



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 10:18 AM GMT

PDB ID : 3LIN
Title : crystal structure of HTLV protease complexed with the inhibitor, KNI-10562
Authors : Satoh, T.; Li, M.; Nguyen, J.; Kiso, Y.; Wlodawer, A.; Gustchina, A.
Deposited on : 2010-01-25
Resolution : 1.96 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

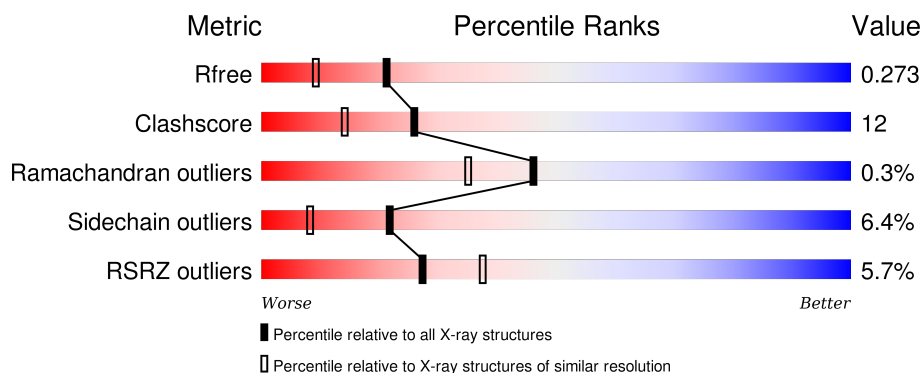
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.96 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	1833 (1.96-1.96)
Clashscore	102246	1953 (1.96-1.96)
Ramachandran outliers	100387	1936 (1.96-1.96)
Sidechain outliers	100360	1936 (1.96-1.96)
RSRZ outliers	91569	1835 (1.96-1.96)

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	116	<div> <div>5%</div> <div>78%</div> <div>21%</div> <div>.</div> </div>
1	B	116	<div> <div>9%</div> <div>79%</div> <div>17%</div> <div>..</div> </div>
1	C	116	<div> <div>5%</div> <div>84%</div> <div>13%</div> <div>.</div> </div>
1	D	116	<div> <div>2%</div> <div>78%</div> <div>19%</div> <div>..</div> </div>
1	E	116	<div> <div>5%</div> <div>75%</div> <div>22%</div> <div>.</div> </div>

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Mol	Chain	Length	Quality of chain
1	F	116	
1	G	116	
1	H	116	
1	I	116	
1	J	116	
1	K	116	
1	L	116	

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	E13	I	117[A]	-	-	-	X
2	E13	I	117[B]	-	-	-	X

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 11892 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 Protease.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	116	Total	C	N	O	S	0	0	0
			883	564	152	164	3			
1	B	116	Total	C	N	O	S	0	0	0
			883	564	152	164	3			
1	C	116	Total	C	N	O	S	0	3	0
			896	576	152	165	3			
1	D	116	Total	C	N	O	S	0	3	0
			901	576	155	167	3			
1	E	116	Total	C	N	O	S	0	0	0
			883	564	152	164	3			
1	F	116	Total	C	N	O	S	0	0	0
			883	564	152	164	3			
1	G	116	Total	C	N	O	S	0	0	0
			883	564	152	164	3			
1	H	116	Total	C	N	O	S	0	0	0
			882	564	152	163	3			
1	I	116	Total	C	N	O	S	0	3	0
			896	576	152	165	3			
1	J	116	Total	C	N	O	S	0	3	0
			901	576	155	167	3			
1	K	116	Total	C	N	O	S	0	0	0
			883	564	152	164	3			
1	L	116	Total	C	N	O	S	0	0	0
			883	564	152	164	3			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	40	ILE	LEU	engineered	UNP Q82134
B	40	ILE	LEU	engineered	UNP Q82134
C	40	ILE	LEU	engineered	UNP Q82134
D	40	ILE	LEU	engineered	UNP Q82134
E	40	ILE	LEU	engineered	UNP Q82134

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Chain	Residue	Modelled	Actual	Comment	Reference
F	40	ILE	LEU	engineered	UNP Q82134
G	40	ILE	LEU	engineered	UNP Q82134
H	40	ILE	LEU	engineered	UNP Q82134
I	40	ILE	LEU	engineered	UNP Q82134
J	40	ILE	LEU	engineered	UNP Q82134
K	40	ILE	LEU	engineered	UNP Q82134
L	40	ILE	LEU	engineered	UNP Q82134

- E13
-
- The image displays a complex chemical structure, likely a protein-ligand complex or a highly substituted molecule. The structure features a central core with multiple substituents, many of which are labeled with codes such as CAC, CAG, CAG1, CAG2, CAG3, CAG4, CAG5, CAG6, CAG7, CAG8, CAG9, CAG10, CAG11, CAG12, CAG13, CAG14, CAG15, CAG16, CAG17, CAG18, CAG19, CAG20, CAG21, CAG22, CAG23, CAG24, CAG25, CAG26, CAG27, CAG28, CAG29, CAG30, CAG31, CAG32, CAG33, CAG34, CAG35, CAG36, CAG37, CAG38, CAG39, CAG40, CAG41, CAG42, CAG43, CAG44, CAG45, CAG46, CAG47, CAG48, CAG49, CAG50, CAG51, CAG52, CAG53, CAG54, CAG55, CAG56, CAG57, CAG58, CAG59, CAG60, CAG61, CAG62, CAG63, CAG64, CAG65, CAG66, CAG67, CAG68, CAG69, CAG70, CAG71, CAG72, CAG73, CAG74, CAG75, CAG76, CAG77, CAG78, CAG79, CAG80, CAG81, CAG82, CAG83, CAG84, CAG85, CAG86, CAG87, CAG88, CAG89, CAG90, CAG91, CAG92, CAG93, CAG94, CAG95, CAG96, CAG97, CAG98, CAG99, CAG100. The structure is rendered in a 3D perspective, showing the spatial arrangement of the atoms and bonds. The labels are color-coded: CAG is green, CAG1 is blue, CAG2 is red, CAG3 is yellow, CAG4 is cyan, CAG5 is magenta, CAG6 is brown, CAG7 is pink, CAG8 is grey, CAG9 is light blue, CAG10 is light green, CAG11 is light red, CAG12 is light yellow, CAG13 is light cyan, CAG14 is light magenta, CAG15 is light brown, CAG16 is light pink, CAG17 is light grey, CAG18 is light light blue, CAG19 is light light green, CAG20 is light light red, CAG21 is light light yellow, CAG22 is light light cyan, CAG23 is light light magenta, CAG24 is light light brown, CAG25 is light light pink, CAG26 is light light grey, CAG27 is light light light blue, CAG28 is light light light green, CAG29 is light light light red, CAG30 is light light light yellow, CAG31 is light light light cyan, CAG32 is light light light magenta, CAG33 is light light light brown, CAG34 is light light light pink, CAG35 is light light light grey, CAG36 is light light light light blue, CAG37 is light light light light green, CAG38 is light light light light red, CAG39 is light light light light yellow, CAG40 is light light light light cyan, CAG41 is light light light light magenta, CAG42 is light light light light brown, CAG43 is light light light light pink, CAG44 is light light light light grey, CAG45 is light light light light light blue, CAG46 is light light light light light green, CAG47 is light light light light light red, CAG48 is light light light light light yellow, CAG49 is light light light light light cyan, CAG50 is light light light light light magenta, CAG51 is light light light light light brown, CAG52 is light light light light light pink, CAG53 is light light light light light grey, CAG54 is light light light light light light blue, CAG55 is light light light light light light green, CAG56 is light light light light light light red, CAG57 is light light light light light light yellow, CAG58 is light light light light light light cyan, CAG59 is light light light light light light magenta, CAG60 is light light light light light light brown, CAG61 is light light light light light light pink, CAG62 is light light light light light light grey, CAG63 is light light light light light light light blue, CAG64 is light light light light light light light green, CAG65 is light light light light light light light red, CAG66 is light light light light light light light yellow, CAG67 is light light light light light light light cyan, CAG68 is light light light light light light light magenta, CAG69 is light light light light light light light brown, CAG70 is light light light light light light light pink, CAG71 is light light light light light light light grey, CAG72 is light light light light light light light light blue, CAG73 is light light light light light light light light green, CAG74 is light light light light light light light light red, CAG75 is light light light light light light light light yellow, CAG76 is light light light light light light light light cyan, CAG77 is light light light light light light light light magenta, CAG78 is light light light light light light light light brown, CAG79 is light light light light light light light light pink, CAG80 is light light light light light light light light grey, CAG81 is light light light light light light light light light blue, CAG82 is light light light light light light light light light green, CAG83 is light light light light light light light light light red, CAG84 is light light light light light light light light light yellow, CAG85 is light light light light light light light light light cyan, CAG86 is light light light light light light light light light magenta, CAG87 is light light light light light light light light light brown, CAG88 is light light light light light light light light light pink, CAG89 is light light light light light light light light light grey, CAG90 is light light light light light light light light light light blue, CAG91 is light light light light light light light light light light green, CAG92 is light light light light light light light light light light red, CAG93 is light light light light light light light light light light yellow, CAG94 is light light light light light light light light light light cyan, CAG95 is light light light light light light light light light light magenta, CAG96 is light light light light light light light light light light brown, CAG97 is light light light light light light light light light light pink, CAG98 is light light light light light light light light light light grey, CAG99 is light light light light light light light light light light light blue, CAG100 is light light light light light light light light light light light green.



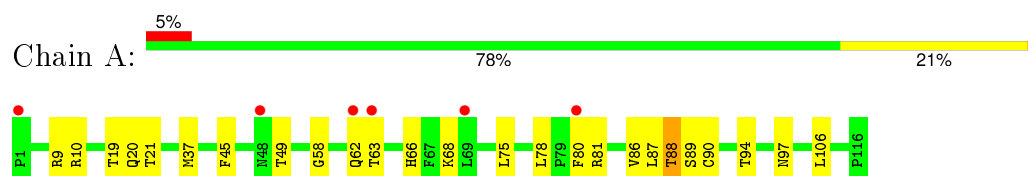
- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	63	Total O 63 63	0	0
3	B	65	Total O 65 65	0	0
3	C	68	Total O 68 68	0	3
3	D	55	Total O 55 55	0	0
3	E	85	Total O 85 85	0	0
3	F	60	Total O 60 60	0	0
3	G	63	Total O 63 63	0	0
3	H	54	Total O 54 54	0	0
3	I	79	Total O 79 79	0	0
3	J	59	Total O 59 59	0	0
3	K	64	Total O 64 64	0	0
3	L	70	Total O 70 70	0	0

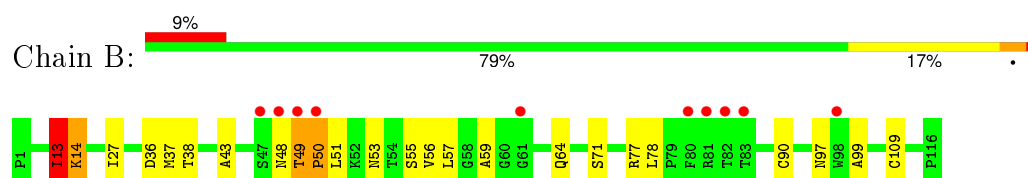
3 Residue-property plots [i](#)

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.

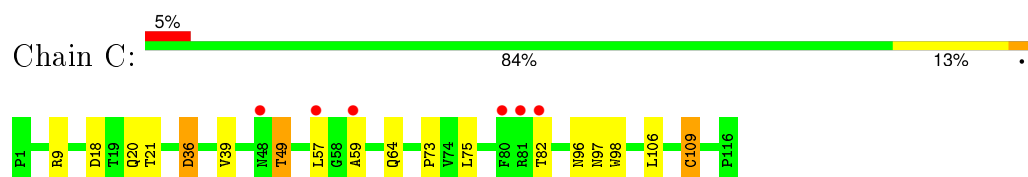
- Molecule 1: Protease



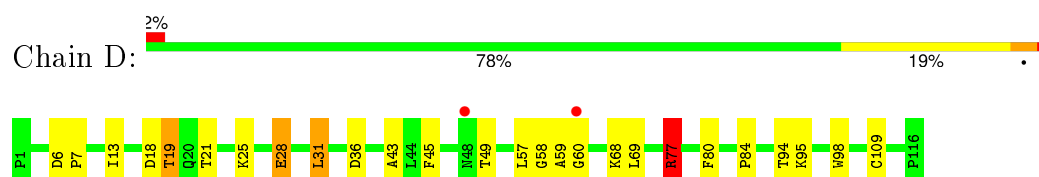
- Molecule 1: Protease



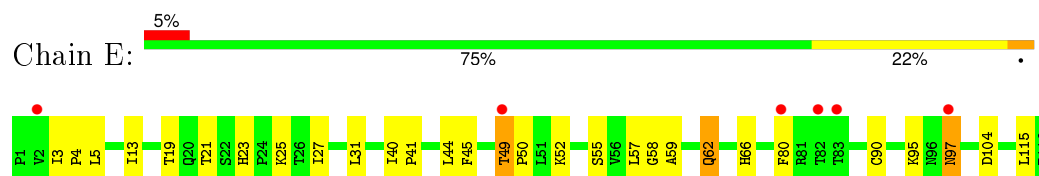
- Molecule 1: Protease



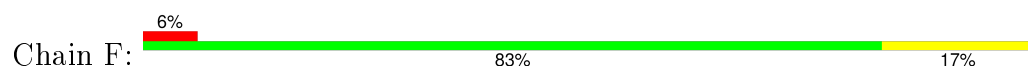
- Molecule 1: Protease



- Molecule 1: Protease

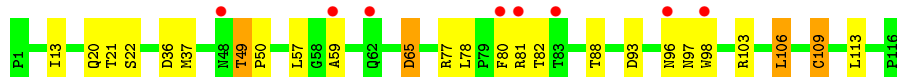
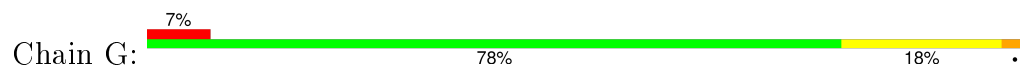


- Molecule 1: Protease

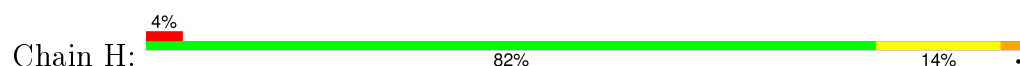




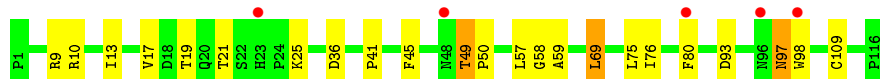
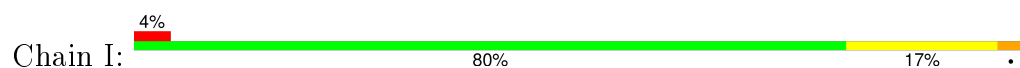
- Molecule 1: Protease



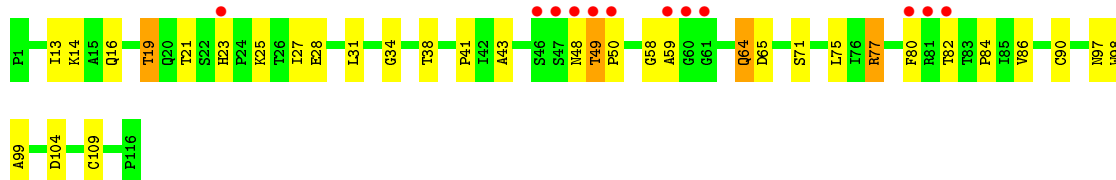
- Molecule 1: Protease



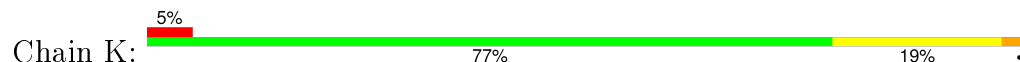
- Molecule 1: Protease



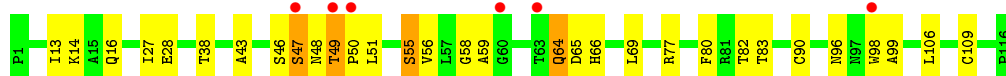
- Molecule 1: Protease



- Molecule 1: Protease



- Molecule 1: Protease



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	134.36Å 77.31Å 159.17Å 90.00° 95.09° 90.00°	Depositor
Resolution (Å)	50.00 – 1.96 49.03 – 1.96	Depositor EDS
% Data completeness (in resolution range)	96.9 (50.00-1.96) 96.9 (49.03-1.96)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.09	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.82 (at 1.97Å)	Xtriage
Refinement program	REFMAC 5.5.0104	Depositor
R, R_{free}	0.213 , 0.262 0.225 , 0.273	Depositor DCC
R_{free} test set	3393 reflections (3.10%)	DCC
Wilson B-factor (Å ²)	30.2	Xtriage
Anisotropy	0.103	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 52.1	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.28$	Xtriage
Outliers	5 of 112736 reflections (0.004%)	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	11892	wwPDB-VP
Average B, all atoms (Å ²)	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 41.41 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 2.3703e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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: E13

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	0.65	0/901	0.78	0/1233
1	B	0.69	0/901	0.84	1/1233 (0.1%)
1	C	0.78	1/923 (0.1%)	0.85	2/1263 (0.2%)
1	D	0.79	1/928 (0.1%)	1.02	6/1269 (0.5%)
1	E	0.74	0/901	0.82	1/1233 (0.1%)
1	F	0.67	0/901	0.83	2/1233 (0.2%)
1	G	0.78	1/901 (0.1%)	0.89	4/1233 (0.3%)
1	H	0.73	1/900 (0.1%)	0.81	0/1233
1	I	0.78	1/923 (0.1%)	0.89	2/1263 (0.2%)
1	J	0.71	1/928 (0.1%)	0.82	1/1269 (0.1%)
1	K	0.72	1/901 (0.1%)	0.82	0/1233
1	L	0.70	0/901	0.85	1/1233 (0.1%)
All	All	0.73	7/10909 (0.1%)	0.85	20/14928 (0.1%)

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	G	109	CYS	CB-SG	-11.83	1.62	1.82
1	C	109	CYS	CB-SG	-11.76	1.62	1.82
1	D	109	CYS	CB-SG	-10.03	1.65	1.82
1	J	109	CYS	CB-SG	-6.46	1.71	1.82
1	I	109	CYS	CB-SG	-6.12	1.71	1.82

The worst 5 of 20 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	77[A]	ARG	NE-CZ-NH2	-7.21	116.70	120.30
1	D	77[B]	ARG	NE-CZ-NH2	-7.21	116.70	120.30
1	B	13	ILE	CB-CA-C	-6.19	99.22	111.60
1	D	109	CYS	CB-CA-C	-6.11	98.19	110.40
1	D	6	ASP	CB-CG-OD1	5.93	123.64	118.30

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	883	0	926	19	0
1	B	883	0	926	18	0
1	C	896	0	953	16	0
1	D	901	0	952	25	0
1	E	883	0	926	25	0
1	F	883	0	926	11	0
1	G	883	0	926	22	0
1	H	882	0	926	15	0
1	I	896	0	953	27	0
1	J	901	0	952	30	0
1	K	883	0	926	28	0
1	L	883	0	926	28	0
2	B	50	0	53	2	0
2	C	100	0	106	24	0
2	E	50	0	52	2	0
2	H	100	0	106	16	0
2	I	100	0	106	21	0
2	L	50	0	53	1	0
3	A	63	0	0	8	1
3	B	65	0	0	10	0
3	C	68	0	0	13	0
3	D	55	0	0	5	0
3	E	85	0	0	9	1
3	F	60	0	0	4	0
3	G	63	0	0	8	0
3	H	54	0	0	9	0
3	I	79	0	0	7	0
3	J	59	0	0	5	0
3	K	64	0	0	10	0
3	L	70	0	0	11	0
All	All	11892	0	11694	283	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 12.

The worst 5 of 283 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)
2:I:117[A]:E13:CAX	2:I:117[A]:E13:HAS	1.43	1.49
2:I:117[A]:E13:CAX	2:I:117[A]:E13:CAS	2.10	1.28
2:C:117[B]:E13:CBM	3:C:840:HOH:O	1.68	1.28
2:H:117[B]:E13:CB1	3:H:839:HOH:O	1.73	1.27
2:H:117[A]:E13:CB2	3:H:838:HOH:O	1.66	1.27

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:535:HOH:O	3:E:237:HOH:O[1_545]	2.13	0.07

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	114/116 (98%)	113 (99%)	1 (1%)	0	100	100
1	B	114/116 (98%)	112 (98%)	1 (1%)	1 (1%)	21	9
1	C	117/116 (101%)	116 (99%)	1 (1%)	0	100	100
1	D	117/116 (101%)	117 (100%)	0	0	100	100
1	E	114/116 (98%)	112 (98%)	1 (1%)	1 (1%)	21	9
1	F	114/116 (98%)	111 (97%)	2 (2%)	1 (1%)	21	9
1	G	114/116 (98%)	111 (97%)	3 (3%)	0	100	100
1	H	114/116 (98%)	113 (99%)	1 (1%)	0	100	100
1	I	117/116 (101%)	115 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	J	117/116 (101%)	116 (99%)	1 (1%)	0	100	100
1	K	114/116 (98%)	112 (98%)	2 (2%)	0	100	100
1	L	114/116 (98%)	110 (96%)	3 (3%)	1 (1%)	21	9
All	All	1380/1392 (99%)	1358 (98%)	18 (1%)	4 (0%)	46	35

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	L	47	SER
1	E	97	ASN
1	F	47	SER
1	B	50	PRO

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	102/102 (100%)	95 (93%)	7 (7%)	19	7
1	B	102/102 (100%)	94 (92%)	8 (8%)	16	4
1	C	105/102 (103%)	99 (94%)	6 (6%)	25	11
1	D	105/102 (103%)	97 (92%)	8 (8%)	16	5
1	E	102/102 (100%)	98 (96%)	4 (4%)	39	24
1	F	102/102 (100%)	96 (94%)	6 (6%)	24	10
1	G	102/102 (100%)	94 (92%)	8 (8%)	16	4
1	H	102/102 (100%)	93 (91%)	9 (9%)	12	3
1	I	105/102 (103%)	101 (96%)	4 (4%)	40	25
1	J	105/102 (103%)	96 (91%)	9 (9%)	13	3
1	K	102/102 (100%)	96 (94%)	6 (6%)	24	10
1	L	102/102 (100%)	94 (92%)	8 (8%)	16	4
All	All	1236/1224 (101%)	1153 (93%)	83 (7%)	22	7

5 of 83 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	F	95	LYS
1	G	109	CYS
1	L	49	THR
1	F	109	CYS
1	G	65	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 14 such sidechains are listed below:

Mol	Chain	Res	Type
1	I	66	HIS
1	I	97	ASN
1	L	23	HIS
1	I	62	GLN
1	J	97	ASN

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](#)

9 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
2	E13	B	117	-	52,52,52	5.39	25 (48%)	72,76,76	1.88	16 (22%)
2	E13	C	117[A]	-	52,52,52	5.30	24 (46%)	72,76,76	2.23	18 (25%)
2	E13	C	117[B]	-	52,52,52	5.31	26 (50%)	72,76,76	2.04	16 (22%)
2	E13	E	117	-	52,52,52	5.32	27 (51%)	72,76,76	2.21	20 (27%)
2	E13	H	117[A]	-	52,52,52	5.36	26 (50%)	72,76,76	2.03	15 (20%)
2	E13	H	117[B]	-	52,52,52	5.33	24 (46%)	72,76,76	2.20	18 (25%)
2	E13	I	117[A]	-	52,52,52	5.47	26 (50%)	72,76,76	2.54	14 (19%)
2	E13	I	117[B]	-	52,52,52	5.32	26 (50%)	72,76,76	2.31	15 (20%)
2	E13	L	117	-	52,52,52	5.49	26 (50%)	72,76,76	1.73	14 (19%)

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
2	E13	B	117	-	-	0/58/74/74	0/3/3/3
2	E13	C	117[A]	-	-	2/58/74/74	0/3/3/3
2	E13	C	117[B]	-	-	0/58/74/74	0/3/3/3
2	E13	E	117	-	-	0/58/74/74	0/3/3/3
2	E13	H	117[A]	-	-	0/58/74/74	0/3/3/3
2	E13	H	117[B]	-	-	2/58/74/74	0/3/3/3
2	E13	I	117[A]	-	-	2/58/74/74	0/3/3/3
2	E13	I	117[B]	-	-	2/58/74/74	0/3/3/3
2	E13	L	117	-	-	2/58/74/74	0/3/3/3

The worst 5 of 230 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	I	117[B]	E13	CAZ-SBE	-5.29	1.69	1.82
2	L	117	E13	CAZ-SBE	-5.28	1.69	1.82
2	C	117[A]	E13	CAZ-SBE	-5.16	1.69	1.82
2	B	117	E13	CAZ-SBE	-5.13	1.69	1.82
2	I	117[A]	E13	CAZ-SBE	-5.10	1.69	1.82

The worst 5 of 146 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	I	117[A]	E13	CBJ-CBA-CBO	-13.44	92.10	113.48

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	I	117[B]	E13	CBM-NAJ-CB1	-10.62	103.93	121.12
2	C	117[B]	E13	CBM-NAJ-CB1	-9.50	105.75	121.12
2	C	117[A]	E13	CBM-NAJ-CB1	-9.34	105.99	121.12
2	I	117[A]	E13	CBM-NAJ-CB1	-8.75	106.96	121.12

There are no chirality outliers.

5 of 10 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	L	117	E13	CB2-OA2-CB1-OA1
2	L	117	E13	CB2-OA2-CB1-NAJ
2	I	117[A]	E13	CB2-OA2-CB1-NAJ
2	I	117[A]	E13	CB2-OA2-CB1-OA1
2	H	117[B]	E13	CB2-OA2-CB1-OA1

There are no ring outliers.

9 monomers are involved in 66 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	117	E13	2	0
2	C	117[A]	E13	14	0
2	C	117[B]	E13	10	0
2	E	117	E13	2	0
2	H	117[A]	E13	10	0
2	H	117[B]	E13	6	0
2	I	117[A]	E13	20	0
2	I	117[B]	E13	1	0
2	L	117	E13	1	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	116/116 (100%)	0.41	6 (5%) 31 42	23, 41, 69, 94	0
1	B	116/116 (100%)	0.45	10 (8%) 13 21	20, 36, 66, 92	0
1	C	116/116 (100%)	0.41	6 (5%) 31 42	22, 38, 64, 92	0
1	D	116/116 (100%)	0.35	2 (1%) 73 81	20, 34, 63, 92	0
1	E	116/116 (100%)	0.27	6 (5%) 31 42	19, 32, 61, 89	0
1	F	116/116 (100%)	0.37	7 (6%) 25 35	22, 39, 64, 94	0
1	G	116/116 (100%)	0.41	8 (6%) 20 30	22, 38, 64, 92	0
1	H	116/116 (100%)	0.32	5 (4%) 39 50	20, 34, 62, 92	0
1	I	116/116 (100%)	0.35	5 (4%) 39 50	19, 33, 62, 90	0
1	J	116/116 (100%)	0.56	12 (10%) 9 14	21, 37, 64, 93	0
1	K	116/116 (100%)	0.40	6 (5%) 31 42	22, 38, 70, 90	0
1	L	116/116 (100%)	0.37	6 (5%) 31 42	21, 36, 69, 92	0
All	All	1392/1392 (100%)	0.39	79 (5%) 27 37	19, 36, 67, 94	0

The worst 5 of 79 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	80	PHE	6.7
1	F	48	ASN	6.3
1	J	48	ASN	5.6
1	K	80	PHE	5.4
1	G	80	PHE	4.8

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
2	E13	I	117[A]	50/50	0.93	0.21	2.82	14,33,46,64	50
2	E13	I	117[B]	50/50	0.93	0.21	2.64	12,24,48,56	50
2	E13	H	117[B]	50/50	0.94	0.19	1.64	14,29,45,66	50
2	E13	H	117[A]	50/50	0.94	0.19	1.58	14,31,44,48	50
2	E13	B	117	50/50	0.94	0.15	1.35	22,37,64,85	0
2	E13	E	117	50/50	0.93	0.15	1.10	23,38,71,84	0
2	E13	L	117	50/50	0.94	0.13	0.62	20,34,63,92	0
2	E13	C	117[B]	50/50	0.95	0.17	0.59	8,23,42,56	50
2	E13	C	117[A]	50/50	0.95	0.17	0.57	15,31,45,54	50

6.5 Other polymers [i](#)

There are no such residues in this entry.