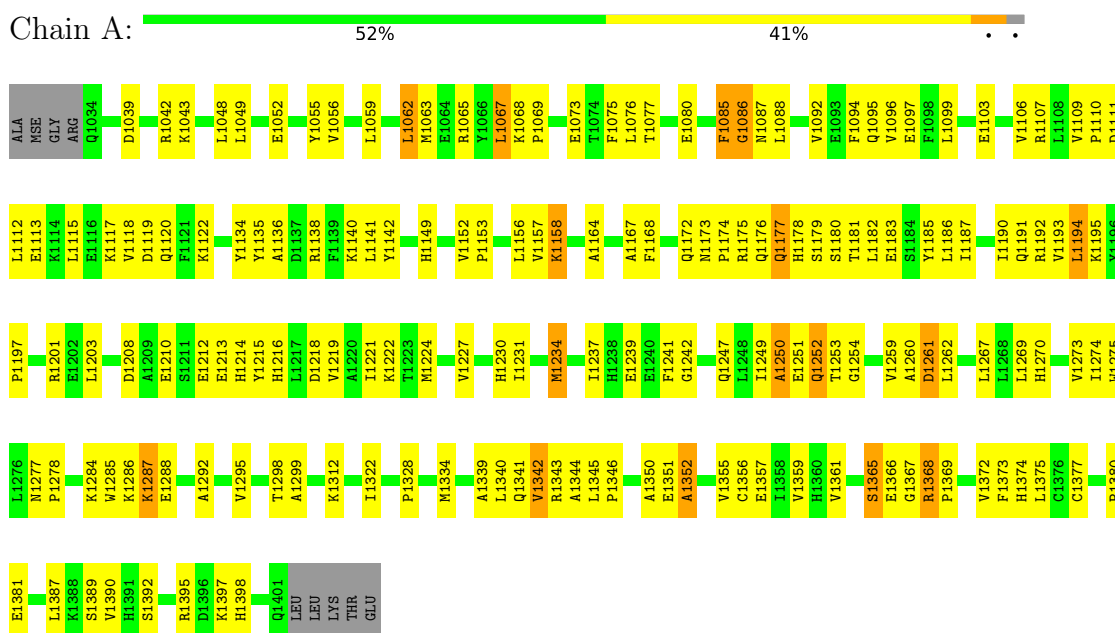
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	14	Total O 14 14	0	0
4	B	6	Total O 6 6	0	0
4	C	8	Total O 8 8	0	0
4	D	6	Total O 6 6	0	0
4	E	7	Total O 7 7	0	0
4	F	7	Total O 7 7	0	0
4	G	19	Total O 19 19	0	0
4	H	26	Total O 26 26	0	0

3 Residue-property plots

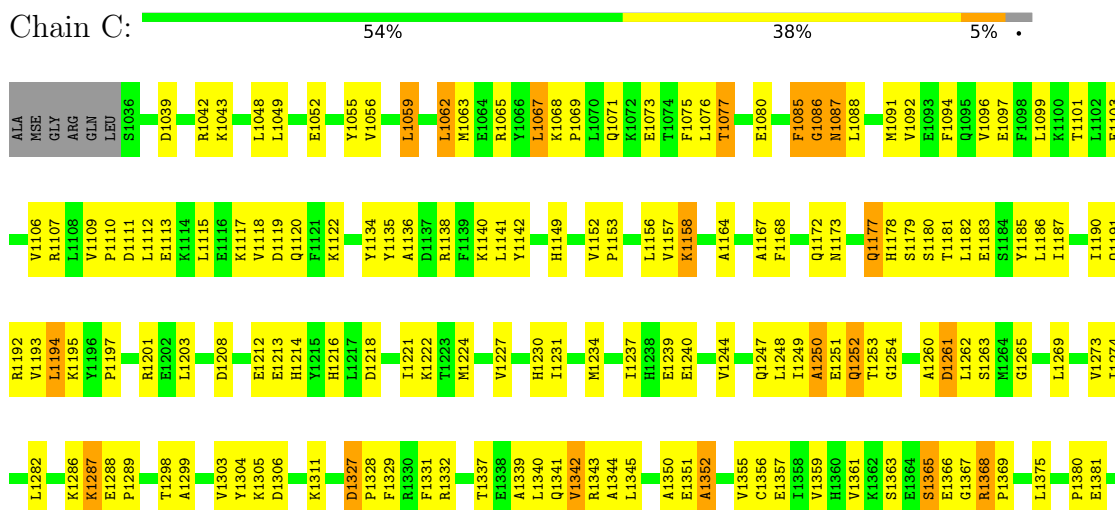
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded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

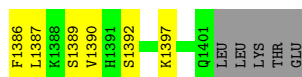
Note EDS was not executed.

• Molecule 1: T-LYMPHOMA INVASION AND METASTASIS INDUCING PROTEIN 1



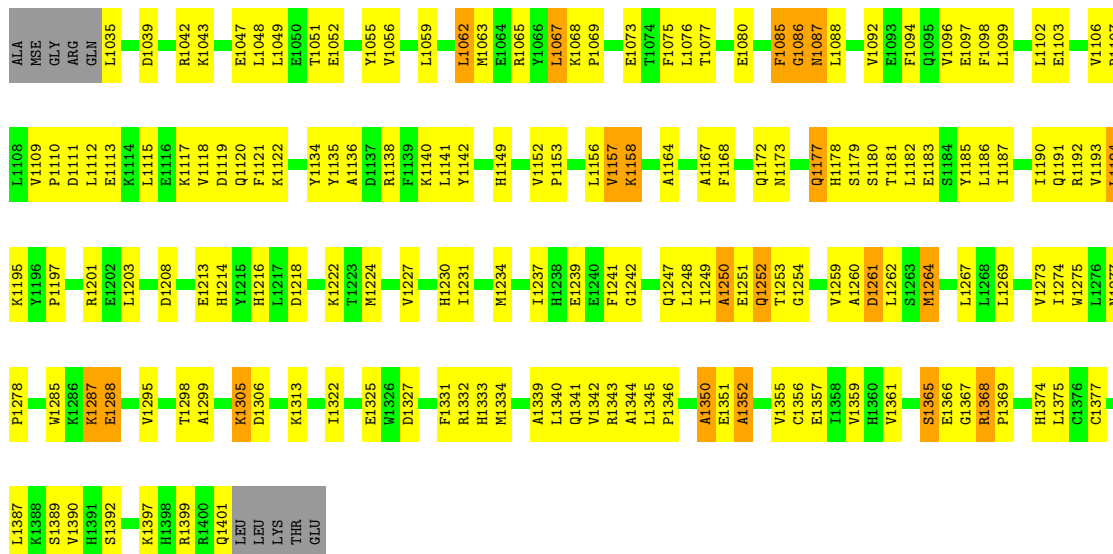
• Molecule 1: T-LYMPHOMA INVASION AND METASTASIS INDUCING PROTEIN 1





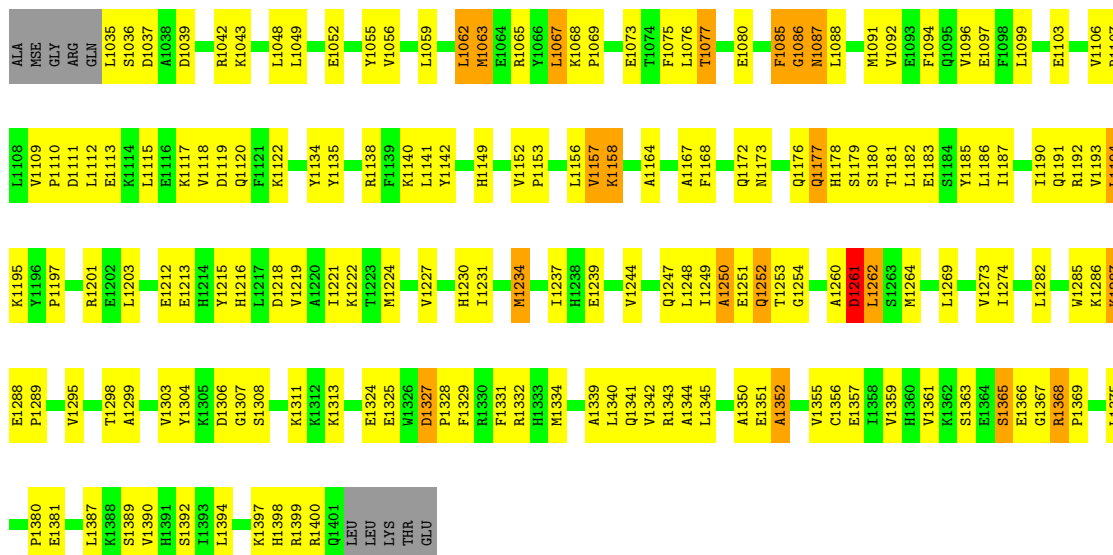
• Molecule 1: T-LYMPHOMA INVASION AND METASTASIS INDUCING PROTEIN 1

Chain E:  53% 39% 5%



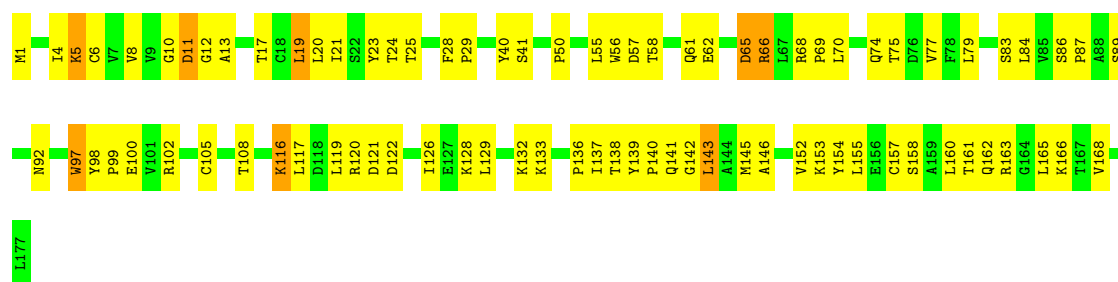
• Molecule 1: T-LYMPHOMA INVASION AND METASTASIS INDUCING PROTEIN 1

Chain G:  52% 40% 5%



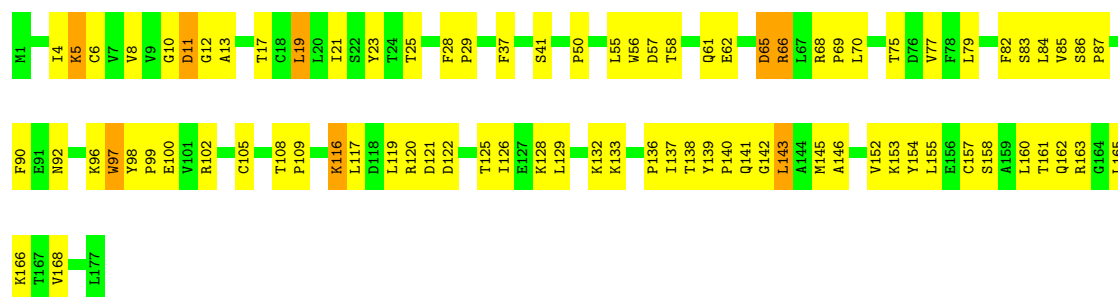
• Molecule 2: RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE

Chain B:  53% 42% 5%



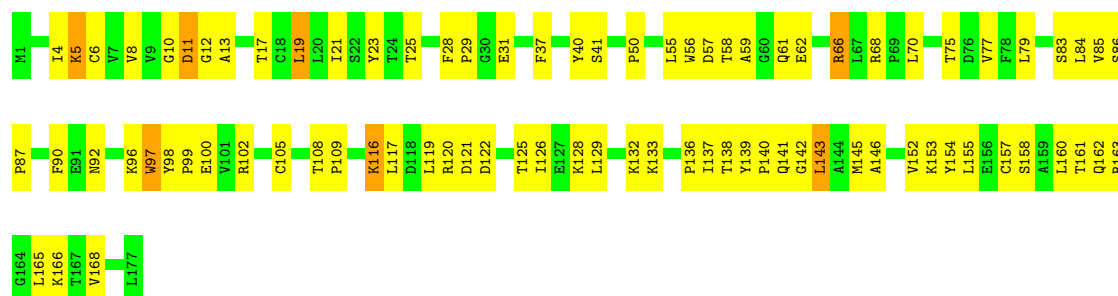
• Molecule 2: RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE

Chain D: 53% 43% 5%



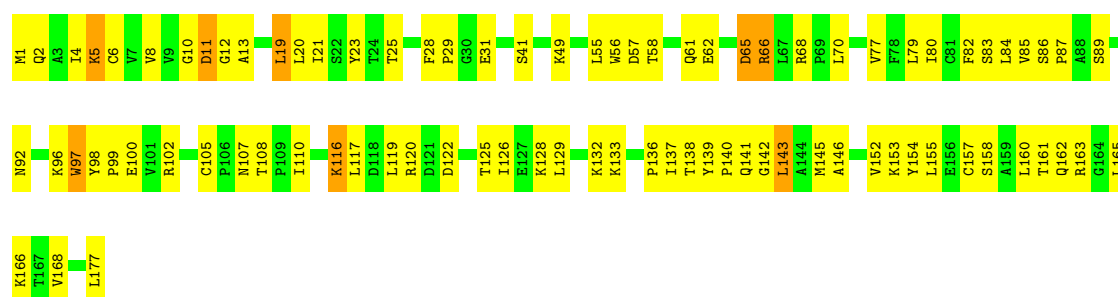
• Molecule 2: RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE

Chain F: 53% 44% .



• Molecule 2: RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE

Chain H: 51% 44% 5%



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	186.95Å 149.27Å 149.21Å 90.00° 121.00° 90.00°	Depositor
Resolution (Å)	15.00 – 2.80	Depositor
% Data completeness (in resolution range)	93.8 (15.00-2.80)	Depositor
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS 0.3	Depositor
R, R_{free}	0.262 , 0.293	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	17570	wwPDB-VP
Average B, all atoms (Å ²)	60.0	wwPDB-VP

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: SO4

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	0.54	4/3045 (0.1%)	0.96	11/4095 (0.3%)
1	C	0.52	2/3028 (0.1%)	0.97	13/4072 (0.3%)
1	E	0.51	3/3036 (0.1%)	0.96	12/4083 (0.3%)
1	G	0.59	8/3036 (0.3%)	0.98	15/4083 (0.4%)
2	B	0.51	0/1414	1.12	7/1922 (0.4%)
2	D	0.49	0/1414	1.12	7/1922 (0.4%)
2	F	0.46	0/1414	1.13	7/1922 (0.4%)
2	H	0.65	0/1414	1.15	8/1922 (0.4%)
All	All	0.54	17/17801 (0.1%)	1.02	80/24021 (0.3%)

The worst 5 of 17 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	G	1234	MSE	SE-CE	-6.97	1.74	1.95
1	C	1224	MSE	SE-CE	-6.12	1.77	1.95
1	G	1264	MSE	SE-CE	-5.83	1.77	1.95
1	G	1334	MSE	SE-CE	-5.82	1.78	1.95
1	G	1264	MSE	CG-SE	-5.78	1.78	1.95

The worst 5 of 80 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	5	LYS	N-CA-CB	-15.86	85.67	110.57
2	H	5	LYS	N-CA-CB	-15.27	86.58	110.55
2	D	5	LYS	N-CA-CB	-15.26	86.59	110.55
2	F	5	LYS	N-CA-CB	-15.13	86.79	110.55
2	F	4	ILE	N-CA-C	-10.62	92.82	108.12

There are no chirality outliers.

There are no planarity outliers.

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	2989	0	3035	179	0
1	C	2972	0	3016	185	0
1	E	2980	0	3027	182	0
1	G	2980	0	3027	179	0
2	B	1384	0	1405	86	0
2	D	1384	0	1405	88	0
2	F	1384	0	1405	84	1
2	H	1384	0	1405	90	1
3	B	5	0	0	0	0
3	D	5	0	0	0	0
3	F	5	0	0	0	0
3	H	5	0	0	0	0
4	A	14	0	0	0	0
4	B	6	0	0	0	0
4	C	8	0	0	0	0
4	D	6	0	0	0	0
4	E	7	0	0	0	0
4	F	7	0	0	0	0
4	G	19	0	0	0	0
4	H	26	0	0	0	0
All	All	17570	0	17725	995	1

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 31.

The worst 5 of 995 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:1285:TRP:HH2	2:D:102:ARG:HG2	1.01	1.09
1:A:1285:TRP:CH2	2:D:102:ARG:HG2	1.88	1.08
2:B:138:THR:H	2:B:141:GLN:HE21	1.09	1.00
1:C:1248:LEU:HD21	1:C:1332:ARG:HG3	1.46	0.97
1:E:1249:ILE:HD12	1:E:1261:ASP:H	1.29	0.96

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the sym-

metry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:139:TYR:OH	2:H:107:ASN:OD1[2_657]	2.06	0.14

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	366/377 (97%)	313 (86%)	43 (12%)	10 (3%)	4	15
1	C	364/377 (97%)	315 (86%)	41 (11%)	8 (2%)	5	19
1	E	365/377 (97%)	322 (88%)	30 (8%)	13 (4%)	2	10
1	G	365/377 (97%)	322 (88%)	31 (8%)	12 (3%)	3	11
2	B	175/177 (99%)	164 (94%)	9 (5%)	2 (1%)	11	36
2	D	175/177 (99%)	164 (94%)	9 (5%)	2 (1%)	11	36
2	F	175/177 (99%)	162 (93%)	12 (7%)	1 (1%)	21	51
2	H	175/177 (99%)	163 (93%)	11 (6%)	1 (1%)	21	51
All	All	2160/2216 (98%)	1925 (89%)	186 (9%)	49 (2%)	5	18

5 of 49 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1087	ASN
1	A	1253	THR
1	A	1261	ASP
1	C	1087	ASN
1	C	1253	THR

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	332/332 (100%)	325 (98%)	7 (2%)	47	79
1	C	330/332 (99%)	324 (98%)	6 (2%)	51	82
1	E	331/332 (100%)	322 (97%)	9 (3%)	39	74
1	G	331/332 (100%)	323 (98%)	8 (2%)	43	77
2	B	153/153 (100%)	146 (95%)	7 (5%)	24	58
2	D	153/153 (100%)	146 (95%)	7 (5%)	24	58
2	F	153/153 (100%)	146 (95%)	7 (5%)	24	58
2	H	153/153 (100%)	147 (96%)	6 (4%)	28	64
All	All	1936/1940 (100%)	1879 (97%)	57 (3%)	37	73

5 of 57 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	1059	LEU
2	H	116	LYS
1	E	1322	ILE
2	H	77	VAL
1	G	1313	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 57 such sidechains are listed below:

Mol	Chain	Res	Type
2	D	74	GLN
2	H	74	GLN
1	E	1230	HIS
2	H	26	ASN
1	G	1230	HIS

5.3.3 RNA ⓘ

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

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	SO4	F	4003	-	4,4,4	0.34	0	6,6,6	0.15	0
3	SO4	H	4004	-	4,4,4	0.42	0	6,6,6	0.29	0
3	SO4	B	4001	-	4,4,4	0.41	0	6,6,6	0.11	0
3	SO4	D	4002	-	4,4,4	0.39	0	6,6,6	0.24	0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

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

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.