



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 04:43 AM GMT

PDB ID : 2NUU  
Title : Regulating the Escherichia coli ammonia channel: the crystal structure of the AmtB-GlnK complex  
Authors : Conroy, M.J.; Durand, A.; Lupo, D.; Li, X.-D.; Bullough, P.A.; Winkler, F.K.; Merrick, M.  
Deposited on : 2006-11-09  
Resolution : 2.50 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.  
We welcome your comments at [validation@mail.wwpdb.org](mailto: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.

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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

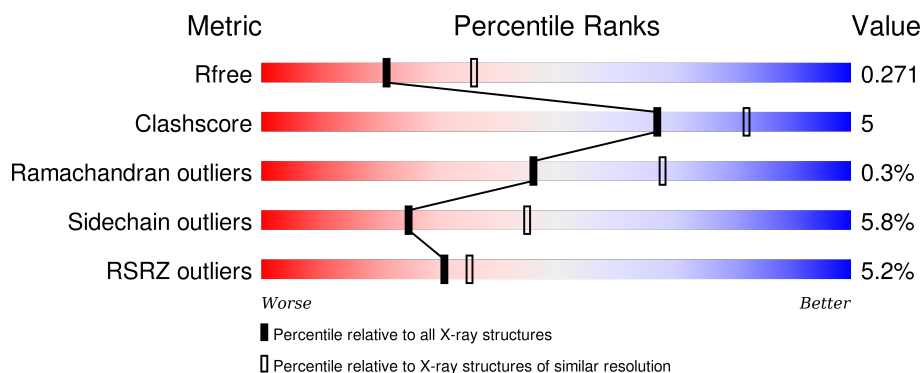
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.50 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))
$R_{free}$	91344	3553 (2.50-2.50)
Clashscore	102246	4242 (2.50-2.50)
Ramachandran outliers	100387	4156 (2.50-2.50)
Sidechain outliers	100360	4158 (2.50-2.50)
RSRZ outliers	91569	3562 (2.50-2.50)

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  $\geq 3$ , 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	415	<div> <div>4%</div> <div>83% 14% ..</div> </div>
1	B	415	<div> <div>5%</div> <div>81% 17% ..</div> </div>
1	C	415	<div> <div>5%</div> <div>84% 13% ..</div> </div>
1	D	415	<div> <div>4%</div> <div>84% 13% ..</div> </div>
1	E	415	<div> <div>4%</div> <div>85% 13% .</div> </div>

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Mol	Chain	Length	Quality of chain
1	F	415	<div><div></div><div>4%</div><div>85%</div><div>13%</div><div>••</div></div>
2	G	112	<div><div></div><div>9%</div><div>86%</div><div>13%</div><div>•</div></div>
2	H	112	<div><div></div><div>8%</div><div>77%</div><div>21%</div><div>•</div></div>
2	I	112	<div><div></div><div>31%</div><div>84%</div><div>15%</div><div>•</div></div>
2	J	112	<div><div></div><div>%</div><div>87%</div><div>12%</div><div>•</div></div>
2	K	112	<div><div></div><div>%</div><div>75%</div><div>25%</div><div></div></div>
2	L	112	<div><div></div><div></div><div>79%</div><div>20%</div><div>•</div></div>

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 24026 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 Ammonia channel.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	409	Total	C	N	O	S	0	0	0
			3020	1981	501	519	19			
1	B	409	Total	C	N	O	S	0	0	0
			3020	1981	501	519	19			
1	C	409	Total	C	N	O	S	0	0	0
			3020	1981	501	519	19			
1	D	410	Total	C	N	O	S	0	0	0
			3030	1987	504	520	19			
1	E	409	Total	C	N	O	S	0	0	0
			3020	1981	501	519	19			
1	F	409	Total	C	N	O	S	0	0	0
			3020	1981	501	519	19			

There are 66 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-8	ALA	-	EXPRESSION TAG	UNP P69681
A	-7	PRO	-	EXPRESSION TAG	UNP P69681
A	-6	ALA	-	EXPRESSION TAG	UNP P69681
A	-5	VAL	-	EXPRESSION TAG	UNP P69681
A	-4	ALA	-	EXPRESSION TAG	UNP P69681
A	-3	HIS	-	EXPRESSION TAG	UNP P69681
A	-2	HIS	-	EXPRESSION TAG	UNP P69681
A	-1	HIS	-	EXPRESSION TAG	UNP P69681
A	0	HIS	-	EXPRESSION TAG	UNP P69681
A	1	HIS	-	EXPRESSION TAG	UNP P69681
A	2	HIS	-	EXPRESSION TAG	UNP P69681
B	-8	ALA	-	EXPRESSION TAG	UNP P69681
B	-7	PRO	-	EXPRESSION TAG	UNP P69681
B	-6	ALA	-	EXPRESSION TAG	UNP P69681
B	-5	VAL	-	EXPRESSION TAG	UNP P69681
B	-4	ALA	-	EXPRESSION TAG	UNP P69681
B	-3	HIS	-	EXPRESSION TAG	UNP P69681

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-2	HIS	-	EXPRESSION TAG	UNP P69681
B	-1	HIS	-	EXPRESSION TAG	UNP P69681
B	0	HIS	-	EXPRESSION TAG	UNP P69681
B	1	HIS	-	EXPRESSION TAG	UNP P69681
B	2	HIS	-	EXPRESSION TAG	UNP P69681
C	-8	ALA	-	EXPRESSION TAG	UNP P69681
C	-7	PRO	-	EXPRESSION TAG	UNP P69681
C	-6	ALA	-	EXPRESSION TAG	UNP P69681
C	-5	VAL	-	EXPRESSION TAG	UNP P69681
C	-4	ALA	-	EXPRESSION TAG	UNP P69681
C	-3	HIS	-	EXPRESSION TAG	UNP P69681
C	-2	HIS	-	EXPRESSION TAG	UNP P69681
C	-1	HIS	-	EXPRESSION TAG	UNP P69681
C	0	HIS	-	EXPRESSION TAG	UNP P69681
C	1	HIS	-	EXPRESSION TAG	UNP P69681
C	2	HIS	-	EXPRESSION TAG	UNP P69681
D	-8	ALA	-	EXPRESSION TAG	UNP P69681
D	-7	PRO	-	EXPRESSION TAG	UNP P69681
D	-6	ALA	-	EXPRESSION TAG	UNP P69681
D	-5	VAL	-	EXPRESSION TAG	UNP P69681
D	-4	ALA	-	EXPRESSION TAG	UNP P69681
D	-3	HIS	-	EXPRESSION TAG	UNP P69681
D	-2	HIS	-	EXPRESSION TAG	UNP P69681
D	-1	HIS	-	EXPRESSION TAG	UNP P69681
D	0	HIS	-	EXPRESSION TAG	UNP P69681
D	1	HIS	-	EXPRESSION TAG	UNP P69681
D	2	HIS	-	EXPRESSION TAG	UNP P69681
E	-8	ALA	-	EXPRESSION TAG	UNP P69681
E	-7	PRO	-	EXPRESSION TAG	UNP P69681
E	-6	ALA	-	EXPRESSION TAG	UNP P69681
E	-5	VAL	-	EXPRESSION TAG	UNP P69681
E	-4	ALA	-	EXPRESSION TAG	UNP P69681
E	-3	HIS	-	EXPRESSION TAG	UNP P69681
E	-2	HIS	-	EXPRESSION TAG	UNP P69681
E	-1	HIS	-	EXPRESSION TAG	UNP P69681
E	0	HIS	-	EXPRESSION TAG	UNP P69681
E	1	HIS	-	EXPRESSION TAG	UNP P69681
E	2	HIS	-	EXPRESSION TAG	UNP P69681
F	-8	ALA	-	EXPRESSION TAG	UNP P69681
F	-7	PRO	-	EXPRESSION TAG	UNP P69681
F	-6	ALA	-	EXPRESSION TAG	UNP P69681
F	-5	VAL	-	EXPRESSION TAG	UNP P69681

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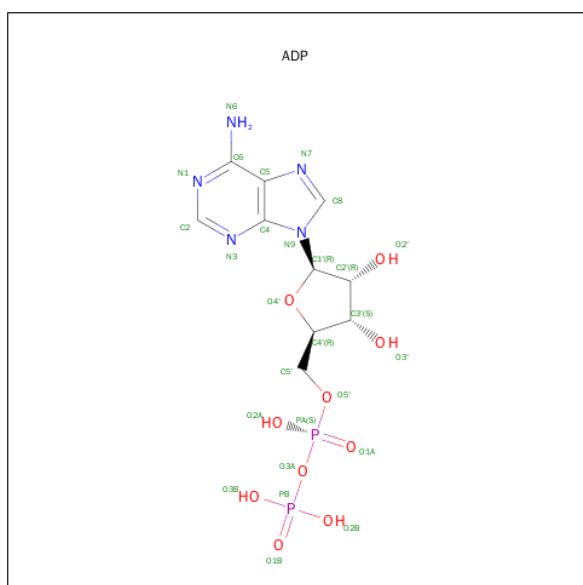
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Chain	Residue	Modelled	Actual	Comment	Reference
F	-4	ALA	-	EXPRESSION TAG	UNP P69681
F	-3	HIS	-	EXPRESSION TAG	UNP P69681
F	-2	HIS	-	EXPRESSION TAG	UNP P69681
F	-1	HIS	-	EXPRESSION TAG	UNP P69681
F	0	HIS	-	EXPRESSION TAG	UNP P69681
F	1	HIS	-	EXPRESSION TAG	UNP P69681
F	2	HIS	-	EXPRESSION TAG	UNP P69681

- Molecule 2 is a protein called Nitrogen regulatory protein P-II 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	G	112	Total	C	N	O	S	0	0	0
			864	552	147	164	1			
2	H	112	Total	C	N	O	S	0	0	0
			864	552	147	164	1			
2	I	112	Total	C	N	O	S	0	0	0
			864	552	147	164	1			
2	J	112	Total	C	N	O	S	0	0	0
			864	552	147	164	1			
2	K	112	Total	C	N	O	S	0	0	0
			864	552	147	164	1			
2	L	112	Total	C	N	O	S	0	0	0
			864	552	147	164	1			

- Molecule 3 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula:  $C_{10}H_{15}N_5O_{10}P_2$ ).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	G	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
3	H	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
3	G	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
3	J	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
3	L	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
3	J	1	Total	C	N	O	P	0	0
			27	10	5	10	2		

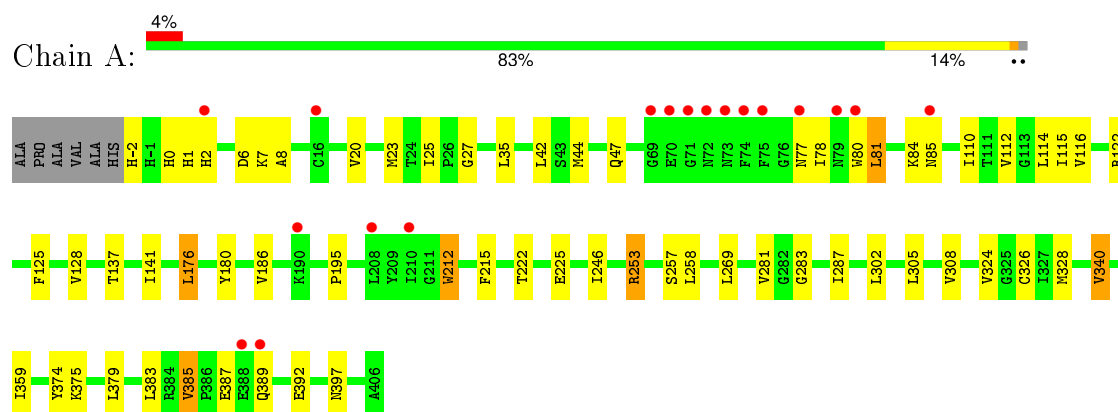
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	60	Total	O	0	0
			60	60		
4	B	64	Total	O	0	0
			64	64		
4	C	82	Total	O	0	0
			82	82		
4	D	66	Total	O	0	0
			66	66		
4	E	68	Total	O	0	0
			68	68		
4	F	69	Total	O	0	0
			69	69		
4	G	19	Total	O	0	0
			19	19		
4	H	23	Total	O	0	0
			23	23		
4	I	16	Total	O	0	0
			16	16		
4	J	31	Total	O	0	0
			31	31		
4	K	21	Total	O	0	0
			21	21		
4	L	31	Total	O	0	0
			31	31		

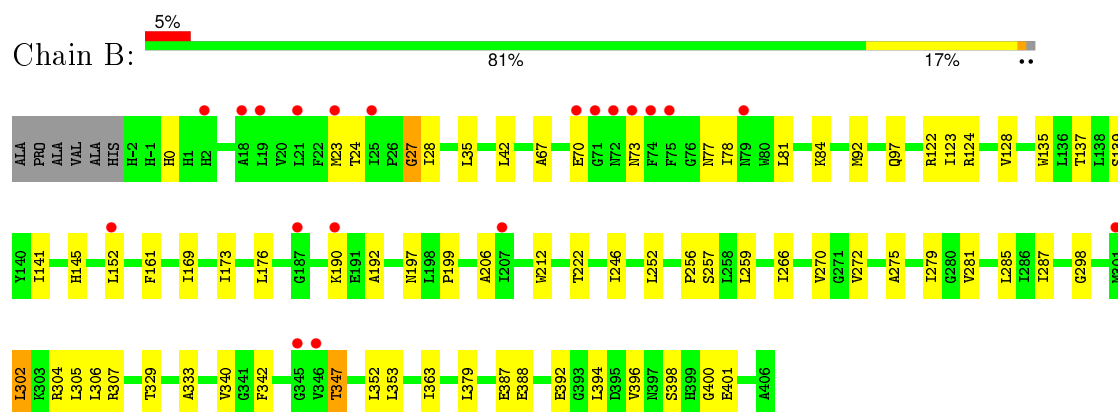
### 3 Residue-property plots

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.

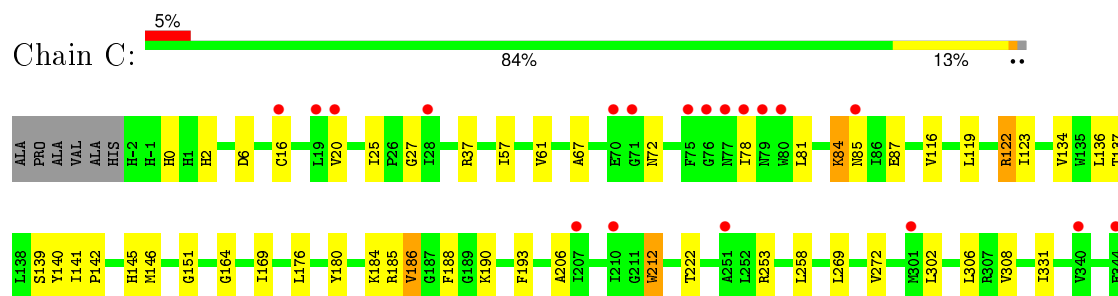
#### • Molecule 1: Ammonia channel



#### • Molecule 1: Ammonia channel



#### • Molecule 1: Ammonia channel







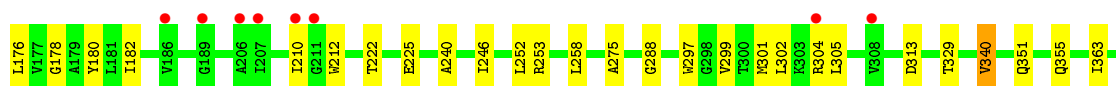
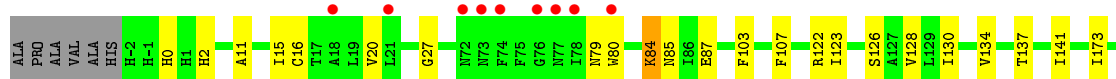
• Molecule 1: Ammonia channel

Chain D: 4% 84% 13% ..



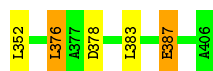
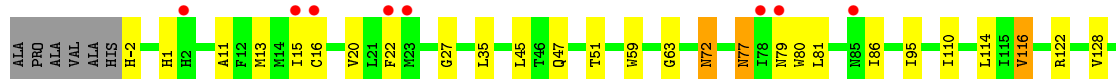
• Molecule 1: Ammonia channel

Chain E: 4% 85% 13% .



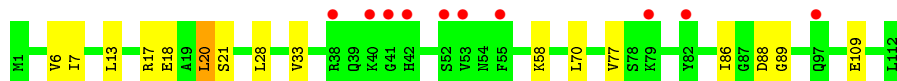
• Molecule 1: Ammonia channel

Chain F: 4% 85% 13% ..

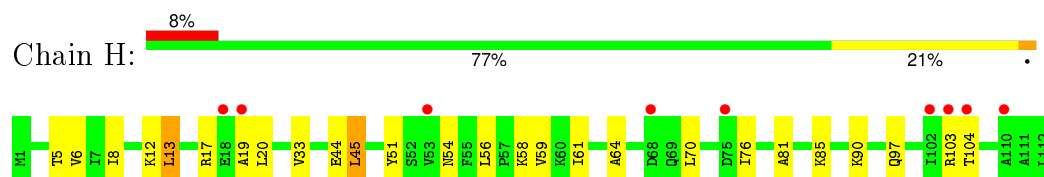


• Molecule 2: Nitrogen regulatory protein P-II 2

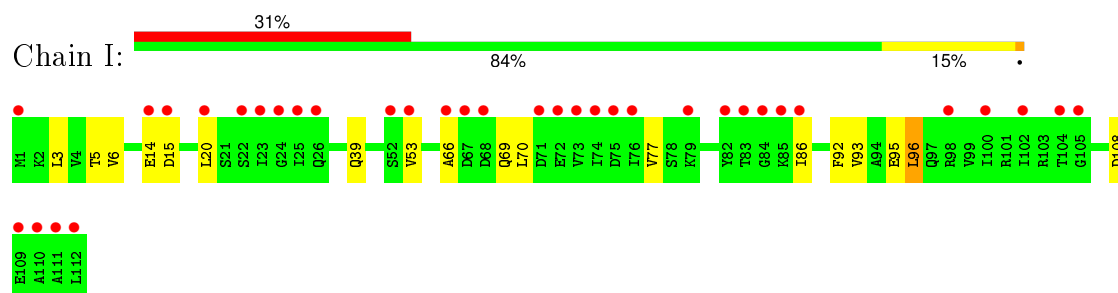
Chain G: 9% 86% 13% .



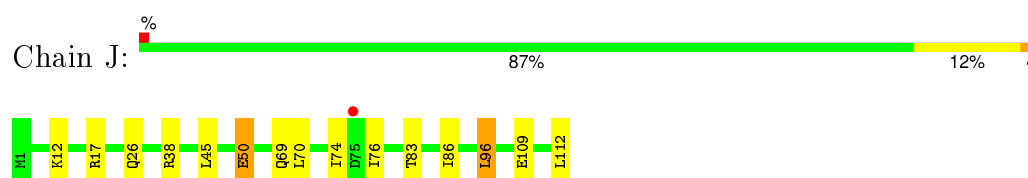
- Molecule 2: Nitrogen regulatory protein P-II 2



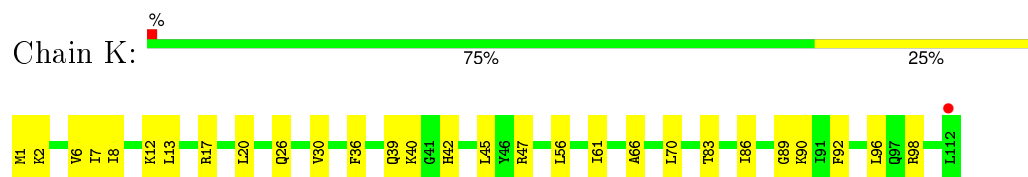
- Molecule 2: Nitrogen regulatory protein P-II 2



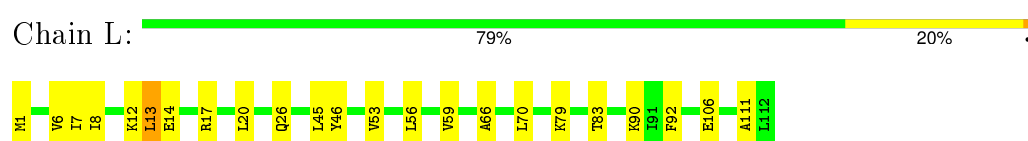
- Molecule 2: Nitrogen regulatory protein P-II 2



- Molecule 2: Nitrogen regulatory protein P-II 2



- Molecule 2: Nitrogen regulatory protein P-II 2



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	99.69Å 107.86Å 280.16Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.00 – 2.50 39.37 – 2.50	Depositor EDS
% Data completeness (in resolution range)	99.8 (40.00-2.50) 99.8 (39.37-2.50)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.10	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.73 (at 2.51Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, $R_{free}$	0.171 , 0.249 0.202 , 0.271	Depositor DCC
$R_{free}$ test set	5272 reflections (5.29%)	DCC
Wilson B-factor (Å <sup>2</sup> )	37.8	Xtriage
Anisotropy	0.096	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 57.2	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.46$ , $\langle L^2 \rangle = 0.28$	Xtriage
Outliers	0 of 105006 reflections	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	24026	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.62% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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 [i](#)

### 5.1 Standard geometry [i](#)

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

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	0.47	0/3092	0.63	0/4209
1	B	0.50	0/3092	0.65	0/4209
1	C	0.46	0/3092	0.64	0/4209
1	D	0.48	0/3103	0.64	1/4224 (0.0%)
1	E	0.47	0/3092	0.60	0/4209
1	F	0.47	0/3092	0.63	0/4209
2	G	0.40	0/873	0.67	0/1173
2	H	0.40	0/873	0.67	1/1173 (0.1%)
2	I	0.38	0/873	0.60	0/1173
2	J	0.45	0/873	0.70	0/1173
2	K	0.45	0/873	0.72	0/1173
2	L	0.45	0/873	0.66	0/1173
All	All	0.47	0/23801	0.64	2/32307 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	81	LEU	CA-CB-CG	6.25	129.67	115.30
2	H	45	LEU	CA-CB-CG	5.85	128.76	115.30

There are no chirality outliers.

There are no planarity outliers.

### 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	3020	0	3068	41	0
1	B	3020	0	3068	35	0
1	C	3020	0	3068	33	0
1	D	3030	0	3075	32	0
1	E	3020	0	3068	31	0
1	F	3020	0	3068	32	0
2	G	864	0	906	5	0
2	H	864	0	906	11	0
2	I	864	0	906	8	0
2	J	864	0	906	5	0
2	K	864	0	906	16	0
2	L	864	0	906	13	0
3	G	54	0	24	0	0
3	H	27	0	12	0	0
3	J	54	0	24	0	0
3	L	27	0	12	1	0
4	A	60	0	0	3	0
4	B	64	0	0	4	0
4	C	82	0	0	0	0
4	D	66	0	0	0	0
4	E	68	0	0	2	0
4	F	69	0	0	3	0
4	G	19	0	0	0	0
4	H	23	0	0	0	0
4	I	16	0	0	0	0
4	J	31	0	0	0	0
4	K	21	0	0	1	0
4	L	31	0	0	0	0
All	All	24026	0	23923	228	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 5.

All (228) 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:E:253:ARG:HE	2:K:45:LEU:HD11	1.45	0.80
1:C:72:ASN:O	1:C:145:HIS:HE1	1.70	0.75
1:C:186:VAL:HG11	1:C:387:GLU:HG3	1.72	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:392:GLU:HG3	1:D:397:ASN:HD21	1.55	0.71
1:A:186:VAL:HG21	1:A:387:GLU:HG3	1.73	0.70
1:A:225:GLU:OE2	1:E:2:HIS:HE1	1.76	0.68
2:L:12:LYS:HE3	2:L:83:THR:HG22	1.77	0.67
1:B:307:ARG:HA	4:B:462:HOH:O	1.95	0.66
1:B:394:LEU:O	1:B:398:SER:HB2	1.95	0.65
1:A:84:LYS:O	1:A:85:ASN:HB2	1.95	0.64
1:A:0:HIS:CD2	1:E:340:VAL:HG21	2.34	0.63
1:F:11:ALA:O	1:F:15:ILE:HG12	2.00	0.62
1:B:304:ARG:HA	4:B:462:HOH:O	2.00	0.61
1:D:137:THR:HA	1:D:141:ILE:HD12	1.81	0.61
1:A:258:LEU:HD22	1:B:42:LEU:HD22	1.83	0.61
1:A:385:VAL:HG13	1:A:389:GLN:HB2	1.83	0.60
2:I:3:LEU:HB2	2:I:96:LEU:HD12	1.84	0.60
1:C:84:LYS:O	1:C:85:ASN:HB2	2.00	0.59
1:A:2:HIS:HE1	1:E:225:GLU:OE2	1.85	0.59
1:C:0:HIS:CD2	1:F:340:VAL:HG21	2.38	0.59
1:B:347:THR:HG21	4:B:459:HOH:O	2.02	0.59
1:E:0:HIS:H	1:E:0:HIS:CD2	2.20	0.58
1:F:331:ILE:HG13	1:F:352:LEU:HD21	1.86	0.58
2:K:7:ILE:O	2:K:89:GLY:HA3	2.03	0.58
2:L:6:VAL:HG12	2:L:8:ILE:HG23	1.86	0.57
1:F:378:ASP:HB2	1:F:383:LEU:HG	1.87	0.57
2:K:17:ARG:HH22	2:L:53:VAL:HG11	1.69	0.57
1:C:180:TYR:CE2	1:C:308:VAL:HG22	2.40	0.57
1:B:396:VAL:O	1:B:400:GLY:HA2	2.05	0.57
1:C:0:HIS:HD2	1:F:340:VAL:HG21	1.70	0.56
1:F:77:ASN:HD22	1:F:77:ASN:C	2.09	0.56
1:C:16:CYS:O	1:C:20:VAL:HG23	2.07	0.55
2:K:96:LEU:HD21	2:L:92:PHE:HB3	1.87	0.55
1:E:178:GLY:O	1:E:182:ILE:HG12	2.06	0.55
1:A:125:PHE:O	1:A:128:VAL:HG12	2.07	0.55
2:K:39:GLN:HB2	2:K:86:ILE:HG22	1.88	0.54
1:D:42:LEU:HD22	1:F:258:LEU:HD22	1.89	0.54
1:B:35:LEU:HD21	1:B:259:LEU:HD11	1.89	0.54
1:D:72:ASN:O	1:D:145:HIS:HE1	1.91	0.54
1:E:258:LEU:CD1	1:F:45:LEU:HB2	2.37	0.54
1:E:84:LYS:O	1:E:85:ASN:HB2	2.08	0.53
1:A:137:THR:HA	1:A:141:ILE:HD12	1.90	0.53
1:C:164:GLY:O	1:C:169:ILE:HG13	2.09	0.53
1:A:112:VAL:HA	1:A:115:ILE:HD12	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:173:ILE:HD11	1:B:363:ILE:HG12	1.91	0.53
1:A:110:ILE:O	1:A:114:LEU:HG	2.09	0.53
1:B:169:ILE:O	1:B:173:ILE:HG12	2.09	0.53
1:A:78:ILE:HG23	1:A:81:LEU:HD23	1.90	0.53
1:C:119:LEU:HD13	1:C:123:ILE:HD13	1.90	0.53
2:H:19:ALA:HB1	2:H:76:ILE:HG12	1.91	0.52
1:A:20:VAL:O	1:A:23:MET:HB2	2.09	0.52
4:B:463:HOH:O	1:D:-1:HIS:HB3	2.09	0.52
2:G:7:ILE:O	2:G:89:GLY:HA3	2.10	0.52
1:F:319:GLY:O	1:F:323:ILE:HG13	2.10	0.52
2:K:30:VAL:HG22	2:K:61:ILE:HG12	1.91	0.52
1:A:-2:HIS:HB3	4:A:434:HOH:O	2.09	0.51
1:F:236:VAL:HG21	1:F:281:VAL:HG23	1.91	0.51
1:B:67:ALA:O	1:B:145:HIS:HD2	1.94	0.51
1:B:73:ASN:HB3	1:B:152:LEU:HB2	1.92	0.51
1:C:122:ARG:HD2	1:C:185:ARG:HG2	1.91	0.51
1:C:137:THR:HA	1:C:141:ILE:HD12	1.92	0.51
1:A:374:TYR:HB3	1:A:383:LEU:HD11	1.93	0.51
1:D:257:SER:HB2	1:E:401:GLU:CD	2.31	0.50
1:D:331:ILE:HG13	1:D:352:LEU:HD21	1.93	0.50
1:A:326:CYS:HB2	1:A:359:ILE:HD11	1.94	0.50
1:A:44:MET:SD	1:A:116:VAL:HG12	2.51	0.50
1:C:134:VAL:HG21	1:C:376:LEU:HD13	1.93	0.50
1:C:2:HIS:HE1	1:F:225:GLU:OE2	1.93	0.49
1:A:-2:HIS:CE1	1:A:1:HIS:HB2	2.48	0.49
1:E:87:GLU:HG3	4:E:435:HOH:O	2.12	0.49
1:B:388:GLU:O	1:B:392:GLU:HG2	2.12	0.49
1:C:67:ALA:O	1:C:145:HIS:HD2	1.96	0.49
1:B:78:ILE:O	1:B:81:LEU:HD13	2.13	0.48
1:E:374:TYR:HB3	1:E:383:LEU:HD11	1.94	0.48
2:J:96:LEU:HD21	2:K:92:PHE:HB3	1.95	0.48
1:C:388:GLU:CD	1:C:388:GLU:H	2.16	0.48
1:B:0:HIS:CD2	1:D:226:ILE:HD12	2.49	0.48
1:E:240:ALA:HB3	1:E:288:GLY:HA3	1.95	0.48
2:K:1:MET:CE	2:K:66:ALA:HA	2.44	0.48
1:A:176:LEU:HD22	1:A:180:TYR:CE1	2.48	0.48
1:A:77:ASN:HB2	4:A:427:HOH:O	2.12	0.48
1:E:253:ARG:NE	2:K:45:LEU:HD11	2.21	0.48
1:A:324:VAL:O	1:A:328:MET:HG3	2.13	0.48
1:D:42:LEU:HD22	1:F:258:LEU:CD2	2.43	0.48
1:B:137:THR:HA	1:B:141:ILE:HD12	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:44:GLU:HG3	2:H:54:ASN:ND2	2.29	0.47
1:F:147:VAL:HG22	1:F:153:LEU:HD12	1.95	0.47
1:F:246:ILE:O	1:F:250:TRP:HB2	2.14	0.47
1:B:257:SER:HB2	1:C:401:GLU:CD	2.35	0.47
1:B:192:ALA:HA	2:H:51:TYR:CE1	2.49	0.47
2:G:20:LEU:HD23	2:G:28:LEU:HD23	1.97	0.47
1:F:-2:HIS:N	4:F:469:HOH:O	2.47	0.47
1:E:173:ILE:HG13	1:E:363:ILE:HA	1.97	0.46
1:D:11:ALA:O	1:D:15:ILE:HG12	2.15	0.46
1:E:103:PHE:CZ	1:E:107:PHE:HE1	2.33	0.46
1:B:123:ILE:HG13	1:B:124:ARG:N	2.30	0.46
1:F:387:GLU:HG2	4:F:425:HOH:O	2.13	0.46
1:A:42:LEU:HD22	1:C:258:LEU:CD2	2.45	0.46
1:A:42:LEU:HD22	1:C:258:LEU:HD23	1.97	0.46
2:L:106:GLU:O	2:L:111:ALA:HB2	2.16	0.46
1:C:375:LYS:HD3	1:C:375:LYS:HA	1.71	0.46
2:K:6:VAL:HG12	2:K:8:ILE:HG23	1.96	0.46
2:J:38:ARG:HB3	2:J:86:ILE:HD11	1.98	0.46
1:F:35:LEU:HD21	1:F:259:LEU:HD11	1.97	0.46
1:F:110:ILE:O	1:F:114:LEU:HG	2.16	0.46
1:C:184:LYS:HD3	1:C:188:PHE:CD2	2.50	0.46
1:A:257:SER:HB2	1:B:401:GLU:CD	2.36	0.46
2:I:6:VAL:HG21	2:I:77:VAL:HG11	1.98	0.46
1:D:84:LYS:HE2	1:D:85:ASN:HD21	1.81	0.45
1:A:35:LEU:HA	1:A:195:PRO:HB3	1.98	0.45
1:D:297:TRP:CD1	1:D:301:MET:HG3	2.51	0.45
1:D:75:PHE:CZ	1:D:142:PRO:HG3	2.52	0.45
2:K:98:ARG:HG3	4:K:122:HOH:O	2.16	0.45
1:F:47:GLN:HB3	1:F:116:VAL:HG11	1.97	0.45
2:K:36:PHE:CZ	2:K:40:LYS:HG2	2.52	0.45
1:E:123:ILE:HG12	1:E:128:VAL:HG23	1.99	0.45
1:C:306:LEU:HB3	1:C:308:VAL:HG23	1.98	0.45
2:L:14:GLU:HA	2:L:14:GLU:OE1	2.17	0.45
1:D:123:ILE:HD12	1:D:128:VAL:HG23	1.97	0.45
2:H:6:VAL:HG12	2:H:8:ILE:HG23	1.99	0.45
2:I:66:ALA:HB3	2:I:69:GLN:HG3	1.99	0.45
1:D:20:VAL:O	1:D:23:MET:HB2	2.17	0.45
1:B:81:LEU:O	1:B:84:LYS:HG2	2.17	0.45
1:B:275:ALA:HB2	1:B:329:THR:OG1	2.16	0.45
2:H:13:LEU:HG	2:H:59:VAL:HG11	1.98	0.45
1:F:13:MET:HG3	1:F:95:ILE:HG21	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:33:VAL:HG23	2:H:58:LYS:HB2	1.99	0.45
1:A:84:LYS:HE2	4:A:432:HOH:O	2.16	0.44
1:B:298:GLY:HA2	1:B:302:LEU:HB3	2.00	0.44
1:E:299:VAL:HG12	1:E:313:ASP:HB3	2.00	0.44
1:C:331:ILE:HG13	1:C:352:LEU:HD21	1.99	0.44
1:B:92:MET:HB2	1:B:97:GLN:HG3	1.97	0.44
1:B:340:VAL:HG21	1:D:0:HIS:ND1	2.33	0.44
1:C:212:TRP:CG	1:C:269:LEU:HD22	2.52	0.44
2:L:13:LEU:HG	2:L:59:VAL:HG11	2.00	0.44
2:K:12:LYS:NZ	2:K:83:THR:HG22	2.31	0.44
1:E:351:GLN:O	1:E:355:GLN:HG2	2.18	0.44
1:B:246:ILE:HG23	1:B:256:PRO:HB3	1.98	0.44
1:B:24:THR:HA	1:B:28:ILE:HG22	1.98	0.44
2:J:12:LYS:HD2	2:J:83:THR:CG2	2.47	0.44
1:A:375:LYS:O	1:A:379:LEU:HG	2.18	0.44
1:F:80:TRP:CD1	1:F:86:ILE:HG13	2.53	0.44
1:F:134:VAL:HG21	1:F:376:LEU:HD12	1.99	0.44
2:I:39:GLN:HB2	2:I:86:ILE:HG22	2.00	0.44
1:C:57:ILE:O	1:C:61:VAL:HG23	2.17	0.44
2:H:12:LYS:HD2	2:H:81:ALA:O	2.17	0.44
2:H:103:ARG:HG2	2:H:104:THR:HG23	1.98	0.44
1:B:135:TRP:O	1:B:139:SER:HB3	2.17	0.44
1:D:25:ILE:HA	1:D:26:PRO:HA	1.88	0.43
2:J:109:GLU:H	2:J:109:GLU:CD	2.21	0.43
1:D:84:LYS:HE2	1:D:85:ASN:ND2	2.33	0.43
1:D:40:ASN:HA	1:D:395:ASP:OD1	2.17	0.43
1:B:279:ILE:HD13	1:B:287:ILE:HD12	2.00	0.43
1:E:11:ALA:O	1:E:15:ILE:HG12	2.19	0.43
1:E:210:ILE:HG13	1:F:22:PHE:CD1	2.54	0.43
1:E:137:THR:HA	1:E:141:ILE:HD12	1.99	0.43
2:L:7:ILE:HD12	2:L:92:PHE:HE2	1.84	0.43
1:D:388:GLU:O	1:D:392:GLU:HG2	2.18	0.43
1:E:297:TRP:CD1	1:E:301:MET:HG3	2.54	0.43
1:D:81:LEU:O	1:D:84:LYS:HG2	2.19	0.43
1:E:16:CYS:O	1:E:20:VAL:HG23	2.19	0.43
1:E:84:LYS:HA	4:E:427:HOH:O	2.19	0.43
1:E:313:ASP:HB2	2:K:47:ARG:NH1	2.33	0.43
1:C:146:MET:HA	1:C:151:GLY:HA3	2.01	0.42
2:I:70:LEU:HD11	2:I:93:VAL:HG11	2.01	0.42
2:K:17:ARG:NH2	2:L:53:VAL:HG11	2.31	0.42
2:L:1:MET:HA	2:L:1:MET:HE2	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:142:PRO:O	1:C:146:MET:HG3	2.20	0.42
1:D:224:ASN:ND2	1:D:227:ALA:H	2.17	0.42
2:G:6:VAL:HG21	2:G:77:VAL:HG11	2.00	0.42
2:H:5:THR:HA	2:H:61:ILE:O	2.19	0.42
1:D:205:THR:HG23	1:D:266:ILE:HD11	2.01	0.42
1:C:139:SER:HB2	1:C:369:VAL:HG11	2.00	0.42
2:K:26:GLN:HB3	2:K:26:GLN:HE21	1.67	0.42
1:A:6:ASP:OD2	1:A:8:ALA:HB3	2.19	0.42
1:A:212:TRP:CE3	1:A:269:LEU:HD13	2.55	0.42
1:B:333:ALA:HB3	1:B:342:PHE:CE1	2.55	0.42
1:C:141:ILE:HB	1:C:142:PRO:HD3	2.02	0.42
1:F:47:GLN:O	1:F:51:THR:HG23	2.20	0.42
1:B:197:ASN:OD1	1:B:199:PRO:HD2	2.20	0.42
2:J:50:GLU:HG3	2:J:50:GLU:O	2.20	0.42
1:F:246:ILE:HA	1:F:246:ILE:HD13	1.92	0.42
1:A:283:GLY:O	1:A:287:ILE:HG13	2.19	0.42
2:H:64:ALA:HB2	2:I:92:PHE:HE1	1.85	0.41
1:F:1:HIS:HD2	4:F:444:HOH:O	2.03	0.41
1:B:266:ILE:O	1:B:270:VAL:HG23	2.20	0.41
1:D:246:ILE:HD13	1:D:246:ILE:HA	1.89	0.41
1:A:80:TRP:HD1	1:A:85:ASN:HB2	1.85	0.41
1:A:47:GLN:HG2	1:A:128:VAL:HG11	2.02	0.41
1:E:126:SER:O	1:E:130:ILE:HG13	2.21	0.41
2:G:17:ARG:HH12	2:G:18:GLU:HG3	1.85	0.41
1:D:401:GLU:HG2	2:L:46:TYR:CE1	2.54	0.41
1:D:67:ALA:O	1:D:145:HIS:HD2	2.03	0.41
1:B:161:PHE:CD1	1:D:-3:HIS:N	2.84	0.41
1:C:37:ARG:NH2	1:C:193:PHE:HE2	2.18	0.41
1:F:16:CYS:O	1:F:20:VAL:HG23	2.20	0.41
1:F:137:THR:HA	1:F:141:ILE:HD12	2.01	0.41
1:A:212:TRP:O	1:A:215:PHE:HB3	2.20	0.41
1:B:23:MET:O	1:B:27:GLY:HA3	2.21	0.41
1:F:304:ARG:HA	1:F:304:ARG:HD2	1.84	0.41
1:F:59:TRP:HA	1:F:63:GLY:HA3	2.03	0.41
1:D:165:THR:OG1	1:D:166:VAL:N	2.53	0.41
1:D:180:TYR:CZ	1:D:308:VAL:HG22	2.55	0.41
1:D:275:ALA:HB2	1:D:329:THR:OG1	2.19	0.41
1:A:78:ILE:CG2	1:A:78:ILE:O	2.68	0.41
2:H:97:GLN:HE21	2:I:95:GLU:HB2	1.86	0.41
1:C:136:LEU:HD12	1:C:140:TYR:HB3	2.03	0.41
2:L:1:MET:CE	2:L:66:ALA:HA	2.51	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:317:VAL:O	1:F:321:CYS:HB2	2.21	0.41
1:D:188:PHE:HA	1:D:193:PHE:CE1	2.56	0.41
1:E:134:VAL:HG21	1:E:376:LEU:HD23	2.03	0.41
1:A:246:ILE:HD13	1:A:246:ILE:HA	1.89	0.41
1:E:275:ALA:HB2	1:E:329:THR:OG1	2.20	0.41
1:A:340:VAL:HG21	1:E:0:HIS:ND1	2.36	0.41
2:G:33:VAL:HG23	2:G:58:LYS:HB2	2.02	0.41
1:B:206:ALA:CB	1:C:25:ILE:HG22	2.51	0.41
1:A:253:ARG:HE	1:A:253:ARG:HA	1.86	0.41
1:A:78:ILE:HA	1:A:78:ILE:HD13	1.93	0.40
2:I:5:THR:HB	2:I:92:PHE:HB2	2.02	0.40
1:F:309:ASP:O	1:F:311:PRO:HD3	2.20	0.40
1:E:80:TRP:HA	1:E:84:LYS:O	2.21	0.40
1:B:67:ALA:O	1:B:145:HIS:CD2	2.74	0.40
1:D:385:VAL:HG13	1:D:389:GLN:HB2	2.04	0.40
1:E:246:ILE:HA	1:E:246:ILE:HD13	1.89	0.40
1:A:392:GLU:HB3	1:A:397:ASN:HD21	1.87	0.40
2:L:90:LYS:HE2	3:L:1600:ADP:O3B	2.21	0.40
1:A:7:LYS:HE3	1:C:6:ASP:OD2	2.22	0.40
1:A:25:ILE:HG22	1:C:206:ALA:CB	2.52	0.40

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	407/415 (98%)	384 (94%)	22 (5%)	1 (0%)	52 75
1	B	407/415 (98%)	388 (95%)	18 (4%)	1 (0%)	52 75
1	C	407/415 (98%)	380 (93%)	26 (6%)	1 (0%)	52 75
1	D	408/415 (98%)	385 (94%)	22 (5%)	1 (0%)	52 75

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	E	407/415 (98%)	379 (93%)	27 (7%)	1 (0%)	52	75
1	F	407/415 (98%)	382 (94%)	22 (5%)	3 (1%)	26	46
2	G	110/112 (98%)	105 (96%)	5 (4%)	0	100	100
2	H	110/112 (98%)	107 (97%)	3 (3%)	0	100	100
2	I	110/112 (98%)	102 (93%)	7 (6%)	1 (1%)	21	37
2	J	110/112 (98%)	105 (96%)	5 (4%)	0	100	100
2	K	110/112 (98%)	105 (96%)	4 (4%)	1 (1%)	21	37
2	L	110/112 (98%)	105 (96%)	5 (4%)	0	100	100
All	All	3103/3162 (98%)	2927 (94%)	166 (5%)	10 (0%)	46	68

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	I	108	ASP
1	B	27	GLY
1	C	27	GLY
1	D	27	GLY
1	E	27	GLY
2	K	42	HIS
1	A	27	GLY
1	F	188	PHE
1	F	72	ASN
1	F	27	GLY

### 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	301/304 (99%)	289 (96%)	12 (4%)	38	64
1	B	301/304 (99%)	281 (93%)	20 (7%)	21	38
1	C	301/304 (99%)	285 (95%)	16 (5%)	28	50
1	D	302/304 (99%)	285 (94%)	17 (6%)	26	47

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	E	301/304 (99%)	288 (96%)	13 (4%)	35	61
1	F	301/304 (99%)	287 (95%)	14 (5%)	32	56
2	G	91/91 (100%)	84 (92%)	7 (8%)	16	30
2	H	91/91 (100%)	83 (91%)	8 (9%)	12	23
2	I	91/91 (100%)	86 (94%)	5 (6%)	27	48
2	J	91/91 (100%)	81 (89%)	10 (11%)	8	14
2	K	91/91 (100%)	85 (93%)	6 (7%)	21	38
2	L	91/91 (100%)	83 (91%)	8 (9%)	12	23
All	All	2353/2370 (99%)	2217 (94%)	136 (6%)	25	45

All (136) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	81	LEU
1	A	122	ARG
1	A	176	LEU
1	A	212	TRP
1	A	222	THR
1	A	253	ARG
1	A	281	VAL
1	A	302	LEU
1	A	305	LEU
1	A	308	VAL
1	A	340	VAL
1	A	385	VAL
1	B	70	GLU
1	B	77	ASN
1	B	122	ARG
1	B	128	VAL
1	B	176	LEU
1	B	190	LYS
1	B	212	TRP
1	B	222	THR
1	B	252	LEU
1	B	272	VAL
1	B	281	VAL
1	B	285	LEU
1	B	302	LEU
1	B	305	LEU

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Mol	Chain	Res	Type
1	B	306	LEU
1	B	347	THR
1	B	352	LEU
1	B	353	LEU
1	B	379	LEU
1	B	387	GLU
1	C	78	ILE
1	C	81	LEU
1	C	84	LYS
1	C	87	GLU
1	C	116	VAL
1	C	122	ARG
1	C	176	LEU
1	C	186	VAL
1	C	190	LYS
1	C	212	TRP
1	C	222	THR
1	C	253	ARG
1	C	272	VAL
1	C	302	LEU
1	C	356	LEU
1	C	388	GLU
1	D	-1	HIS
1	D	4	VAL
1	D	122	ARG
1	D	123	ILE
1	D	124	ARG
1	D	156	HIS
1	D	176	LEU
1	D	212	TRP
1	D	222	THR
1	D	224	ASN
1	D	250	TRP
1	D	285	LEU
1	D	304	ARG
1	D	308	VAL
1	D	340	VAL
1	D	385	VAL
1	D	387	GLU
1	E	79	ASN
1	E	84	LYS
1	E	122	ARG

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Mol	Chain	Res	Type
1	E	176	LEU
1	E	180	TYR
1	E	212	TRP
1	E	222	THR
1	E	252	LEU
1	E	302	LEU
1	E	304	ARG
1	E	305	LEU
1	E	340	VAL
1	E	379	LEU
1	F	72	ASN
1	F	77	ASN
1	F	79	ASN
1	F	81	LEU
1	F	116	VAL
1	F	122	ARG
1	F	128	VAL
1	F	176	LEU
1	F	212	TRP
1	F	222	THR
1	F	307	ARG
1	F	340	VAL
1	F	376	LEU
1	F	387	GLU
2	G	13	LEU
2	G	20	LEU
2	G	21	SER
2	G	70	LEU
2	G	86	ILE
2	G	88	ASP
2	G	109	GLU
2	H	13	LEU
2	H	17	ARG
2	H	20	LEU
2	H	45	LEU
2	H	56	LEU
2	H	70	LEU
2	H	85	LYS
2	H	90	LYS
2	I	14	GLU
2	I	15	ASP
2	I	20	LEU

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Mol	Chain	Res	Type
2	I	53	VAL
2	I	96	LEU
2	J	17	ARG
2	J	26	GLN
2	J	45	LEU
2	J	50	GLU
2	J	69	GLN
2	J	70	LEU
2	J	74	ILE
2	J	76	ILE
2	J	96	LEU
2	J	112	LEU
2	K	2	LYS
2	K	13	LEU
2	K	20	LEU
2	K	56	LEU
2	K	70	LEU
2	K	90	LYS
2	L	13	LEU
2	L	17	ARG
2	L	20	LEU
2	L	26	GLN
2	L	45	LEU
2	L	56	LEU
2	L	70	LEU
2	L	79	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (26) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	2	HIS
1	A	145	HIS
1	A	402	ASN
1	B	77	ASN
1	B	79	ASN
1	B	145	HIS
1	C	-2	HIS
1	C	2	HIS
1	C	145	HIS
1	C	156	HIS
1	C	402	ASN
1	D	79	ASN

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Mol	Chain	Res	Type
1	D	145	HIS
1	D	224	ASN
1	D	397	ASN
1	D	402	ASN
1	E	0	HIS
1	E	2	HIS
1	E	79	ASN
1	E	145	HIS
1	F	1	HIS
1	F	77	ASN
1	F	79	ASN
1	F	402	ASN
2	I	69	GLN
2	K	26	GLN

### 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](#)

6 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	ADP	G	1200	-	22,29,29	1.06	2 (9%)	27,45,45	1.86	3 (11%)
3	ADP	G	1400	-	22,29,29	1.10	1 (4%)	27,45,45	1.78	3 (11%)
3	ADP	H	1300	-	22,29,29	1.10	2 (9%)	27,45,45	1.70	3 (11%)
3	ADP	J	1500	-	22,29,29	1.02	1 (4%)	27,45,45	2.00	4 (14%)
3	ADP	J	1700	-	22,29,29	1.15	2 (9%)	27,45,45	1.80	2 (7%)
3	ADP	L	1600	-	22,29,29	1.12	2 (9%)	27,45,45	1.79	2 (7%)

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	G	1200	-	-	0/12/32/32	0/3/3/3
3	ADP	G	1400	-	-	0/12/32/32	0/3/3/3
3	ADP	H	1300	-	-	0/12/32/32	0/3/3/3
3	ADP	J	1500	-	-	0/12/32/32	0/3/3/3
3	ADP	J	1700	-	-	0/12/32/32	0/3/3/3
3	ADP	L	1600	-	-	0/12/32/32	0/3/3/3

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	H	1300	ADP	O4'-C1'	2.03	1.43	1.41
3	J	1700	ADP	O4'-C1'	2.30	1.44	1.41
3	G	1200	ADP	O4'-C1'	2.69	1.44	1.41
3	L	1600	ADP	O4'-C1'	2.83	1.44	1.41
3	G	1200	ADP	C5-C4	2.90	1.47	1.40
3	J	1500	ADP	C5-C4	3.15	1.47	1.40
3	L	1600	ADP	C5-C4	3.17	1.47	1.40
3	H	1300	ADP	C5-C4	3.35	1.48	1.40
3	G	1400	ADP	C5-C4	3.42	1.48	1.40
3	J	1700	ADP	C5-C4	3.44	1.48	1.40

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	J	1500	ADP	N3-C2-N1	-8.06	122.72	128.89
3	G	1200	ADP	N3-C2-N1	-7.73	122.97	128.89
3	L	1600	ADP	N3-C2-N1	-7.61	123.07	128.89
3	G	1400	ADP	N3-C2-N1	-7.18	123.39	128.89

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Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
3	J	1700	ADP	N3-C2-N1	-7.11	123.45	128.89
3	H	1300	ADP	N3-C2-N1	-6.94	123.58	128.89
3	J	1500	ADP	C4-C5-N7	-3.87	105.92	109.48
3	H	1300	ADP	C4-C5-N7	-3.24	106.50	109.48
3	J	1700	ADP	C4-C5-N7	-3.08	106.64	109.48
3	G	1400	ADP	C4-C5-N7	-3.08	106.65	109.48
3	G	1200	ADP	C4-C5-N7	-2.93	106.78	109.48
3	L	1600	ADP	C4-C5-N7	-2.90	106.81	109.48
3	H	1300	ADP	PA-O3A-PB	-2.26	125.10	132.67
3	G	1400	ADP	C2-N1-C6	2.00	122.35	118.77
3	J	1500	ADP	C2-N1-C6	2.06	122.45	118.77
3	G	1200	ADP	O3B-PB-O2B	2.13	115.51	107.38
3	J	1500	ADP	O3A-PA-O5'	2.30	109.03	102.94

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	L	1600	ADP	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

### 6.1 Protein, DNA and RNA chains

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	409/415 (98%)	0.03	18 (4%) 38 43	16, 27, 47, 86	10 (2%)
1	B	409/415 (98%)	0.05	20 (4%) 33 38	17, 27, 47, 65	11 (2%)
1	C	409/415 (98%)	0.04	21 (5%) 32 36	16, 26, 45, 65	11 (2%)
1	D	410/415 (98%)	0.01	15 (3%) 45 50	14, 26, 42, 82	11 (2%)
1	E	409/415 (98%)	0.02	17 (4%) 40 45	17, 27, 49, 72	11 (2%)
1	F	409/415 (98%)	0.04	15 (3%) 45 50	17, 27, 45, 68	11 (2%)
2	G	112/112 (100%)	0.44	10 (8%) 12 13	14, 27, 45, 56	0
2	H	112/112 (100%)	0.24	9 (8%) 15 16	16, 27, 43, 49	0
2	I	112/112 (100%)	1.22	35 (31%) 1 0	12, 30, 41, 54	0
2	J	112/112 (100%)	-0.15	1 (0%) 85 88	17, 28, 41, 48	0
2	K	112/112 (100%)	-0.27	1 (0%) 85 88	17, 26, 43, 49	0
2	L	112/112 (100%)	-0.20	0 100 100	17, 28, 41, 50	0
All	All	3127/3162 (98%)	0.07	162 (5%) 31 35	12, 27, 45, 86	65 (2%)

All (162) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	G	53	VAL	5.6
2	I	112	LEU	5.6
1	A	75	PHE	5.0
1	E	74	PHE	4.5
1	B	74	PHE	4.2
2	I	22	SER	4.1
1	A	72	ASN	4.1
1	C	75	PHE	4.0
2	G	52	SER	4.0
2	I	84	GLY	3.8
2	G	79	LYS	3.8

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Mol	Chain	Res	Type	RSRZ
1	C	78	ILE	3.6
2	I	71	ASP	3.6
2	I	100	ILE	3.6
1	E	77	ASN	3.6
1	E	304	ARG	3.5
2	I	82	TYR	3.5
2	I	110	ALA	3.4
1	A	85	ASN	3.3
1	A	69	GLY	3.3
1	E	78	ILE	3.2
2	I	67	ASP	3.2
2	I	73	VAL	3.2
2	H	18	GLU	3.2
2	I	24	GLY	3.2
1	B	73	ASN	3.2
1	B	71	GLY	3.2
2	I	66	ALA	3.2
1	B	70	GLU	3.2
1	A	74	PHE	3.2
1	B	72	ASN	3.1
2	I	72	GLU	3.1
1	B	18	ALA	3.1
1	F	15	ILE	3.1
1	B	190	LYS	3.0
1	A	77	ASN	3.0
2	I	76	ILE	3.0
1	B	345	GLY	3.0
2	I	14	GLU	3.0
2	I	105	GLY	3.0
1	A	73	ASN	3.0
1	C	251	ALA	3.0
2	I	83	THR	3.0
2	I	26	GLN	2.9
1	E	211	GLY	2.9
1	B	79	ASN	2.9
1	E	206	ALA	2.9
1	A	70	GLU	2.9
2	I	79	LYS	2.9
1	E	207	ILE	2.9
1	D	180	TYR	2.8
1	C	19	LEU	2.8
1	C	346	VAL	2.8

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	C	71	GLY	2.8
2	I	74	ILE	2.8
2	G	38	ARG	2.8
2	I	75	ASP	2.8
1	A	208	LEU	2.8
2	G	40	LYS	2.8
1	F	2	HIS	2.8
2	I	25	ILE	2.7
1	F	206	ALA	2.7
1	F	344	GLU	2.7
2	I	23	ILE	2.7
1	B	152	LEU	2.7
1	C	79	ASN	2.7
1	D	265	ALA	2.7
1	C	77	ASN	2.7
1	F	78	ILE	2.6
1	B	23	MET	2.6
1	F	346	VAL	2.6
1	A	80	TRP	2.6
1	B	75	PHE	2.6
2	H	110	ALA	2.6
1	D	-2	HIS	2.6
1	D	207	ILE	2.5
2	G	42	HIS	2.5
1	E	189	GLY	2.5
1	E	76	GLY	2.5
1	C	16	CYS	2.5
2	H	75	ASP	2.5
1	D	23	MET	2.5
2	I	15	ASP	2.5
1	F	22	PHE	2.5
1	C	80	TRP	2.4
2	I	104	THR	2.4
2	H	102	ILE	2.4
1	F	345	GLY	2.4
1	D	206	ALA	2.4
1	E	210	ILE	2.4
1	F	211	GLY	2.4
1	C	20	VAL	2.4
1	D	22	PHE	2.4
1	C	301	MET	2.4
2	G	41	GLY	2.3

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Mol	Chain	Res	Type	RSRZ
2	I	68	ASP	2.3
1	D	21	LEU	2.3
2	I	52	SER	2.3
1	B	301	MET	2.3
1	D	208	LEU	2.3
1	F	16	CYS	2.3
2	I	53	VAL	2.3
1	F	207	ILE	2.3
2	I	85	LYS	2.3
2	G	55	PHE	2.3
1	C	344	GLU	2.3
1	F	85	ASN	2.3
2	H	104	THR	2.3
2	I	109	GLU	2.2
1	E	80	TRP	2.2
2	I	1	MET	2.2
1	A	16	CYS	2.2
1	B	21	LEU	2.2
2	H	103	ARG	2.2
2	H	53	VAL	2.2
1	D	406	ALA	2.2
1	C	210	ILE	2.2
1	F	23	MET	2.2
1	D	15	ILE	2.2
2	H	68	ASP	2.2
2	I	86	ILE	2.2
1	C	340	VAL	2.2
2	I	98	ARG	2.2
1	C	353	LEU	2.2
1	D	211	GLY	2.2
1	A	210	ILE	2.2
2	I	102	ILE	2.1
1	A	190	LYS	2.1
1	E	21	LEU	2.1
2	K	112	LEU	2.1
1	E	72	ASN	2.1
2	I	111	ALA	2.1
1	A	79	ASN	2.1
1	F	79	ASN	2.1
2	I	20	LEU	2.1
1	A	71	GLY	2.1
1	B	207	ILE	2.1

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Mol	Chain	Res	Type	RSRZ
1	F	210	ILE	2.1
1	A	388	GLU	2.1
1	C	207	ILE	2.1
1	D	209	TYR	2.1
1	E	73	ASN	2.1
1	B	187	GLY	2.1
2	J	75	ASP	2.1
2	H	19	ALA	2.1
1	E	186	VAL	2.1
1	C	28	ILE	2.1
1	D	17	THR	2.1
1	D	24	THR	2.1
1	E	308	VAL	2.0
1	B	19	LEU	2.0
1	E	18	ALA	2.0
1	A	2	HIS	2.0
1	A	389	GLN	2.0
2	G	82	TYR	2.0
2	G	97	GLN	2.0
1	C	70	GLU	2.0
1	C	85	ASN	2.0
1	B	2	HIS	2.0
1	B	346	VAL	2.0
1	C	76	GLY	2.0
1	B	25	ILE	2.0

## 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, 95<sup>th</sup> 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( $\text{\AA}^2$ )	Q<0.9
3	ADP	G	1400	27/27	0.97	0.17	-0.36	11,30,42,46	0
3	ADP	H	1300	27/27	0.95	0.13	-0.88	2,23,30,41	0
3	ADP	L	1600	27/27	0.97	0.09	-1.05	10,20,31,33	0
3	ADP	J	1500	27/27	0.97	0.09	-1.39	4,17,31,37	0
3	ADP	G	1200	27/27	0.98	0.08	-1.42	8,18,23,34	0
3	ADP	J	1700	27/27	0.98	0.07	-1.85	9,22,30,34	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.