



wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 31, 2016 – 09:21 PM GMT

PDB ID : 1OFI
Title : ASYMMETRIC COMPLEX BETWEEN HSLV AND I-DOMAIN DELETED
HSLU (H. INFLUENZAE)
Authors : Kwon, A.R.; Kessler, B.M.; Overkleeft, H.S.; Mckay, D.B.
Deposited on : 2003-04-14
Resolution : 3.20 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) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

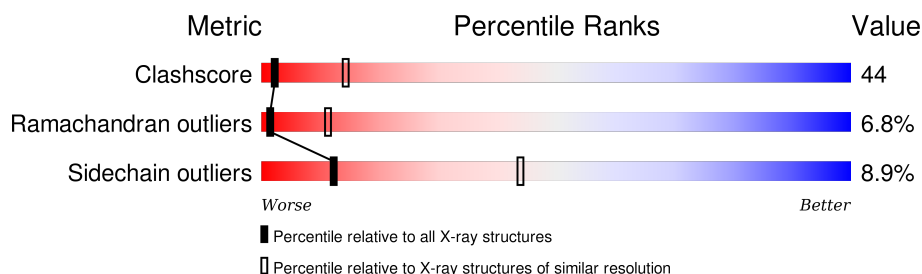
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.20 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	102246	1024 (3.22-3.18)
Ramachandran outliers	100387	1004 (3.22-3.18)
Sidechain outliers	100360	1003 (3.22-3.18)


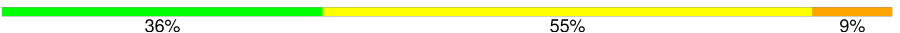
The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey 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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	310	
1	B	310	
1	C	310	
2	G	174	
2	H	174	
2	I	174	
2	L	174	

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Mol	Chain	Length	Quality of chain
2	M	174	
2	N	174	

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
5	PO4	B	452	-	-	X	-

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 15050 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 ATP-DEPENDENT HSL PROTEASE ATP-BINDING SUB-UNIT HSLU.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	299	Total	C	N	O	S	0	0	0
			2312	1446	411	446	9			
1	B	295	Total	C	N	O	S	0	0	0
			2284	1430	407	438	9			
1	C	296	Total	C	N	O	S	0	0	0
			2288	1431	407	441	9			

- Molecule 2 is a protein called ATP-DEPENDENT PROTEASE HSLV.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	G	174	Total	C	N	O	S	0	0	1
			1319	826	236	253	4			
2	H	174	Total	C	N	O	S	0	0	1
			1319	826	236	253	4			
2	I	174	Total	C	N	O	S	0	0	1
			1319	826	236	253	4			
2	L	174	Total	C	N	O	S	0	0	1
			1319	826	236	253	4			
2	M	174	Total	C	N	O	S	0	0	1
			1319	826	236	253	4			
2	N	174	Total	C	N	O	S	0	0	1
			1319	826	236	253	4			

- Molecule 3 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula: C₁₀H₁₅N₅O₁₀P₂).

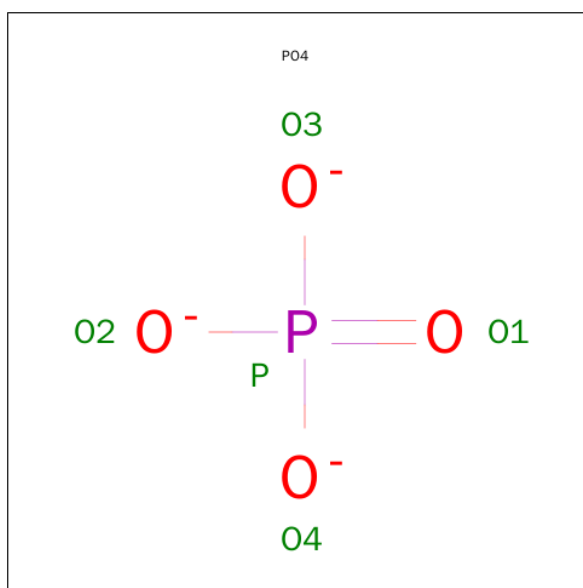


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
3	B	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
3	C	1	Total	C	N	O	P	0	0
			27	10	5	10	2		

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

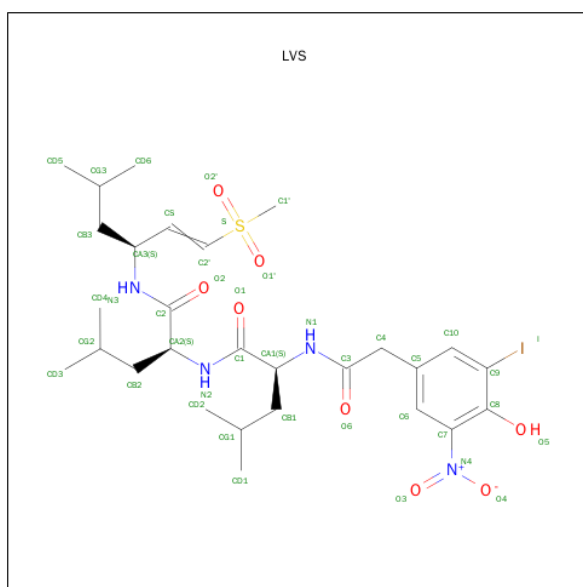
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	G	1	Total	Mg	0	0
			1	1		
4	H	1	Total	Mg	0	0
			1	1		
4	B	2	Total	Mg	0	0
			2	2		
4	I	1	Total	Mg	0	0
			1	1		
4	C	2	Total	Mg	0	0
			2	2		
4	A	2	Total	Mg	0	0
			2	2		
4	N	1	Total	Mg	0	0
			1	1		
4	L	1	Total	Mg	0	0
			1	1		
4	M	1	Total	Mg	0	0
			1	1		

- Molecule 5 is PHOSPHATE ION (three-letter code: PO4) (formula: O₄P).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	O	P	0	0
			5	4	1		
5	B	1	Total	O	P	0	0
			5	4	1		
5	C	1	Total	O	P	0	0
			5	4	1		

- Molecule 6 is 4-iodo-3-nitrophenyl acetyl-leucinyll-leucinyll-leucinyll-vinylsulfone (three-letter code: LVS) (formula: C₂₈H₄₃IN₄O₈S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
6	G	1	Total 41	C 28	N 4	O 8	S 1	0	0
6	H	1	Total 41	C 28	N 4	O 8	S 1	0	0
6	I	1	Total 41	C 28	N 4	O 8	S 1	0	0

- Molecule 7 is water.

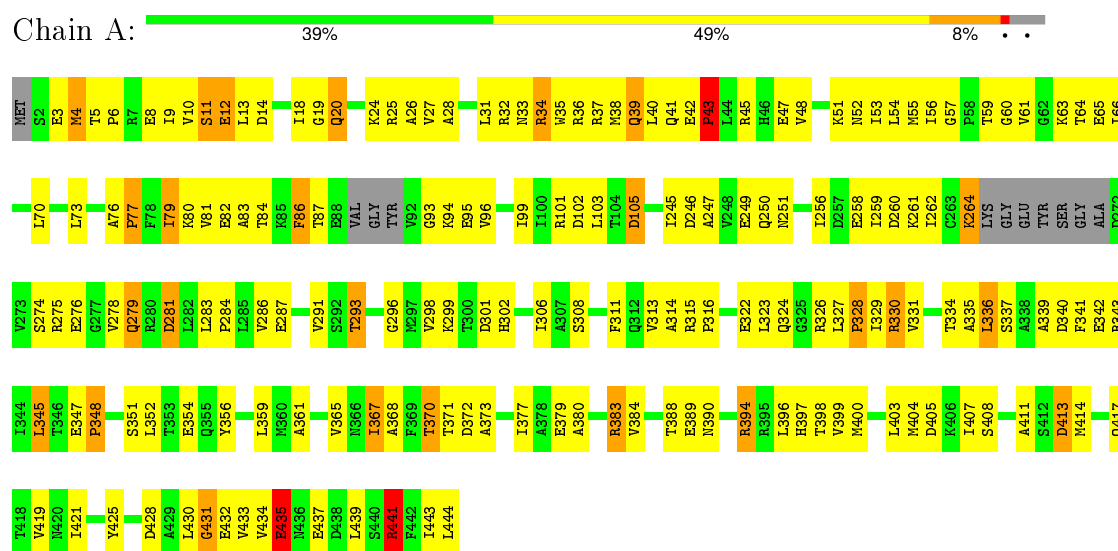
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	7	Total 7	O 7	0	0
7	B	7	Total 7	O 7	0	0
7	C	7	Total 7	O 7	0	0

3 Residue-property plots

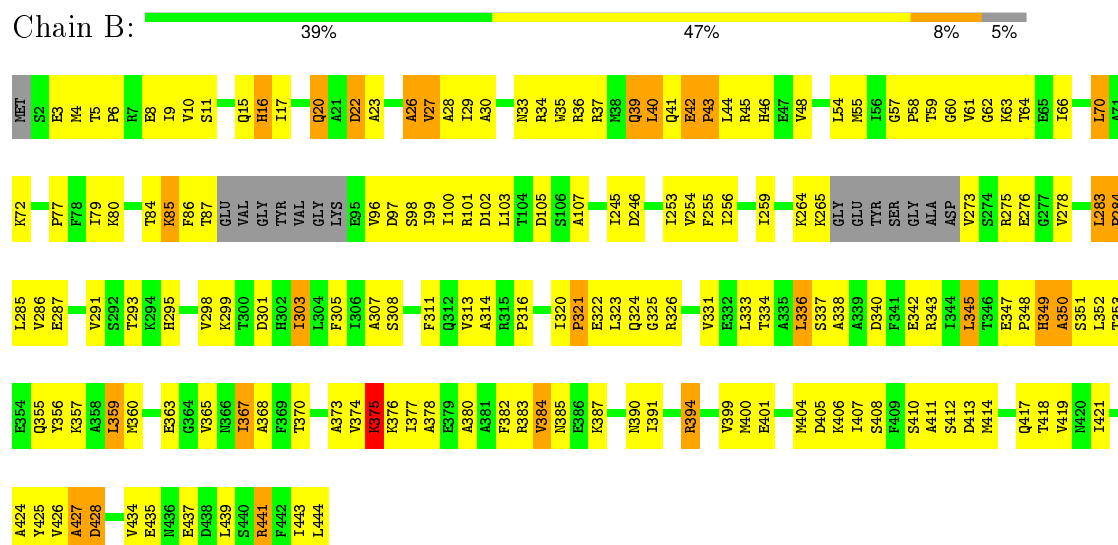
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according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

Note EDS was not executed.

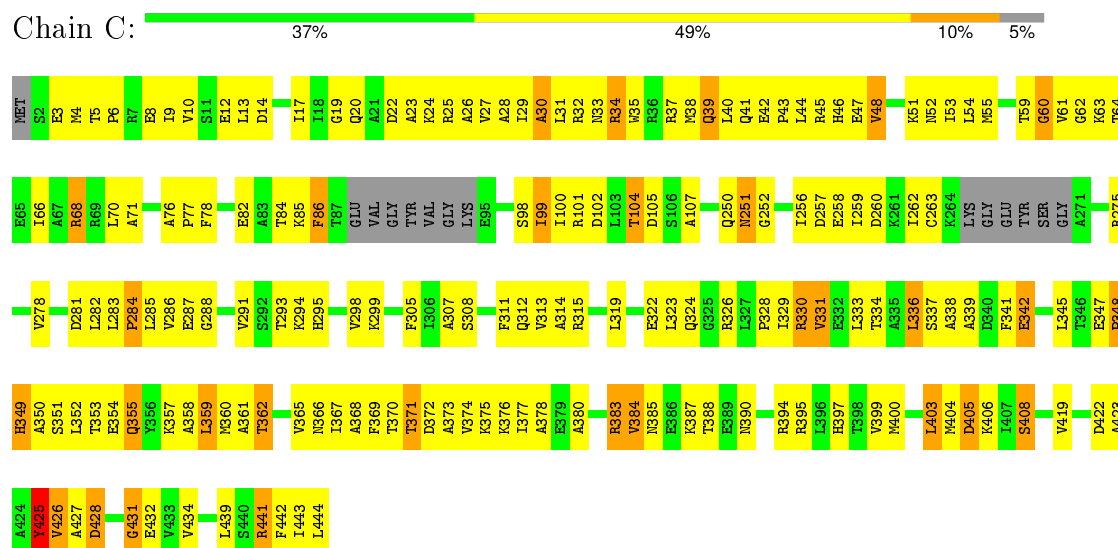
• Molecule 1: ATP-DEPENDENT HSL PROTEASE ATP-BINDING SUBUNIT HSLU

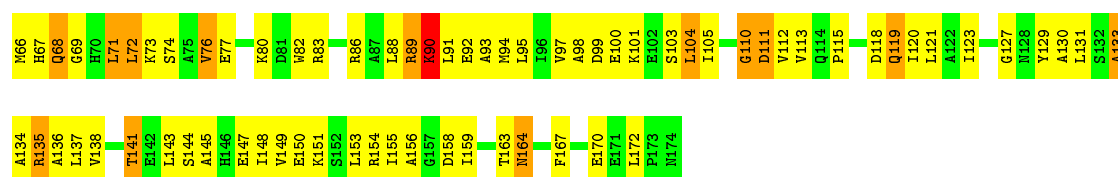


• Molecule 1: ATP-DEPENDENT HSL PROTEASE ATP-BINDING SUBUNIT HSLU



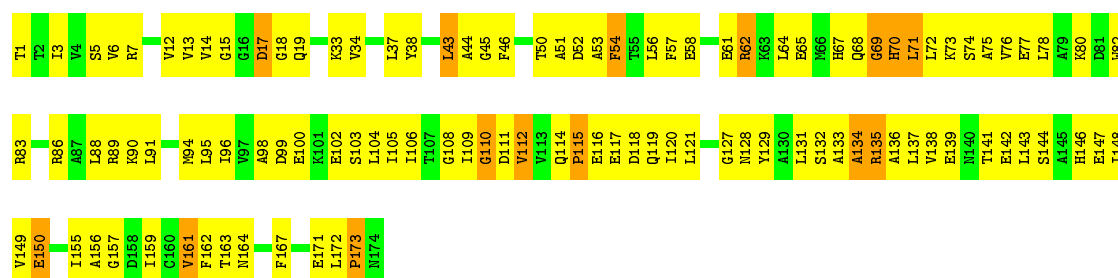
- Molecule 1: ATP-DEPENDENT HSL PROTEASE ATP-BINDING SUBUNIT HSLU





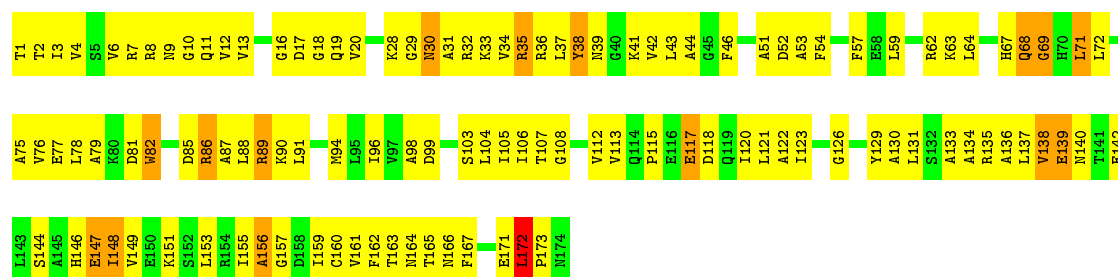
• Molecule 2: ATP-DEPENDENT PROTEASE HSLV

Chain L: 37% 54% 9%



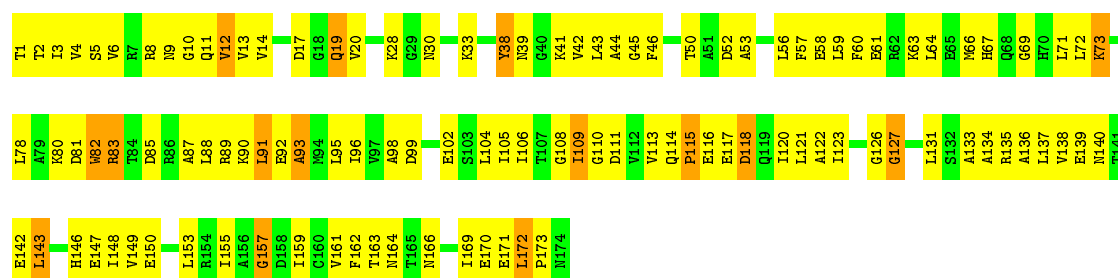
• Molecule 2: ATP-DEPENDENT PROTEASE HSLV

Chain M: 33% 57% 9%



• Molecule 2: ATP-DEPENDENT PROTEASE HSLV

Chain N: 36% 55% 9%



4 Data and refinement statistics

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

Property	Value	Source
Space group	P 6	Depositor
Cell constants a, b, c, α , β , γ	190.18Å 190.18Å 114.51Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	50.00 – 3.20	Depositor
% Data completeness (in resolution range)	96.7 (50.00-3.20)	Depositor
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.232 , 0.327	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	15050	wwPDB-VP
Average B, all atoms (Å ²)	64.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MG, PO4, ADP, LVS

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	0.44	0/2339	0.71	0/3156
1	B	0.44	0/2311	0.70	0/3118
1	C	0.41	0/2315	0.69	1/3125 (0.0%)
2	G	0.38	0/1333	0.63	0/1798
2	H	0.38	0/1333	0.61	0/1798
2	I	0.36	0/1333	0.62	0/1798
2	L	0.34	0/1333	0.60	0/1798
2	M	0.33	0/1333	0.58	0/1798
2	N	0.34	0/1333	0.60	0/1798
All	All	0.39	0/14963	0.65	1/20187 (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	A	0	1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	345	LEU	CA-CB-CG	6.12	129.39	115.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	356	TYR	Sidechain

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	2312	0	2358	190	0
1	B	2284	0	2336	182	0
1	C	2288	0	2332	187	0
2	G	1319	0	1347	135	0
2	H	1319	0	1347	151	0
2	I	1319	0	1347	144	0
2	L	1319	0	1348	116	0
2	M	1319	0	1348	140	0
2	N	1319	0	1348	127	0
3	A	27	0	12	4	0
3	B	27	0	12	6	0
3	C	27	0	12	4	0
4	A	2	0	0	0	0
4	B	2	0	0	0	0
4	C	2	0	0	0	0
4	G	1	0	0	0	0
4	H	1	0	0	0	0
4	I	1	0	0	0	0
4	L	1	0	0	0	0
4	M	1	0	0	0	0
4	N	1	0	0	0	0
5	A	5	0	0	0	0
5	B	5	0	0	2	0
5	C	5	0	0	1	0
6	G	41	0	38	9	0
6	H	41	0	38	5	0
6	I	41	0	38	5	0
7	A	7	0	0	0	0
7	B	7	0	0	0	0
7	C	7	0	0	0	0
All	All	15050	0	15261	1331	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 44.

The worst 5 of 1331 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:3:GLU:HG3	1:C:4:MET:H	1.10	1.14
1:B:441:ARG:HH11	1:B:441:ARG:HB3	1.07	1.09
1:C:406:LYS:H	1:C:406:LYS:HD2	1.15	1.04
2:N:105:ILE:HG13	2:N:121:LEU:HD13	1.40	1.03
1:A:441:ARG:HH11	1:A:441:ARG:HB3	1.21	1.03

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	293/310 (94%)	229 (78%)	50 (17%)	14 (5%)	3	22
1	B	289/310 (93%)	217 (75%)	54 (19%)	18 (6%)	2	14
1	C	290/310 (94%)	219 (76%)	53 (18%)	18 (6%)	2	14
2	G	172/174 (99%)	128 (74%)	33 (19%)	11 (6%)	2	13
2	H	172/174 (99%)	131 (76%)	31 (18%)	10 (6%)	2	17
2	I	172/174 (99%)	128 (74%)	31 (18%)	13 (8%)	1	9
2	L	172/174 (99%)	122 (71%)	35 (20%)	15 (9%)	1	5
2	M	172/174 (99%)	109 (63%)	49 (28%)	14 (8%)	1	7
2	N	172/174 (99%)	121 (70%)	35 (20%)	16 (9%)	1	5
All	All	1904/1974 (96%)	1404 (74%)	371 (20%)	129 (7%)	1	11

5 of 129 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	96	VAL
1	A	435	GLU
1	B	42	GLU
1	B	85	LYS
1	C	47	GLU

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	249/256 (97%)	216 (87%)	33 (13%)	5	23
1	B	246/256 (96%)	224 (91%)	22 (9%)	12	44
1	C	246/256 (96%)	220 (89%)	26 (11%)	8	34
2	G	139/140 (99%)	130 (94%)	9 (6%)	21	61
2	H	139/140 (99%)	128 (92%)	11 (8%)	15	53
2	I	139/140 (99%)	122 (88%)	17 (12%)	6	27
2	L	139/140 (99%)	131 (94%)	8 (6%)	25	66
2	M	139/140 (99%)	129 (93%)	10 (7%)	18	57
2	N	139/140 (99%)	135 (97%)	4 (3%)	50	83
All	All	1575/1608 (98%)	1435 (91%)	140 (9%)	12	44

5 of 140 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	104	THR
1	C	425	TYR
2	M	71	LEU
1	C	281	ASP
1	C	355	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 45 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	312	GLN
2	G	164	ASN
2	N	67	HIS
2	G	19	GLN
2	H	19	GLN

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 carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 21 ligands modelled in this entry, 12 are monoatomic - leaving 9 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	ADP	A	450	4	22,29,29	2.49	9 (40%)	27,45,45	2.87	5 (18%)
5	PO4	A	452	4	4,4,4	0.99	0	6,6,6	0.27	0
3	ADP	B	450	4	22,29,29	2.44	10 (45%)	27,45,45	2.77	4 (14%)
5	PO4	B	452	4	4,4,4	0.97	0	6,6,6	0.27	0
3	ADP	C	450	4	22,29,29	2.50	10 (45%)	27,45,45	2.93	5 (18%)
5	PO4	C	452	4	4,4,4	0.78	0	6,6,6	0.27	0
6	LVS	G	0	2	37,41,42	4.39	11 (29%)	45,57,59	1.70	7 (15%)
6	LVS	H	0	2	37,41,42	4.52	11 (29%)	45,57,59	1.62	6 (13%)
6	LVS	I	0	2	37,41,42	4.64	11 (29%)	45,57,59	1.69	6 (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	ADP	A	450	4	-	0/12/32/32	0/3/3/3
5	PO4	A	452	4	-	0/0/0/0	0/0/0/0
3	ADP	B	450	4	-	0/12/32/32	0/3/3/3
5	PO4	B	452	4	-	0/0/0/0	0/0/0/0
3	ADP	C	450	4	-	0/12/32/32	0/3/3/3
5	PO4	C	452	4	-	0/0/0/0	0/0/0/0
6	LVS	G	0	2	-	0/44/46/46	0/1/1/1
6	LVS	H	0	2	-	0/44/46/46	0/1/1/1
6	LVS	I	0	2	-	0/44/46/46	0/1/1/1

The worst 5 of 62 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	G	0	LVS	CD5-CG3	-4.72	1.23	1.51
6	H	0	LVS	CD5-CG3	-4.61	1.23	1.51
6	I	0	LVS	CD5-CG3	-4.47	1.24	1.51
3	C	450	ADP	C8-N7	-2.99	1.28	1.34
3	B	450	ADP	C8-N7	-2.88	1.29	1.34

The worst 5 of 33 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	450	ADP	N3-C2-N1	-11.22	120.30	128.89
3	C	450	ADP	N3-C2-N1	-11.20	120.32	128.89
3	B	450	ADP	N3-C2-N1	-10.88	120.56	128.89
3	C	450	ADP	PA-O3A-PB	-7.80	106.51	132.67
3	B	450	ADP	PA-O3A-PB	-7.14	108.73	132.67

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

8 monomers are involved in 36 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	450	ADP	4	0
3	B	450	ADP	6	0
5	B	452	PO4	2	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	450	ADP	4	0
5	C	452	PO4	1	0
6	G	0	LVS	9	0
6	H	0	LVS	5	0
6	I	0	LVS	5	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 ⓘ

6.1 Protein, DNA and RNA chains ⓘ

EDS was not executed - this section will therefore be empty.

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

EDS was not executed - this section will therefore be empty.

6.3 Carbohydrates ⓘ

EDS was not executed - this section will therefore be empty.

6.4 Ligands ⓘ

EDS was not executed - this section will therefore be empty.

6.5 Other polymers ⓘ

EDS was not executed - this section will therefore be empty.