



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 06:14 PM GMT

PDB ID : 4KVM  
Title : The NatA (Naa10p/Naa15p) amino-terminal acetyltransferase complex bound to a bisubstrate analog  
Authors : Liszczak, G.P.; Marmorstein, R.Q.  
Deposited on : 2013-05-22  
Resolution : 2.60 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

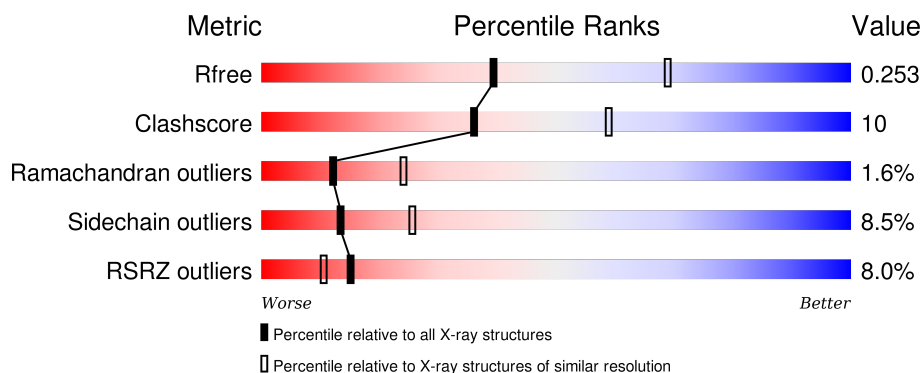
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.60 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	2328 (2.60-2.60)
Clashscore	102246	2679 (2.60-2.60)
Ramachandran outliers	100387	2635 (2.60-2.60)
Sidechain outliers	100360	2635 (2.60-2.60)
RSRZ outliers	91569	2334 (2.60-2.60)

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	734	<div> <div>6%</div> <div> <div></div> <div>72%</div> <div>22%</div> <div>• •</div> </div> </div>
1	B	734	<div> <div>11%</div> <div> <div></div> <div>74%</div> <div>21%</div> <div>• •</div> </div> </div>
1	C	734	<div> <div>9%</div> <div> <div></div> <div>72%</div> <div>23%</div> <div>• •</div> </div> </div>
1	D	734	<div> <div>9%</div> <div> <div></div> <div>72%</div> <div>23%</div> <div>• • •</div> </div> </div>
2	E	156	<div> <div>%</div> <div> <div></div> <div>78%</div> <div>18%</div> <div>• •</div> </div> </div>

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Mol	Chain	Length	Quality of chain
2	F	156	
2	G	156	
2	H	156	
3	I	5	
3	J	5	
3	K	5	
3	L	5	

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
4	CL	A	801	-	-	-	X
4	CL	A	810	-	-	X	-
4	CL	A	814	-	-	X	-
4	CL	B	802	-	-	-	X
4	CL	B	804	-	-	-	X
4	CL	B	805	-	-	-	X
4	CL	C	802	-	-	-	X
4	CL	C	810	-	-	X	-
4	CL	C	812	-	-	-	X
4	CL	D	805	-	-	-	X
4	CL	D	811	-	-	X	-
4	CL	D	814	-	-	-	X

## 2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 28749 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 N-terminal acetyltransferase A complex subunit nat1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	718	Total	C	N	O	S	0	3	0
			5782	3689	976	1099	18			
1	B	722	Total	C	N	O	S	0	1	0
			5777	3686	971	1102	18			
1	C	717	Total	C	N	O	S	0	1	0
			5753	3671	968	1096	18			
1	D	718	Total	C	N	O	S	0	1	0
			5766	3681	970	1097	18			

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	730	ALA	-	EXPRESSION TAG	UNP O74985
A	731	ALA	-	EXPRESSION TAG	UNP O74985
A	732	ALA	-	EXPRESSION TAG	UNP O74985
A	733	ALA	-	EXPRESSION TAG	UNP O74985
A	734	ALA	-	EXPRESSION TAG	UNP O74985
B	730	ALA	-	EXPRESSION TAG	UNP O74985
B	731	ALA	-	EXPRESSION TAG	UNP O74985
B	732	ALA	-	EXPRESSION TAG	UNP O74985
B	733	ALA	-	EXPRESSION TAG	UNP O74985
B	734	ALA	-	EXPRESSION TAG	UNP O74985
C	730	ALA	-	EXPRESSION TAG	UNP O74985
C	731	ALA	-	EXPRESSION TAG	UNP O74985
C	732	ALA	-	EXPRESSION TAG	UNP O74985
C	733	ALA	-	EXPRESSION TAG	UNP O74985
C	734	ALA	-	EXPRESSION TAG	UNP O74985
D	730	ALA	-	EXPRESSION TAG	UNP O74985
D	731	ALA	-	EXPRESSION TAG	UNP O74985
D	732	ALA	-	EXPRESSION TAG	UNP O74985
D	733	ALA	-	EXPRESSION TAG	UNP O74985
D	734	ALA	-	EXPRESSION TAG	UNP O74985

- Molecule 2 is a protein called N-terminal acetyltransferase A complex catalytic subunit ard1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	E	153	Total	C	N	O	S	0	1	0
			1247	790	221	225	11			
2	F	153	Total	C	N	O	S	0	0	0
			1239	785	220	224	10			
2	G	153	Total	C	N	O	S	0	0	0
			1239	785	220	224	10			
2	H	153	Total	C	N	O	S	0	0	0
			1239	785	220	224	10			

- Molecule 3 is a protein called bisubstrate analog inhibitor.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	I	4	Total	C	N	O	0	0	0
			26	14	4	8			
3	J	4	Total	C	N	O	0	0	0
			26	14	4	8			
3	K	4	Total	C	N	O	0	0	0
			26	14	4	8			
3	L	4	Total	C	N	O	0	0	0
			26	14	4	8			

- Molecule 4 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

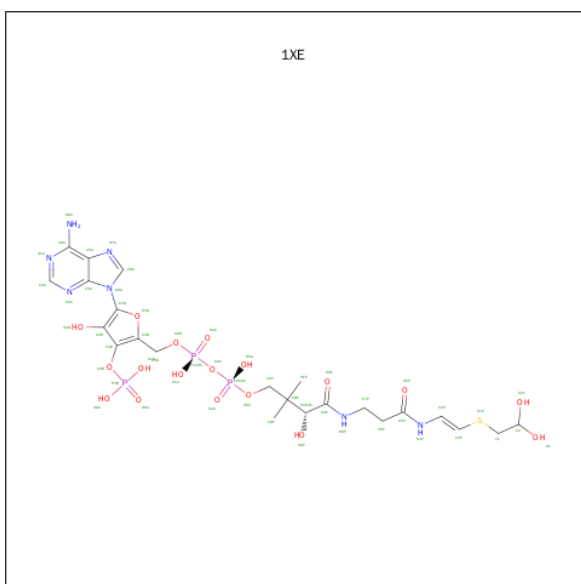
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	G	1	Total	Cl	0	0
			1	1		
4	D	15	Total	Cl	0	0
			15	15		
4	E	3	Total	Cl	0	0
			3	3		
4	H	1	Total	Cl	0	0
			1	1		
4	B	16	Total	Cl	0	0
			16	16		
4	C	13	Total	Cl	0	0
			13	13		
4	A	14	Total	Cl	0	0
			14	14		
4	F	1	Total	Cl	0	0
			1	1		

- Molecule 5 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	O	S	0	0
			5	4	1		
5	D	1	Total	O	S	0	0
			5	4	1		

- Molecule 6 is [5-(6-AMINO-9H-PURIN-9-YL)-4-HYDROXY-3-(PHOSPHONOOXY)FURAN-2-YL]METHYL (3R)-4-{[3-({(E)-2-[(2,2-DIHYDROXYETHYL)SULFANYL]ETHENYL}AMINO)-3-OXOPROPYL]AMINO}-3-HYDROXY-2,2-DIMETHYL-4-OXOBUTYL DIHYDROGEN DIPHOSPHATE (three-letter code: 1XE) (formula: C<sub>23</sub>H<sub>34</sub>N<sub>7</sub>O<sub>18</sub>P<sub>3</sub>S).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
6	I	1	Total	C	N	O	P	S	0	0
			51	23	7	17	3	1		
6	J	1	Total	C	N	O	P	S	0	0
			51	23	7	17	3	1		
6	K	1	Total	C	N	O	P	S	0	0
			51	23	7	17	3	1		
6	L	1	Total	C	N	O	P	S	0	0
			51	23	7	17	3	1		

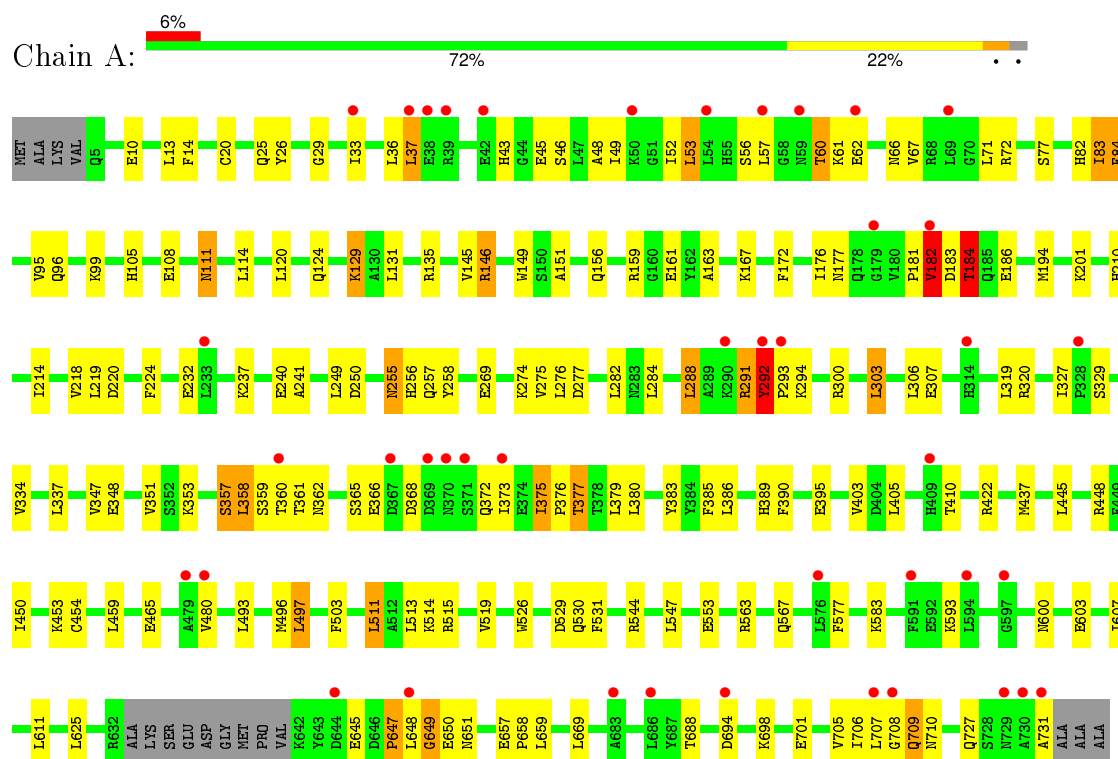
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	79	Total	O	0	0
			79	79		
7	B	50	Total	O	0	0
			50	50		
7	C	80	Total	O	0	0
			80	80		
7	D	64	Total	O	0	0
			64	64		
7	E	20	Total	O	0	0
			20	20		
7	F	6	Total	O	0	0
			6	6		
7	G	5	Total	O	0	0
			5	5		
7	H	18	Total	O	0	0
			18	18		
7	I	1	Total	O	0	0
			1	1		
7	J	1	Total	O	0	0
			1	1		
7	L	1	Total	O	0	0
			1	1		

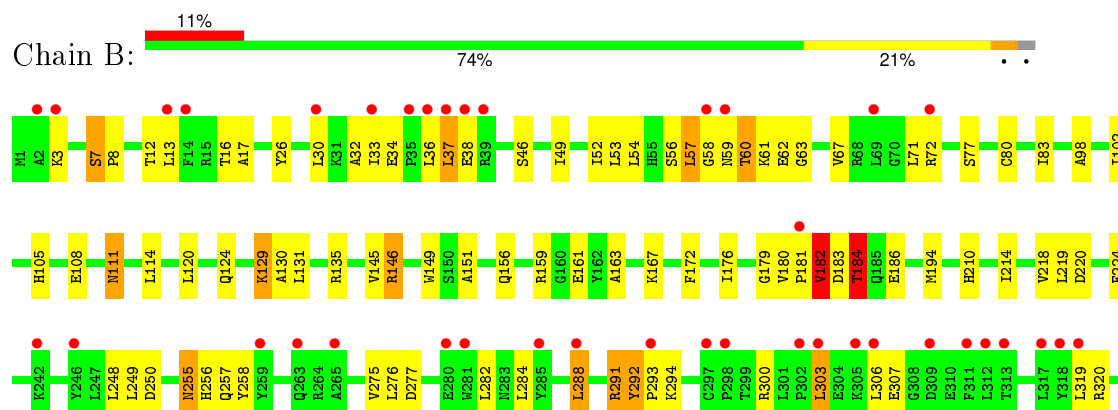
### 3 Residue-property plots

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.

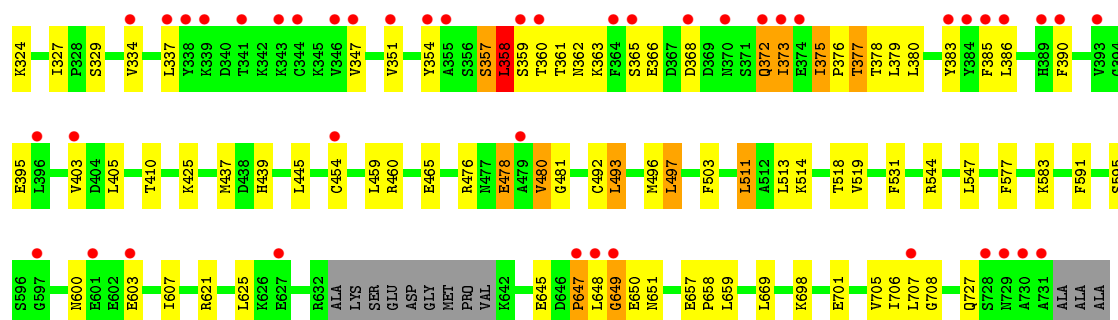
- Molecule 1: N-terminal acetyltransferase A complex subunit nat1



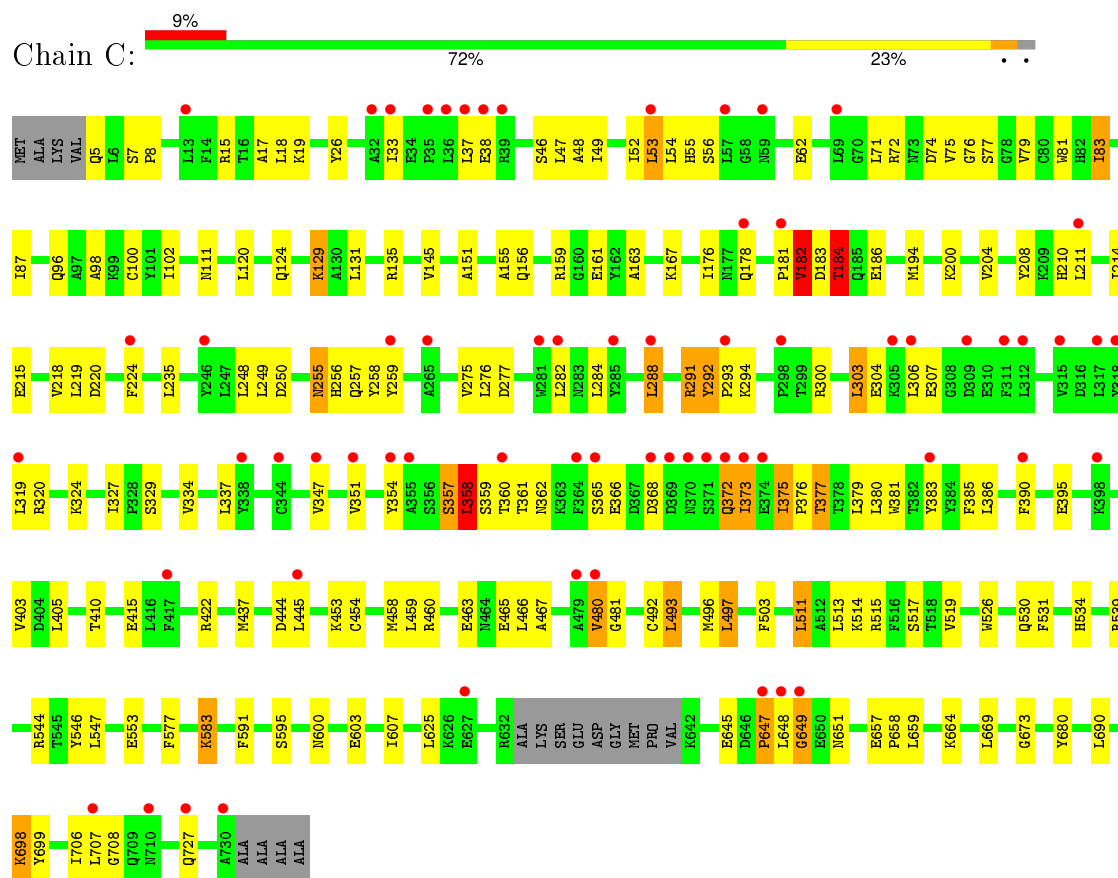
- Molecule 1: N-terminal acetyltransferase A complex subunit nat1



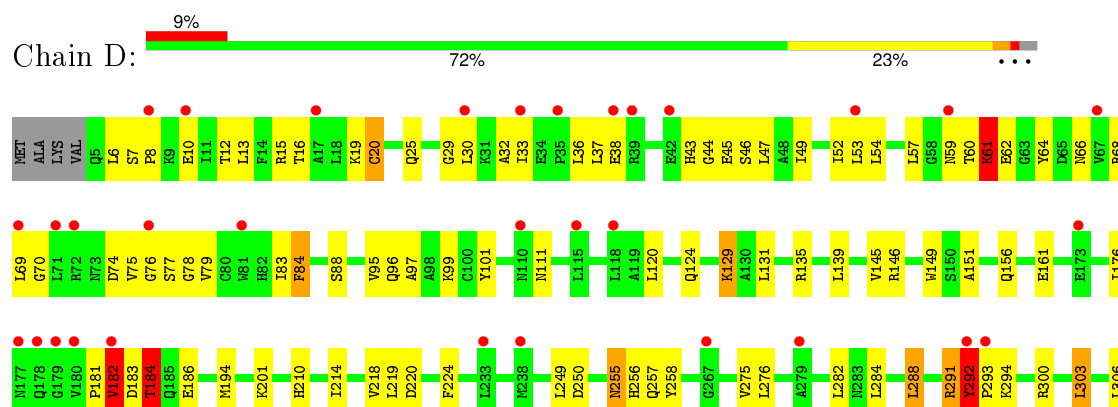


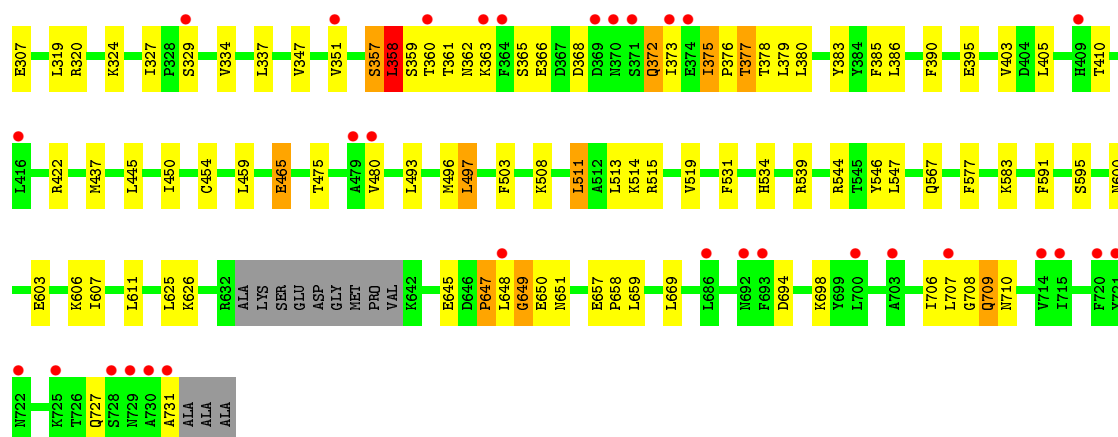


- Molecule 1: N-terminal acetyltransferase A complex subunit nat1

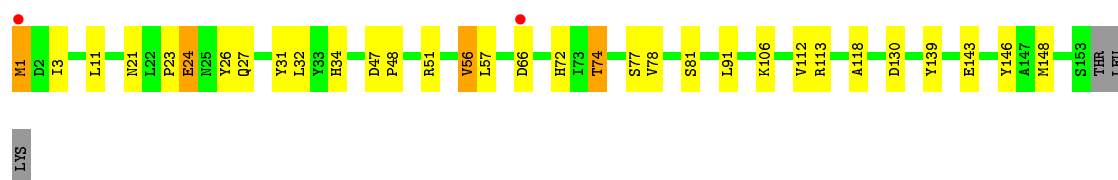
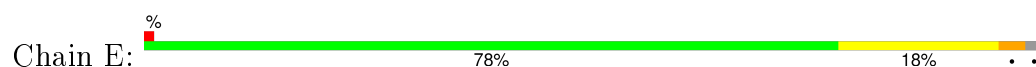


- Molecule 1: N-terminal acetyltransferase A complex subunit nat1

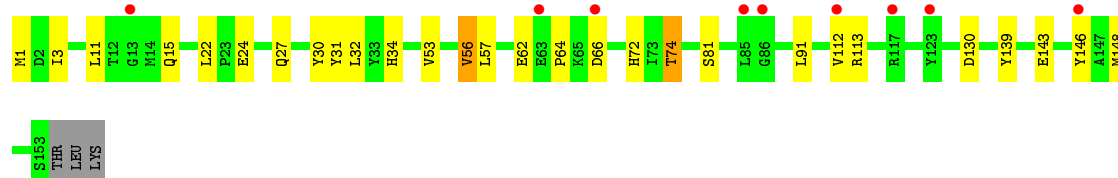
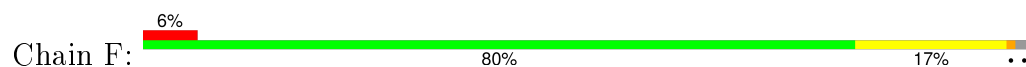




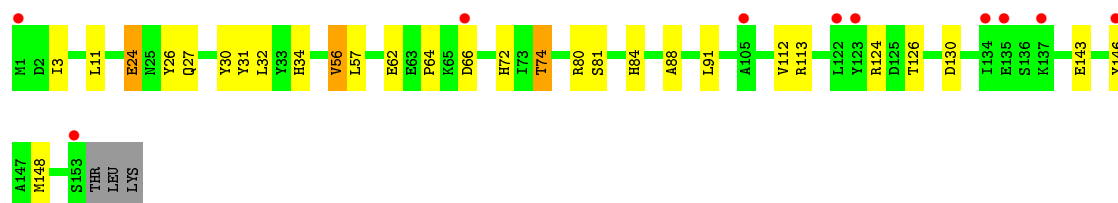
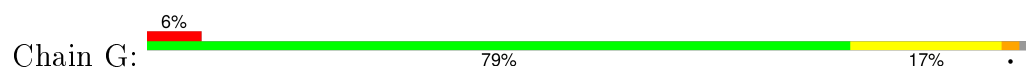
- Molecule 2: N-terminal acetyltransferase A complex catalytic subunit ard1



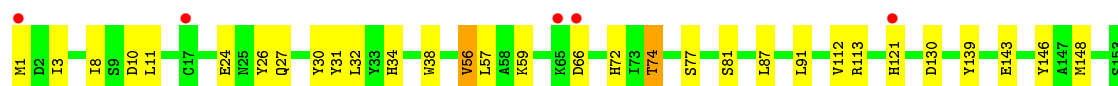
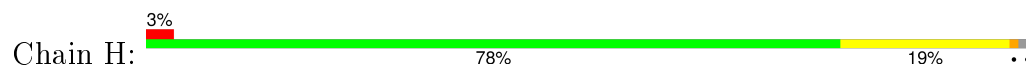
- Molecule 2: N-terminal acetyltransferase A complex catalytic subunit ard1



- Molecule 2: N-terminal acetyltransferase A complex catalytic subunit ard1

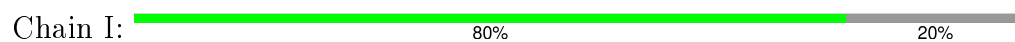


- Molecule 2: N-terminal acetyltransferase A complex catalytic subunit ard1





- Molecule 3: bisubstrate analog inhibitor



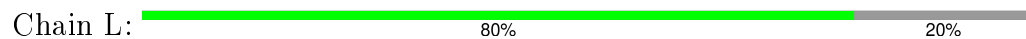
- Molecule 3: bisubstrate analog inhibitor



- Molecule 3: bisubstrate analog inhibitor



- Molecule 3: bisubstrate analog inhibitor



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	81.44Å 119.38Å 134.06Å 80.20° 76.60° 70.42°	Depositor
Resolution (Å)	49.59 – 2.60 49.59 – 2.60	Depositor EDS
% Data completeness (in resolution range)	96.8 (49.59-2.60) 87.4 (49.59-2.60)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.42 (at 2.61Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7.3_928)	Depositor
R, $R_{free}$	0.222 , 0.260 0.218 , 0.253	Depositor DCC
$R_{free}$ test set	6916 reflections (5.71%)	DCC
Wilson B-factor (Å <sup>2</sup> )	64.6	Xtriage
Anisotropy	0.667	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.29 , 59.5	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 137695 reflections	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	28749	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	105.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.81% 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

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: CL, SO4, 1XE

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	0.45	0/5896	0.59	1/7952 (0.0%)
1	B	0.40	0/5891	0.56	0/7948
1	C	0.41	0/5867	0.55	0/7915
1	D	0.43	0/5881	0.56	0/7934
2	E	0.52	0/1277	0.63	0/1722
2	F	0.40	0/1269	0.56	0/1712
2	G	0.41	0/1269	0.56	0/1712
2	H	0.48	0/1269	0.62	0/1712
3	I	0.71	0/25	0.74	0/32
3	J	0.50	0/25	0.58	0/32
3	K	0.34	0/25	0.43	0/32
3	L	0.63	0/25	0.65	0/32
All	All	0.43	0/28719	0.57	1/38735 (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	2
1	B	0	2
1	C	0	2
1	D	0	2
All	All	0	8

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	60	THR	N-CA-C	-5.16	97.08	111.00

There are no chirality outliers.

All (8) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	357	SER	Peptide
1	A	649	GLY	Peptide
1	B	357	SER	Peptide
1	B	649	GLY	Peptide
1	C	357	SER	Peptide
1	C	649	GLY	Peptide
1	D	357	SER	Peptide
1	D	649	GLY	Peptide

## 5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	5782	0	5705	124	1
1	B	5777	0	5697	114	0
1	C	5753	0	5675	123	0
1	D	5766	0	5691	115	0
2	E	1247	0	1233	21	0
2	F	1239	0	1223	13	0
2	G	1239	0	1223	19	0
2	H	1239	0	1223	15	0
3	I	26	0	20	0	0
3	J	26	0	20	2	0
3	K	26	0	20	1	0
3	L	26	0	20	0	0
4	A	14	0	0	10	0
4	B	16	0	0	3	0
4	C	13	0	0	4	0
4	D	15	0	0	7	0
4	E	3	0	0	0	0
4	F	1	0	0	0	0
4	G	1	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	H	1	0	0	0	0
5	A	5	0	0	0	0
5	D	5	0	0	0	0
6	I	51	0	29	5	0
6	J	51	0	30	2	0
6	K	51	0	30	7	0
6	L	51	0	29	3	0
7	A	79	0	0	19	0
7	B	50	0	0	6	0
7	C	80	0	0	22	0
7	D	64	0	0	10	0
7	E	20	0	0	3	0
7	F	6	0	0	1	0
7	G	5	0	0	0	1
7	H	18	0	0	1	0
7	I	1	0	0	0	0
7	J	1	0	0	0	0
7	L	1	0	0	0	0
All	All	28749	0	27868	542	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 10.

All (542) 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:237:LYS:O	7:A:957:HOH:O	1.83	0.96
1:C:211:LEU:O	7:C:942:HOH:O	1.86	0.92
1:A:291:ARG:NH2	4:A:813:CL:CL	2.39	0.92
1:A:129[B]:LYS:NZ	4:A:805:CL:CL	2.41	0.91
1:C:463:GLU:O	7:C:915:HOH:O	1.90	0.90
1:D:606:LYS:NZ	4:D:802:CL:CL	2.42	0.89
1:A:567:GLN:OE1	7:A:912:HOH:O	1.93	0.87
1:B:647:PRO:HB3	1:B:651:ASN:HB2	1.59	0.84
1:C:647:PRO:HB3	1:C:651:ASN:HB2	1.60	0.84
4:C:808:CL:CL	7:C:901:HOH:O	2.34	0.82
1:D:647:PRO:HB3	1:D:651:ASN:HB2	1.61	0.81
1:D:465:GLU:OE2	7:D:952:HOH:O	1.97	0.80
1:A:647:PRO:HB3	1:A:651:ASN:HB2	1.62	0.80
1:D:731:ALA:O	7:D:901:HOH:O	2.00	0.78
1:B:57:LEU:HD12	1:B:58:GLY:H	1.47	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:108:GLU:O	7:B:913:HOH:O	2.02	0.77
1:A:108:GLU:O	7:A:930:HOH:O	2.02	0.77
1:A:232:GLU:HB3	7:A:957:HOH:O	1.85	0.76
1:D:77:SER:OG	1:D:78:GLY:N	2.18	0.75
1:D:358:LEU:HD12	1:D:379:LEU:HG	1.69	0.75
1:A:183:ASP:HB3	1:A:186:GLU:HB2	1.70	0.73
1:A:181:PRO:HA	1:A:182:VAL:HG22	1.71	0.73
1:D:181:PRO:HA	1:D:182:VAL:HG22	1.71	0.73
1:A:241:ALA:N	7:A:957:HOH:O	2.20	0.73
1:C:52:ILE:HB	1:C:83:ILE:HD11	1.70	0.73
1:B:358:LEU:HD12	1:B:379:LEU:HG	1.72	0.72
1:C:553:GLU:OE2	7:C:955:HOH:O	2.08	0.72
1:C:181:PRO:HA	1:C:182:VAL:HG22	1.70	0.72
1:A:358:LEU:HD12	1:A:379:LEU:HG	1.72	0.71
1:C:358:LEU:HD12	1:C:379:LEU:HG	1.72	0.71
1:A:526:TRP:O	7:A:914:HOH:O	2.06	0.71
1:B:181:PRO:HA	1:B:182:VAL:HG22	1.71	0.71
2:E:106:LYS:HE2	7:E:315:HOH:O	1.91	0.71
1:D:650:GLU:OE1	7:D:903:HOH:O	2.09	0.71
1:C:467:ALA:N	7:C:915:HOH:O	2.22	0.70
1:D:320:ARG:NH1	1:D:368:ASP:OD2	2.18	0.70
1:C:458:MET:HB3	7:C:915:HOH:O	1.89	0.70
2:G:84:HIS:NE2	6:K:5201:1XE:H1	2.07	0.69
1:C:526:TRP:O	7:C:955:HOH:O	2.11	0.68
1:B:183:ASP:HB3	1:B:186:GLU:HB2	1.74	0.68
1:A:553:GLU:OE2	7:A:914:HOH:O	2.11	0.68
1:A:320:ARG:NH1	1:A:368:ASP:OD2	2.20	0.67
1:C:129:LYS:HD2	1:C:129:LYS:H	1.59	0.67
2:E:24:GLU:OE2	7:E:319:HOH:O	2.11	0.67
1:D:567:GLN:OE1	7:D:942:HOH:O	2.12	0.67
1:A:62:GLU:O	1:A:66:ASN:ND2	2.27	0.67
1:B:320:ARG:NH1	1:B:368:ASP:OD2	2.19	0.67
1:D:475:THR:O	7:D:964:HOH:O	2.11	0.67
1:A:177:ASN:HA	1:B:621:ARG:HH21	1.58	0.67
1:B:650:GLU:OE1	7:B:934:HOH:O	2.13	0.67
1:C:54:LEU:HD13	1:C:62:GLU:HG3	1.76	0.66
1:C:320:ARG:NH1	1:C:368:ASP:OD2	2.20	0.66
1:B:497:LEU:HD13	1:B:519:VAL:HG21	1.76	0.66
1:A:269:GLU:HG3	1:A:274:LYS:HA	1.77	0.66
1:D:124:GLN:HG3	1:D:531:PHE:CD1	2.31	0.66
1:D:183:ASP:HB3	1:D:186:GLU:HB2	1.78	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:390:PHE:HD1	1:B:395:GLU:HG3	1.61	0.65
1:A:497:LEU:HD13	1:A:519:VAL:HG21	1.78	0.65
1:A:563:ARG:NH1	4:A:814:CL:CL	2.62	0.65
1:D:422:ARG:NH2	4:D:811:CL:CL	2.67	0.65
1:D:124:GLN:HG3	1:D:531:PHE:HD1	1.61	0.65
1:A:709:GLN:HG2	1:A:710:ASN:H	1.61	0.65
1:D:497:LEU:HD13	1:D:519:VAL:HG21	1.80	0.64
2:E:51:ARG:HD2	7:E:312:HOH:O	1.97	0.64
1:C:124:GLN:HG3	1:C:531:PHE:CD1	2.33	0.64
1:A:688:THR:O	7:A:927:HOH:O	2.15	0.64
1:D:709:GLN:HG2	1:D:710:ASN:H	1.62	0.64
1:C:183:ASP:HB3	1:C:186:GLU:HB2	1.79	0.64
1:D:61:LYS:HD3	1:D:64:TYR:HB2	1.80	0.64
2:E:77:SER:HB2	6:I:5201:1XE:H24	1.80	0.64
1:C:390:PHE:HD1	1:C:395:GLU:HG3	1.62	0.63
2:E:118:ALA:HA	6:I:5201:1XE:N7A	2.12	0.63
1:A:659:LEU:HD22	1:A:659:LEU:H	1.63	0.63
1:C:659:LEU:HD22	1:C:659:LEU:H	1.64	0.63
1:C:5:GLN:NE2	7:C:903:HOH:O	2.27	0.63
1:D:390:PHE:HD1	1:D:395:GLU:HG3	1.63	0.63
1:A:422:ARG:NH2	4:A:810:CL:CL	2.69	0.63
1:A:563:ARG:HD2	4:A:814:CL:CL	2.36	0.63
1:B:124:GLN:HG3	1:B:531:PHE:CD1	2.34	0.63
2:E:56:VAL:HG12	2:E:91:LEU:HB3	1.80	0.62
1:A:390:PHE:HD1	1:A:395:GLU:HG3	1.64	0.62
1:D:156:GLN:HG3	1:D:161:GLU:HB2	1.80	0.62
2:G:56:VAL:HG12	2:G:91:LEU:HB3	1.81	0.62
2:F:56:VAL:HG12	2:F:91:LEU:HB3	1.80	0.62
1:B:129[A]:LYS:HD2	1:B:129[A]:LYS:H	1.65	0.62
1:A:709:GLN:HG2	1:A:710:ASN:N	2.15	0.62
1:A:124:GLN:HG3	1:A:531:PHE:CD1	2.35	0.62
1:D:659:LEU:HD22	1:D:659:LEU:H	1.64	0.62
2:H:56:VAL:HG12	2:H:91:LEU:HB3	1.81	0.62
1:C:183:ASP:O	1:C:184:THR:HB	1.98	0.62
1:A:183:ASP:O	1:A:184:THR:HB	1.98	0.61
1:D:183:ASP:O	1:D:184:THR:HB	1.98	0.61
1:A:156:GLN:HG3	1:A:161:GLU:HB2	1.81	0.61
1:A:48:ALA:HB1	1:A:83:ILE:HD12	1.82	0.61
1:C:514:LYS:NZ	1:C:645:GLU:OE1	2.23	0.61
1:A:124:GLN:HG3	1:A:531:PHE:HD1	1.65	0.61
1:A:292:TYR:O	1:A:294:LYS:N	2.34	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:124:GLN:HG3	1:B:531:PHE:HD1	1.66	0.61
1:D:709:GLN:HG2	1:D:710:ASN:N	2.16	0.60
1:C:215:GLU:HB2	7:C:942:HOH:O	2.01	0.60
1:A:250:ASP:OD2	1:A:291:ARG:NH1	2.34	0.60
1:B:183:ASP:O	1:B:184:THR:HB	1.99	0.60
2:E:112:VAL:HG12	6:I:5201:1XE:S1P	2.40	0.60
1:D:359:SER:OG	1:D:360:THR:N	2.35	0.60
1:C:497:LEU:HD13	1:C:519:VAL:HG21	1.82	0.60
1:C:124:GLN:HG3	1:C:531:PHE:HD1	1.65	0.60
1:A:52:ILE:HB	1:A:83:ILE:HG13	1.83	0.60
1:B:659:LEU:HD22	1:B:659:LEU:H	1.67	0.60
1:B:156:GLN:HG3	1:B:161:GLU:HB2	1.82	0.60
1:B:292:TYR:O	1:B:294:LYS:N	2.34	0.60
1:C:304:GLU:O	7:C:948:HOH:O	2.16	0.59
2:E:34:HIS:NE2	2:E:74:THR:HG21	2.18	0.59
1:D:503:PHE:CD2	1:D:511:LEU:HB3	2.37	0.59
1:C:292:TYR:O	1:C:294:LYS:N	2.35	0.59
1:A:359:SER:OG	1:A:360:THR:N	2.36	0.59
1:B:390:PHE:CD1	1:B:395:GLU:HG3	2.36	0.59
2:H:34:HIS:NE2	2:H:74:THR:HG21	2.18	0.59
1:A:129[A]:LYS:NZ	4:A:811:CL:CL	2.58	0.59
2:G:84:HIS:CD2	6:K:5201:1XE:H1	2.38	0.59
1:B:13:LEU:HD22	1:B:32:ALA:HB1	1.82	0.59
1:C:503:PHE:CD2	1:C:511:LEU:HB3	2.37	0.59
1:C:444:ASP:OD1	2:G:80:ARG:NH2	2.33	0.59
1:C:156:GLN:HG3	1:C:161:GLU:HB2	1.83	0.59
1:A:503:PHE:CD2	1:A:511:LEU:HB3	2.38	0.59
1:D:292:TYR:O	1:D:294:LYS:N	2.36	0.59
1:C:390:PHE:CD1	1:C:395:GLU:HG3	2.37	0.58
1:D:390:PHE:CD1	1:D:395:GLU:HG3	2.38	0.58
1:D:47:LEU:HD13	1:D:69:LEU:HB3	1.85	0.58
1:A:159[B]:ARG:NH2	4:A:807:CL:CL	2.74	0.58
1:A:71:LEU:HD22	1:A:84:PHE:HD2	1.68	0.58
1:C:250:ASP:OD2	1:C:291:ARG:NH1	2.37	0.58
1:A:390:PHE:CD1	1:A:395:GLU:HG3	2.38	0.58
1:C:135:ARG:HD2	7:C:937:HOH:O	2.04	0.58
1:C:359:SER:OG	1:C:360:THR:N	2.35	0.58
1:B:359:SER:OG	1:B:360:THR:N	2.36	0.58
1:C:466:LEU:HB3	7:C:915:HOH:O	2.03	0.57
2:F:34:HIS:NE2	2:F:74:THR:HG21	2.19	0.57
1:B:250:ASP:OD2	1:B:291:ARG:NH1	2.38	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:496:MET:HE2	1:B:518:THR:HG21	1.86	0.57
1:D:250:ASP:OD2	1:D:291:ARG:NH1	2.37	0.57
1:B:33:ILE:HG13	1:B:37:LEU:HD21	1.85	0.57
1:A:146[B]:ARG:HB3	1:A:172:PHE:CZ	2.39	0.57
2:H:77:SER:HB2	6:L:5201:1XE:H24	1.85	0.57
1:C:178:GLN:OE1	7:C:918:HOH:O	2.18	0.57
1:D:183:ASP:OD2	7:D:930:HOH:O	2.18	0.56
2:G:124:ARG:HD3	4:G:201:CL:CL	2.42	0.56
1:A:67:VAL:HG22	1:A:83:ILE:HD11	1.87	0.56
2:F:112:VAL:HG12	6:J:5201:1XE:S1P	2.46	0.56
1:A:437:MET:HG2	1:A:454:CYS:HA	1.87	0.56
1:C:577:PHE:CD1	1:C:659:LEU:HD21	2.41	0.56
1:B:503:PHE:CD2	1:B:511:LEU:HB3	2.41	0.56
1:C:255:ASN:HD22	1:C:255:ASN:C	2.09	0.56
1:D:625:LEU:HB3	1:D:648:LEU:HG	1.87	0.56
1:B:129[A]:LYS:CD	1:B:129[A]:LYS:H	2.19	0.55
1:A:351:VAL:HG23	1:A:386:LEU:HD21	1.89	0.55
1:D:577:PHE:CD1	1:D:659:LEU:HD21	2.41	0.55
1:A:625:LEU:HB3	1:A:648:LEU:HG	1.88	0.55
1:A:146[B]:ARG:HH22	1:A:182:VAL:HG12	1.72	0.55
1:D:135:ARG:HD3	1:D:151:ALA:HB1	1.89	0.54
1:C:422:ARG:NH2	4:C:810:CL:CL	2.77	0.54
1:D:201:LYS:NZ	4:D:809:CL:CL	2.70	0.54
1:C:37:LEU:HD13	1:C:47:LEU:HD23	1.89	0.54
1:B:135:ARG:HD3	1:B:151:ALA:HB1	1.88	0.54
1:A:255:ASN:C	1:A:255:ASN:HD22	2.11	0.54
1:D:84:PHE:O	1:D:88:SER:OG	2.20	0.54
1:B:625:LEU:HB3	1:B:648:LEU:HG	1.90	0.54
1:C:625:LEU:HB3	1:C:648:LEU:HG	1.90	0.54
1:B:114:LEU:HD12	7:B:913:HOH:O	2.08	0.54
1:C:17:ALA:HB1	1:C:33:ILE:HD11	1.90	0.54
1:A:129[A]:LYS:H	1:A:129[A]:LYS:HD2	1.73	0.53
1:A:114:LEU:HD12	7:A:930:HOH:O	2.08	0.53
2:G:34:HIS:NE2	2:G:74:THR:HG21	2.22	0.53
1:C:381:TRP:HB3	7:C:949:HOH:O	2.07	0.53
2:G:126:THR:HG21	6:K:5201:1XE:P3B	2.49	0.53
1:C:182:VAL:HG23	1:C:184:THR:H	1.74	0.53
1:C:235:LEU:HD11	7:C:941:HOH:O	2.08	0.53
1:C:52:ILE:HD12	1:C:83:ILE:HG12	1.91	0.53
1:D:15:ARG:HD3	1:D:19:LYS:HE2	1.90	0.53
1:A:237:LYS:NZ	4:A:812:CL:CL	2.68	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:111:ASN:HB3	7:B:913:HOH:O	2.08	0.53
1:C:48:ALA:HB1	1:C:83:ILE:HG21	1.90	0.53
1:B:577:PHE:CD1	1:B:659:LEU:HD21	2.44	0.53
1:D:351:VAL:HG23	1:D:386:LEU:HD21	1.91	0.53
1:A:334:VAL:HG13	1:A:337:LEU:HD12	1.91	0.53
1:D:437:MET:HG2	1:D:454:CYS:HA	1.90	0.53
1:C:664:LYS:NZ	7:C:926:HOH:O	2.42	0.53
1:A:43:HIS:ND1	1:A:46:SER:OG	2.41	0.52
2:G:113:ARG:NH1	2:G:143:GLU:OE2	2.39	0.52
1:B:476:ARG:HH21	1:B:478:GLU:HG3	1.73	0.52
1:B:514:LYS:NZ	1:B:645:GLU:OE1	2.29	0.52
1:D:60:THR:O	1:D:62:GLU:N	2.42	0.52
1:B:255:ASN:HD22	1:B:255:ASN:C	2.13	0.52
1:B:34:GLU:O	1:B:38:GLU:HB2	2.09	0.52
1:A:577:PHE:CD1	1:A:659:LEU:HD21	2.43	0.52
1:A:593:LYS:NZ	7:A:968:HOH:O	2.43	0.52
1:A:201:LYS:HE3	4:A:803:CL:CL	2.47	0.52
1:B:282:LEU:HD21	1:B:306:LEU:HD21	1.91	0.52
1:C:282:LEU:HD21	1:C:306:LEU:HD21	1.91	0.52
1:A:292:TYR:C	1:A:294:LYS:H	2.12	0.52
1:B:292:TYR:C	1:B:294:LYS:H	2.13	0.52
1:D:324:LYS:HB3	4:D:810:CL:CL	2.47	0.52
1:B:351:VAL:HG23	1:B:386:LEU:HD21	1.91	0.52
1:C:292:TYR:C	1:C:294:LYS:H	2.13	0.52
1:B:706:ILE:O	1:B:708:GLY:N	2.43	0.52
1:D:52:ILE:HD12	1:D:83:ILE:HG23	1.92	0.52
1:C:351:VAL:HG23	1:C:386:LEU:HD21	1.91	0.52
1:B:357:SER:N	1:B:359:SER:H	2.08	0.52
1:C:357:SER:N	1:C:359:SER:H	2.08	0.51
1:B:327:ILE:HG22	1:B:329:SER:H	1.75	0.51
1:A:514:LYS:NZ	1:A:645:GLU:OE1	2.25	0.51
1:A:383:TYR:CZ	1:A:405:LEU:HD13	2.45	0.51
2:G:84:HIS:HE2	6:K:5201:1XE:H1	1.75	0.51
1:A:437:MET:HE2	1:A:450:ILE:HD11	1.91	0.51
1:D:255:ASN:HD22	1:D:255:ASN:C	2.13	0.51
1:D:357:SER:N	1:D:359:SER:H	2.08	0.51
1:D:291:ARG:NH2	7:D:932:HOH:O	2.42	0.51
1:A:135:ARG:HD2	7:A:925:HOH:O	2.10	0.51
1:C:49:ILE:O	1:C:53:LEU:HD22	2.10	0.51
1:C:334:VAL:HG13	1:C:337:LEU:HD12	1.92	0.51
1:C:437:MET:HG2	1:C:454:CYS:HA	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:129[A]:LYS:H	1:A:129[A]:LYS:CD	2.24	0.51
1:B:182:VAL:HG23	1:B:184:THR:H	1.76	0.50
2:H:113:ARG:NH1	2:H:143:GLU:OE2	2.40	0.50
2:E:113:ARG:NH1	2:E:143:GLU:OE2	2.38	0.50
1:D:146:ARG:NH1	4:D:807:CL:CL	2.79	0.50
1:B:288:LEU:O	1:B:291:ARG:HB3	2.11	0.50
2:F:113:ARG:NH1	2:F:143:GLU:OE2	2.41	0.50
1:D:13:LEU:HD12	1:D:36:LEU:HD11	1.93	0.50
2:G:112:VAL:HG12	6:K:5201:1XE:S1P	2.51	0.50
1:C:204:VAL:HG12	7:C:941:HOH:O	2.11	0.50
1:C:135:ARG:HD3	1:C:151:ALA:HB1	1.92	0.50
2:G:24:GLU:HG3	3:K:5122:SER:OG	2.11	0.50
1:D:383:TYR:CZ	1:D:405:LEU:HD13	2.47	0.50
1:D:79:VAL:O	1:D:83:ILE:HG12	2.11	0.50
1:A:220:ASP:OD2	1:A:544:ARG:NH2	2.45	0.50
1:D:292:TYR:C	1:D:294:LYS:H	2.14	0.50
1:A:706:ILE:O	1:A:708:GLY:N	2.44	0.50
1:D:365:SER:OG	1:D:366:GLU:N	2.45	0.50
1:A:184:THR:CG2	1:A:219:LEU:HD11	2.41	0.49
1:C:259:TYR:HA	7:C:947:HOH:O	2.11	0.49
1:D:282:LEU:HD21	1:D:306:LEU:HD21	1.93	0.49
1:C:46:SER:HA	1:C:49:ILE:HG12	1.93	0.49
2:G:88:ALA:HB3	6:K:5201:1XE:O2A	2.12	0.49
2:H:112:VAL:HG12	6:L:5201:1XE:S1P	2.52	0.49
1:D:706:ILE:O	1:D:708:GLY:N	2.45	0.49
1:C:377:THR:O	1:C:377:THR:OG1	2.26	0.49
1:A:357:SER:N	1:A:359:SER:H	2.11	0.49
1:D:184:THR:CG2	1:D:219:LEU:HD11	2.42	0.49
1:B:30:LEU:O	1:B:34:GLU:HG2	2.13	0.49
1:C:319:LEU:HD21	1:C:334:VAL:HG21	1.95	0.49
1:C:155:ALA:HB2	7:C:937:HOH:O	2.13	0.49
1:B:52:ILE:HB	1:B:83:ILE:HD13	1.94	0.49
1:A:111:ASN:HB3	7:A:930:HOH:O	2.13	0.49
1:A:530:GLN:N	7:A:914:HOH:O	2.31	0.49
1:B:334:VAL:HG13	1:B:337:LEU:HD12	1.94	0.49
1:D:603:GLU:O	1:D:607:ILE:HG12	2.12	0.49
1:B:383:TYR:CZ	1:B:405:LEU:HD13	2.48	0.49
1:D:351:VAL:HG21	1:D:385:PHE:CE2	2.48	0.49
1:A:357:SER:OG	1:A:358:LEU:N	2.46	0.48
1:C:291:ARG:NH2	4:C:801:CL:CL	2.83	0.48
1:C:327:ILE:HG22	1:C:329:SER:H	1.78	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:288:LEU:O	1:A:291:ARG:HB3	2.13	0.48
1:A:135:ARG:HD3	1:A:151:ALA:HB1	1.94	0.48
1:D:437:MET:HE2	1:D:450:ILE:HD11	1.95	0.48
1:B:105:HIS:HD2	7:B:913:HOH:O	1.95	0.48
1:A:351:VAL:HG21	1:A:385:PHE:CE2	2.49	0.48
1:C:383:TYR:CZ	1:C:405:LEU:HD13	2.48	0.48
1:D:534:HIS:HD1	1:D:546:TYR:HH	1.54	0.48
1:C:358:LEU:HD13	1:C:358:LEU:HA	1.80	0.48
1:A:10:GLU:O	1:A:14:PHE:N	2.38	0.48
1:D:44:GLY:HA2	1:D:70:GLY:HA2	1.95	0.48
1:B:377:THR:O	1:B:377:THR:OG1	2.27	0.48
1:C:657:GLU:N	1:C:657:GLU:OE2	2.47	0.48
1:C:75:VAL:N	1:C:76:GLY:HA3	2.28	0.48
1:B:319:LEU:HD21	1:B:334:VAL:HG21	1.96	0.48
1:C:71:LEU:HD11	1:C:81:TRP:CD2	2.49	0.48
1:B:476:ARG:HG2	1:B:478:GLU:HG2	1.94	0.48
1:D:534:HIS:ND1	1:D:546:TYR:OH	2.35	0.48
1:B:184:THR:CG2	1:B:219:LEU:HD11	2.44	0.48
1:B:255:ASN:O	1:B:257:GLN:N	2.47	0.48
1:D:10:GLU:HG2	1:D:36:LEU:HD13	1.96	0.48
1:C:15:ARG:O	1:C:19:LYS:HG2	2.13	0.48
1:D:514:LYS:NZ	1:D:645:GLU:OE1	2.23	0.48
1:D:30:LEU:HG	1:D:53:LEU:HD12	1.94	0.48
1:C:288:LEU:O	1:C:291:ARG:HB3	2.14	0.48
1:B:347:VAL:O	1:B:351:VAL:HG22	2.14	0.48
1:D:16:THR:O	1:D:20:CYS:N	2.47	0.48
1:C:351:VAL:HG21	1:C:385:PHE:CE2	2.49	0.47
1:A:379:LEU:HD23	1:A:379:LEU:HA	1.80	0.47
1:D:422:ARG:CZ	4:D:811:CL:CL	3.00	0.47
1:A:37:LEU:HD21	1:A:46:SER:HB3	1.96	0.47
1:D:220:ASP:OD2	1:D:544:ARG:NH2	2.47	0.47
1:D:319:LEU:HD21	1:D:334:VAL:HG21	1.95	0.47
1:C:255:ASN:O	1:C:257:GLN:N	2.47	0.47
1:C:33:ILE:HG22	1:C:37:LEU:HG	1.96	0.47
1:A:319:LEU:HD21	1:A:334:VAL:HG21	1.96	0.47
2:H:113:ARG:HB3	2:H:139:TYR:CE2	2.50	0.47
1:A:365:SER:OG	1:A:366:GLU:N	2.48	0.47
1:D:97:ALA:O	1:D:101:TYR:HD2	1.97	0.47
1:A:129[B]:LYS:H	1:A:129[B]:LYS:HG3	1.47	0.47
1:A:347:VAL:O	1:A:351:VAL:HG22	2.14	0.47
1:B:437:MET:HG2	1:B:454:CYS:HA	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:23:PRO:HD2	2:E:24:GLU:OE2	2.14	0.47
1:B:13:LEU:HD12	1:B:36:LEU:HD21	1.96	0.47
2:F:22:LEU:HD21	6:J:5201:1XE:N4P	2.29	0.47
1:D:327:ILE:HG22	1:D:329:SER:H	1.79	0.47
1:A:327:ILE:HG22	1:A:329:SER:H	1.79	0.47
1:D:288:LEU:O	1:D:291:ARG:HB3	2.15	0.47
1:D:255:ASN:O	1:D:257:GLN:N	2.47	0.47
1:B:365:SER:OG	1:B:366:GLU:N	2.47	0.47
1:B:358:LEU:HD13	1:B:358:LEU:HA	1.81	0.47
1:C:362:ASN:HB3	1:C:375:ILE:H	1.80	0.47
1:B:129[B]:LYS:HE3	1:B:130:ALA:N	2.19	0.46
1:A:422:ARG:CZ	4:A:810:CL:CL	3.00	0.46
1:A:282:LEU:HD21	1:A:306:LEU:HD21	1.96	0.46
1:B:184:THR:HG22	1:B:219:LEU:HD11	1.97	0.46
2:F:56:VAL:CG1	2:F:91:LEU:HB3	2.45	0.46
1:C:706:ILE:O	1:C:708:GLY:N	2.49	0.46
1:C:163:ALA:O	1:C:167:LYS:HG2	2.15	0.46
1:C:347:VAL:O	1:C:351:VAL:HG22	2.15	0.46
1:C:365:SER:OG	1:C:366:GLU:N	2.48	0.46
1:B:71:LEU:HD13	1:B:80:CYS:HB3	1.97	0.46
1:C:530:GLN:N	7:C:955:HOH:O	2.30	0.46
2:H:10:ASP:HA	7:H:308:HOH:O	2.15	0.46
1:A:362:ASN:HB3	1:A:375:ILE:H	1.80	0.46
1:D:515:ARG:NH2	7:D:963:HOH:O	2.46	0.46
1:A:377:THR:OG1	1:A:377:THR:O	2.28	0.46
1:C:300:ARG:O	1:C:303:LEU:HB2	2.16	0.46
2:E:56:VAL:CG1	2:E:91:LEU:HB3	2.45	0.46
1:D:377:THR:OG1	1:D:377:THR:O	2.28	0.46
1:D:275:VAL:HA	1:D:276:LEU:HA	1.60	0.46
1:A:453:LYS:HD3	1:A:453:LYS:HA	1.79	0.46
1:D:95:VAL:O	1:D:99:LYS:HG3	2.15	0.46
1:A:105:HIS:HD2	7:A:930:HOH:O	1.98	0.46
1:C:184:THR:CG2	1:C:219:LEU:HD11	2.46	0.46
2:E:113:ARG:HB3	2:E:139:TYR:CE2	2.51	0.46
1:B:460:ARG:HD2	4:B:813:CL:CL	2.53	0.46
1:C:81:TRP:O	1:C:100:CYS:HB3	2.15	0.45
1:B:362:ASN:HB3	1:B:375:ILE:H	1.81	0.45
1:D:363:LYS:NZ	1:D:372:GLN:O	2.43	0.45
1:A:95:VAL:O	1:A:99:LYS:HG3	2.16	0.45
1:D:657:GLU:HB2	7:D:960:HOH:O	2.17	0.45
1:D:362:ASN:HB3	1:D:375:ILE:H	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:362:ASN:ND2	1:A:375:ILE:O	2.44	0.45
1:D:61:LYS:HE2	1:D:68:ARG:HH12	1.81	0.45
1:B:7:SER:HA	1:B:8:PRO:HD3	1.84	0.45
1:B:300:ARG:O	1:B:303:LEU:HB2	2.16	0.45
2:F:74:THR:O	3:J:5122:SER:HA	2.16	0.45
1:D:12:THR:O	1:D:16:THR:HG23	2.17	0.45
1:B:351:VAL:HG21	1:B:385:PHE:CE2	2.51	0.45
1:A:275:VAL:HA	1:A:276:LEU:HA	1.61	0.45
1:B:439:HIS:HD2	4:B:801:CL:CL	2.36	0.45
1:C:248:LEU:HB3	1:C:258:TYR:CE1	2.51	0.45
1:B:220:ASP:OD2	1:B:544:ARG:NH2	2.48	0.45
1:A:184:THR:HG22	1:A:219:LEU:HD11	1.99	0.45
1:C:422:ARG:CZ	4:C:810:CL:CL	3.01	0.45
1:A:45:GLU:O	1:A:49:ILE:HG13	2.16	0.45
1:D:43:HIS:ND1	1:D:46:SER:OG	2.44	0.45
1:D:362:ASN:ND2	1:D:375:ILE:O	2.45	0.45
1:A:210:HIS:CE1	1:A:214:ILE:HD13	2.51	0.45
1:B:476:ARG:NH2	1:B:478:GLU:HG3	2.31	0.45
1:D:496:MET:HE1	1:D:515:ARG:HD3	1.99	0.45
1:D:694:ASP:N	1:D:694:ASP:OD1	2.50	0.45
1:C:218:VAL:HG21	1:C:224:PHE:CD1	2.52	0.45
1:D:75:VAL:N	1:D:76:GLY:HA3	2.32	0.45
1:A:657:GLU:HA	1:A:658:PRO:HD2	1.82	0.45
1:C:534:HIS:ND1	1:C:546:TYR:OH	2.31	0.45
1:B:218:VAL:HG21	1:B:224:PHE:CD1	2.52	0.45
1:A:603:GLU:O	1:A:607:ILE:HG12	2.16	0.45
1:B:163:ALA:O	1:B:167:LYS:HG2	2.17	0.45
1:A:218:VAL:HG21	1:A:224:PHE:CD1	2.52	0.44
1:A:650:GLU:HA	7:A:962:HOH:O	2.17	0.44
1:D:45:GLU:O	1:D:49:ILE:HG12	2.16	0.44
2:G:84:HIS:CD2	6:K:5201:1XE:C2A	3.00	0.44
2:G:56:VAL:CG1	2:G:91:LEU:HB3	2.47	0.44
1:D:74:ASP:OD2	1:D:77:SER:HB2	2.18	0.44
1:B:54:LEU:HD13	1:B:62:GLU:HB3	1.99	0.44
1:D:358:LEU:HA	1:D:358:LEU:HD13	1.78	0.44
2:E:78:VAL:H	6:I:5201:1XE:H22	1.65	0.44
1:A:657:GLU:HG2	1:A:657:GLU:O	2.18	0.44
2:E:1[A]:MET:HE3	2:E:1[A]:MET:HB3	1.79	0.44
2:E:1[B]:MET:CE	2:E:48:PRO:HD3	2.47	0.44
1:B:480:VAL:HB	1:B:481:GLY:H	1.55	0.44
1:B:63:GLY:O	1:B:67:VAL:HG23	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:52:ILE:HB	1:C:83:ILE:CD1	2.44	0.44
2:H:56:VAL:CG1	2:H:91:LEU:HB3	2.47	0.44
1:C:55:HIS:CD2	1:C:87:ILE:HB	2.53	0.44
1:A:694:ASP:OD1	1:A:694:ASP:N	2.51	0.44
1:C:210:HIS:CE1	1:C:214:ILE:HD13	2.52	0.44
1:B:98:ALA:O	1:B:102:ILE:HG12	2.18	0.44
1:B:478:GLU:H	1:B:478:GLU:HG2	1.41	0.44
2:F:113:ARG:HB3	2:F:139:TYR:CE2	2.52	0.43
2:H:11:LEU:HD22	2:H:31:TYR:HB3	1.99	0.43
1:B:372:GLN:HB3	1:B:373:ILE:H	1.63	0.43
1:A:496:MET:HE3	1:A:515:ARG:HD3	2.00	0.43
1:D:657:GLU:HA	1:D:658:PRO:HD2	1.83	0.43
1:B:363:LYS:HA	1:B:363:LYS:HD2	1.83	0.43
1:C:460:ARG:HD2	7:C:954:HOH:O	2.16	0.43
1:B:58:GLY:HA2	1:B:59:ASN:HA	1.50	0.43
1:D:218:VAL:HG21	1:D:224:PHE:CD1	2.53	0.43
1:C:79:VAL:O	1:C:83:ILE:HG22	2.19	0.43
2:G:30:TYR:CZ	2:G:34:HIS:HE1	2.36	0.43
1:C:18:LEU:HD21	1:C:49:ILE:HD12	2.00	0.43
1:C:657:GLU:HA	1:C:658:PRO:HD2	1.81	0.43
1:D:210:HIS:CE1	1:D:214:ILE:HD13	2.53	0.43
1:C:220:ASP:OD2	1:C:544:ARG:NH2	2.49	0.43
2:F:11:LEU:HD22	2:F:31:TYR:HB3	1.99	0.43
1:A:149:TRP:CE3	1:A:172:PHE:HB2	2.53	0.43
1:A:292:TYR:C	1:A:294:LYS:N	2.72	0.43
1:A:249:LEU:CD1	1:A:258:TYR:HB3	2.48	0.43
1:C:200:LYS:HA	1:C:200:LYS:HD2	1.89	0.43
1:B:275:VAL:HA	1:B:276:LEU:HA	1.61	0.43
1:C:480:VAL:HB	1:C:481:GLY:H	1.56	0.43
1:A:240:GLU:HB2	7:A:957:HOH:O	2.17	0.43
1:C:275:VAL:HA	1:C:276:LEU:HA	1.62	0.43
1:C:98:ALA:O	1:C:102:ILE:HG12	2.18	0.43
1:D:54:LEU:HD13	1:D:62:GLU:HG3	1.99	0.43
1:A:26:TYR:CZ	1:A:56:SER:HB3	2.54	0.43
1:C:415:GLU:OE1	2:G:80:ARG:HD3	2.19	0.43
1:A:255:ASN:O	1:A:257:GLN:N	2.51	0.43
1:C:282:LEU:HD23	1:C:282:LEU:HA	1.90	0.43
1:A:13:LEU:HB3	1:A:36:LEU:HD11	2.01	0.43
1:D:709:GLN:HB3	1:D:709:GLN:HE21	1.61	0.43
1:C:372:GLN:HB3	1:C:373:ILE:H	1.63	0.43
1:B:657:GLU:HA	1:B:658:PRO:HD2	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:53:LEU:HD12	1:A:53:LEU:HA	1.76	0.43
1:B:379:LEU:HA	1:B:379:LEU:HD23	1.79	0.42
1:D:657:GLU:N	1:D:657:GLU:OE2	2.52	0.42
1:A:657:GLU:HB2	7:A:979:HOH:O	2.19	0.42
1:D:129:LYS:HE3	4:D:806:CL:CL	2.56	0.42
1:C:583:LYS:HG3	1:C:583:LYS:H	1.62	0.42
1:D:292:TYR:C	1:D:294:LYS:N	2.73	0.42
2:G:11:LEU:HD22	2:G:31:TYR:HB3	2.00	0.42
1:C:492:CYS:O	1:C:496:MET:HG2	2.20	0.42
1:A:448:ARG:HH11	2:E:23:PRO:HA	1.83	0.42
1:A:709:GLN:HE21	1:A:709:GLN:HB3	1.62	0.42
1:C:208:TYR:HB2	7:C:941:HOH:O	2.20	0.42
1:D:607:ILE:O	1:D:611:LEU:HG	2.19	0.42
1:D:334:VAL:HG13	1:D:337:LEU:HD12	2.01	0.42
1:B:248:LEU:HB3	1:B:258:TYR:CE1	2.54	0.42
1:D:300:ARG:O	1:D:303:LEU:HB2	2.19	0.42
1:A:105:HIS:CD2	7:A:930:HOH:O	2.71	0.42
2:H:121:HIS:HB3	6:L:5201:1XE:C8A	2.49	0.42
1:D:626:LYS:HG2	1:D:648:LEU:HD23	2.01	0.42
1:A:607:ILE:O	1:A:611:LEU:HG	2.20	0.42
1:A:300:ARG:O	1:A:303:LEU:HB2	2.20	0.42
1:B:57:LEU:CD1	1:B:58:GLY:H	2.26	0.42
1:D:184:THR:HG22	1:D:219:LEU:HD11	2.02	0.42
1:D:657:GLU:HG2	1:D:657:GLU:O	2.20	0.42
1:C:184:THR:HG22	1:C:219:LEU:HD11	2.01	0.42
1:C:354:TYR:O	1:C:358:LEU:HB2	2.19	0.42
2:H:112:VAL:HG23	2:H:146:TYR:HB2	2.01	0.42
1:B:405:LEU:HA	1:B:405:LEU:HD23	1.90	0.42
2:F:112:VAL:HG23	2:F:146:TYR:HB2	2.02	0.42
1:D:591:PHE:O	1:D:595:SER:HB2	2.19	0.42
1:C:673:GLY:HA3	1:C:680:TYR:CZ	2.55	0.42
1:B:249:LEU:CD1	1:B:258:TYR:HB3	2.50	0.42
1:B:603:GLU:O	1:B:607:ILE:HG12	2.20	0.42
2:G:112:VAL:HG23	2:G:146:TYR:HB2	2.02	0.42
2:E:112:VAL:HG23	2:E:146:TYR:HB2	2.01	0.42
1:C:71:LEU:HD11	1:C:81:TRP:CE2	2.55	0.42
1:C:591:PHE:O	1:C:595:SER:HB2	2.19	0.42
1:A:353:LYS:HB3	1:A:353:LYS:HE2	1.79	0.42
1:B:105:HIS:CD2	7:B:913:HOH:O	2.70	0.42
1:A:437:MET:HE2	1:A:450:ILE:CD1	2.50	0.42
1:D:47:LEU:HB3	1:D:66:ASN:O	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:30:TYR:CE1	2:H:34:HIS:HE1	2.37	0.41
1:D:37:LEU:HD21	1:D:46:SER:HB3	2.01	0.41
1:B:60:THR:O	1:B:63:GLY:N	2.51	0.41
1:B:129[B]:LYS:H	1:B:129[B]:LYS:HG3	1.47	0.41
1:B:292:TYR:C	1:B:294:LYS:N	2.73	0.41
1:B:657:GLU:N	1:B:657:GLU:OE2	2.54	0.41
1:D:7:SER:HA	1:D:8:PRO:HD3	1.78	0.41
1:C:292:TYR:C	1:C:294:LYS:N	2.73	0.41
1:C:405:LEU:HD23	1:C:405:LEU:HA	1.91	0.41
1:A:657:GLU:N	1:A:657:GLU:OE2	2.53	0.41
1:B:149:TRP:CE3	1:B:172:PHE:HB2	2.54	0.41
1:D:508:LYS:NZ	7:D:952:HOH:O	2.53	0.41
1:B:354:TYR:O	1:B:358:LEU:HB2	2.20	0.41
2:E:21:ASN:HB3	6:I:5201:1XE:H24	2.02	0.41
1:B:37:LEU:N	1:B:37:LEU:HD23	2.35	0.41
1:D:13:LEU:HD22	1:D:32:ALA:HB1	2.03	0.41
1:A:701:GLU:O	1:A:705:VAL:HG23	2.20	0.41
1:D:249:LEU:CD1	1:D:258:TYR:HB3	2.50	0.41
1:B:493:LEU:HA	1:B:493:LEU:HD12	1.88	0.41
1:C:181:PRO:HA	1:C:182:VAL:CG2	2.45	0.41
1:A:348:GLU:HB2	1:A:389:HIS:NE2	2.36	0.41
1:C:493:LEU:HA	1:C:493:LEU:HD12	1.90	0.41
2:H:8:ILE:HA	2:H:8:ILE:HD13	1.91	0.41
1:D:181:PRO:HA	1:D:182:VAL:CG2	2.46	0.41
1:C:159:ARG:NH1	1:C:161:GLU:HG3	2.35	0.41
1:D:347:VAL:O	1:D:351:VAL:HG22	2.21	0.41
1:D:405:LEU:HA	1:D:405:LEU:HD23	1.85	0.41
1:B:146:ARG:HB2	1:B:172:PHE:CZ	2.56	0.41
2:F:62:GLU:O	2:F:64:PRO:HD3	2.20	0.41
1:A:181:PRO:HA	1:A:182:VAL:CG2	2.46	0.41
2:H:30:TYR:CZ	2:H:34:HIS:HE1	2.38	0.41
1:B:511:LEU:HD12	1:B:511:LEU:HA	1.85	0.41
1:C:362:ASN:ND2	1:C:375:ILE:O	2.46	0.41
1:B:362:ASN:ND2	1:B:375:ILE:O	2.46	0.41
1:B:210:HIS:CE1	1:B:214:ILE:HD13	2.55	0.41
1:A:529:ASP:N	7:A:914:HOH:O	2.53	0.41
1:B:135:ARG:CD	1:B:151:ALA:HB1	2.51	0.41
1:C:324:LYS:HG2	1:C:375:ILE:HD13	2.03	0.41
2:E:1[B]:MET:HE3	2:E:48:PRO:HD3	2.03	0.41
1:B:701:GLU:O	1:B:705:VAL:HG23	2.21	0.41
1:A:29:GLY:O	1:A:33:ILE:HG13	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:62:GLU:O	2:G:64:PRO:HD3	2.20	0.41
2:E:11:LEU:HD22	2:E:31:TYR:HB3	2.02	0.41
2:H:38:TRP:CZ3	2:H:59:LYS:HB2	2.56	0.41
1:B:591:PHE:O	1:B:595:SER:HB2	2.20	0.41
1:B:26:TYR:HD2	1:B:57:LEU:HD23	1.86	0.41
1:A:497:LEU:HD12	1:A:497:LEU:HA	1.98	0.41
2:F:15:GLN:HG3	2:F:31:TYR:CE1	2.56	0.41
1:C:496:MET:HE1	1:C:515:ARG:HD3	2.03	0.41
1:D:29:GLY:O	1:D:33:ILE:HG13	2.21	0.41
1:B:425:LYS:NZ	4:B:814:CL:CL	2.68	0.41
1:C:26:TYR:CZ	1:C:56:SER:HB3	2.56	0.41
1:A:182:VAL:HG23	1:A:184:THR:H	1.86	0.40
2:F:30:TYR:CZ	2:F:34:HIS:HE1	2.39	0.40
1:C:249:LEU:CD1	1:C:258:TYR:HB3	2.52	0.40
1:C:603:GLU:O	1:C:607:ILE:HG12	2.22	0.40
1:C:453:LYS:HA	1:C:453:LYS:HD3	1.80	0.40
1:B:324:LYS:HG2	1:B:375:ILE:HD13	2.03	0.40
1:D:379:LEU:HA	1:D:379:LEU:HD23	1.81	0.40
1:C:368:ASP:N	1:C:368:ASP:OD1	2.54	0.40
1:B:17:ALA:CB	1:B:33:ILE:HD13	2.52	0.40
1:B:37:LEU:HD22	1:B:46:SER:HB3	2.02	0.40
1:D:324:LYS:HG2	1:D:375:ILE:HD13	2.04	0.40
2:E:47:ASP:HB2	2:E:48:PRO:HD2	2.04	0.40
1:B:12:THR:O	1:B:16:THR:HG23	2.21	0.40
1:B:129[A]:LYS:HD2	1:B:129[A]:LYS:N	2.34	0.40
7:F:305:HOH:O	3:J:5122:SER:HB2	2.21	0.40
1:B:492:CYS:O	1:B:496:MET:HG2	2.22	0.40
1:D:139:LEU:HD11	1:D:149:TRP:CE2	2.57	0.40
1:B:179:GLY:HA3	1:B:180:VAL:HA	1.62	0.40
1:C:7:SER:HA	1:C:8:PRO:HD3	1.88	0.40
1:B:181:PRO:HA	1:B:182:VAL:CG2	2.46	0.40
1:A:163:ALA:O	1:A:167:LYS:HG2	2.21	0.40
1:C:698:LYS:HG3	1:C:699:TYR:N	2.37	0.40

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)
1:A:731:ALA:O	7:G:304:HOH:O[1_556]	2.08	0.12

## 5.3 Torsion angles

### 5.3.1 Protein backbone

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	717/734 (98%)	658 (92%)	46 (6%)	13 (2%)	11	21
1	B	719/734 (98%)	660 (92%)	45 (6%)	14 (2%)	10	19
1	C	714/734 (97%)	660 (92%)	42 (6%)	12 (2%)	11	22
1	D	715/734 (97%)	657 (92%)	43 (6%)	15 (2%)	9	16
2	E	151/156 (97%)	144 (95%)	7 (5%)	0	100	100
2	F	151/156 (97%)	147 (97%)	4 (3%)	0	100	100
2	G	151/156 (97%)	146 (97%)	5 (3%)	0	100	100
2	H	151/156 (97%)	145 (96%)	6 (4%)	0	100	100
3	I	2/5 (40%)	2 (100%)	0	0	100	100
3	J	2/5 (40%)	2 (100%)	0	0	100	100
3	K	2/5 (40%)	2 (100%)	0	0	100	100
3	L	2/5 (40%)	2 (100%)	0	0	100	100
All	All	3477/3580 (97%)	3225 (93%)	198 (6%)	54 (2%)	12	24

All (54) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	182	VAL
1	A	184	THR
1	A	256	HIS
1	A	293	PRO
1	A	358	LEU
1	A	373	ILE
1	B	182	VAL
1	B	256	HIS
1	B	293	PRO
1	B	373	ILE
1	C	182	VAL
1	C	256	HIS

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Mol	Chain	Res	Type
1	C	293	PRO
1	C	373	ILE
1	D	25	GLN
1	D	182	VAL
1	D	184	THR
1	D	256	HIS
1	D	373	ILE
1	A	647	PRO
1	B	184	THR
1	B	358	LEU
1	B	647	PRO
1	C	184	THR
1	C	358	LEU
1	C	647	PRO
1	D	61	LYS
1	D	293	PRO
1	D	358	LEU
1	D	647	PRO
1	A	376	PRO
1	B	60	THR
1	B	376	PRO
1	C	77	SER
1	C	376	PRO
1	D	59	ASN
1	D	376	PRO
1	D	6	LEU
1	A	77	SER
1	B	649	GLY
1	C	649	GLY
1	A	25	GLN
1	A	649	GLY
1	B	3	LYS
1	B	77	SER
1	D	649	GLY
1	A	480	VAL
1	B	480	VAL
1	C	480	VAL
1	D	480	VAL
1	A	292	TYR
1	D	292	TYR
1	B	292	TYR
1	C	292	TYR

### 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	611/638 (96%)	558 (91%)	53 (9%)	13	24
1	B	610/638 (96%)	559 (92%)	51 (8%)	14	26
1	C	609/638 (96%)	561 (92%)	48 (8%)	15	30
1	D	610/638 (96%)	562 (92%)	48 (8%)	15	30
2	E	133/135 (98%)	118 (89%)	15 (11%)	7	13
2	F	132/135 (98%)	118 (89%)	14 (11%)	8	15
2	G	132/135 (98%)	119 (90%)	13 (10%)	10	19
2	H	132/135 (98%)	117 (89%)	15 (11%)	7	12
3	I	3/3 (100%)	3 (100%)	0	100	100
3	J	3/3 (100%)	2 (67%)	1 (33%)	0	0
3	K	3/3 (100%)	3 (100%)	0	100	100
3	L	3/3 (100%)	3 (100%)	0	100	100
All	All	2981/3104 (96%)	2723 (91%)	258 (9%)	13	24

All (258) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	20	CYS
1	A	37	LEU
1	A	53	LEU
1	A	57	LEU
1	A	60	THR
1	A	61	LYS
1	A	72	ARG
1	A	82	HIS
1	A	83	ILE
1	A	84	PHE
1	A	96	GLN
1	A	111	ASN
1	A	120	LEU
1	A	129[A]	LYS

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Mol	Chain	Res	Type
1	A	129[B]	LYS
1	A	131	LEU
1	A	145	VAL
1	A	146[A]	ARG
1	A	146[B]	ARG
1	A	176	ILE
1	A	182	VAL
1	A	184	THR
1	A	194	MET
1	A	255	ASN
1	A	277	ASP
1	A	284	LEU
1	A	288	LEU
1	A	291	ARG
1	A	292	TYR
1	A	303	LEU
1	A	307	GLU
1	A	361	THR
1	A	372	GLN
1	A	375	ILE
1	A	377	THR
1	A	380	LEU
1	A	403	VAL
1	A	410	THR
1	A	445	LEU
1	A	459	LEU
1	A	465	GLU
1	A	493	LEU
1	A	497	LEU
1	A	511	LEU
1	A	513	LEU
1	A	547	LEU
1	A	583	LYS
1	A	600	ASN
1	A	669	LEU
1	A	698	LYS
1	A	707	LEU
1	A	709	GLN
1	A	727	GLN
1	B	7	SER
1	B	37	LEU
1	B	49	ILE

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Mol	Chain	Res	Type
1	B	53	LEU
1	B	56	SER
1	B	57	LEU
1	B	61	LYS
1	B	72	ARG
1	B	111	ASN
1	B	120	LEU
1	B	129[A]	LYS
1	B	129[B]	LYS
1	B	131	LEU
1	B	145	VAL
1	B	146	ARG
1	B	159	ARG
1	B	176	ILE
1	B	182	VAL
1	B	184	THR
1	B	194	MET
1	B	255	ASN
1	B	277	ASP
1	B	284	LEU
1	B	288	LEU
1	B	291	ARG
1	B	303	LEU
1	B	307	GLU
1	B	358	LEU
1	B	361	THR
1	B	372	GLN
1	B	375	ILE
1	B	377	THR
1	B	378	THR
1	B	380	LEU
1	B	403	VAL
1	B	410	THR
1	B	445	LEU
1	B	459	LEU
1	B	465	GLU
1	B	478	GLU
1	B	493	LEU
1	B	497	LEU
1	B	511	LEU
1	B	513	LEU
1	B	547	LEU

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Mol	Chain	Res	Type
1	B	583	LYS
1	B	600	ASN
1	B	669	LEU
1	B	698	LYS
1	B	707	LEU
1	B	727	GLN
1	C	38	GLU
1	C	53	LEU
1	C	72	ARG
1	C	74	ASP
1	C	83	ILE
1	C	96	GLN
1	C	111	ASN
1	C	120	LEU
1	C	129	LYS
1	C	131	LEU
1	C	145	VAL
1	C	176	ILE
1	C	182	VAL
1	C	184	THR
1	C	194	MET
1	C	255	ASN
1	C	277	ASP
1	C	284	LEU
1	C	288	LEU
1	C	291	ARG
1	C	303	LEU
1	C	307	GLU
1	C	358	LEU
1	C	361	THR
1	C	372	GLN
1	C	375	ILE
1	C	377	THR
1	C	380	LEU
1	C	403	VAL
1	C	410	THR
1	C	445	LEU
1	C	459	LEU
1	C	465	GLU
1	C	493	LEU
1	C	497	LEU
1	C	511	LEU

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Mol	Chain	Res	Type
1	C	513	LEU
1	C	517	SER
1	C	539[A]	ARG
1	C	539[B]	ARG
1	C	547	LEU
1	C	583	LYS
1	C	600	ASN
1	C	669	LEU
1	C	690	LEU
1	C	698	LYS
1	C	707	LEU
1	C	727	GLN
1	D	20	CYS
1	D	38	GLU
1	D	57	LEU
1	D	61	LYS
1	D	84	PHE
1	D	96	GLN
1	D	111	ASN
1	D	120	LEU
1	D	129	LYS
1	D	131	LEU
1	D	145	VAL
1	D	176	ILE
1	D	182	VAL
1	D	184	THR
1	D	194	MET
1	D	255	ASN
1	D	284	LEU
1	D	288	LEU
1	D	291	ARG
1	D	292	TYR
1	D	303	LEU
1	D	307	GLU
1	D	358	LEU
1	D	361	THR
1	D	372	GLN
1	D	375	ILE
1	D	377	THR
1	D	378	THR
1	D	380	LEU
1	D	403	VAL

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Mol	Chain	Res	Type
1	D	410	THR
1	D	445	LEU
1	D	459	LEU
1	D	465	GLU
1	D	493	LEU
1	D	497	LEU
1	D	511	LEU
1	D	513	LEU
1	D	539[A]	ARG
1	D	539[B]	ARG
1	D	547	LEU
1	D	583	LYS
1	D	600	ASN
1	D	669	LEU
1	D	698	LYS
1	D	707	LEU
1	D	709	GLN
1	D	727	GLN
2	E	1[A]	MET
2	E	1[B]	MET
2	E	3	ILE
2	E	24	GLU
2	E	26	TYR
2	E	27	GLN
2	E	32	LEU
2	E	56	VAL
2	E	57	LEU
2	E	66	ASP
2	E	72	HIS
2	E	74	THR
2	E	81	SER
2	E	130	ASP
2	E	148	MET
2	F	1	MET
2	F	3	ILE
2	F	24	GLU
2	F	27	GLN
2	F	32	LEU
2	F	53	VAL
2	F	56	VAL
2	F	57	LEU
2	F	66	ASP

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Mol	Chain	Res	Type
2	F	72	HIS
2	F	74	THR
2	F	81	SER
2	F	130	ASP
2	F	148	MET
2	G	3	ILE
2	G	24	GLU
2	G	26	TYR
2	G	27	GLN
2	G	32	LEU
2	G	56	VAL
2	G	57	LEU
2	G	66	ASP
2	G	72	HIS
2	G	74	THR
2	G	81	SER
2	G	130	ASP
2	G	148	MET
2	H	1	MET
2	H	3	ILE
2	H	24	GLU
2	H	26	TYR
2	H	27	GLN
2	H	32	LEU
2	H	56	VAL
2	H	57	LEU
2	H	66	ASP
2	H	72	HIS
2	H	74	THR
2	H	81	SER
2	H	87	LEU
2	H	130	ASP
2	H	148	MET
3	J	5125	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (20) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	96	GLN
1	A	111	ASN
1	A	255	ASN
1	A	600	ASN

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Mol	Chain	Res	Type
1	A	709	GLN
1	B	111	ASN
1	B	255	ASN
1	B	439	HIS
1	B	600	ASN
1	C	111	ASN
1	C	255	ASN
1	C	256	HIS
1	C	600	ASN
1	D	111	ASN
1	D	255	ASN
1	D	600	ASN
1	D	709	GLN
2	E	27	GLN
2	G	27	GLN
2	H	27	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](#)

Of 70 ligands modelled in this entry, 64 are monoatomic - leaving 6 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
5	SO4	A	815	-	4,4,4	0.14	0	6,6,6	0.11	0
5	SO4	D	816	-	4,4,4	0.11	0	6,6,6	0.13	0
6	1XE	I	5201	3	42,53,54	2.49	12 (28%)	44,78,80	3.14	20 (45%)
6	1XE	J	5201	3	42,53,54	2.56	11 (26%)	44,78,80	2.60	16 (36%)
6	1XE	K	5201	3	42,53,54	2.48	10 (23%)	44,78,80	2.89	15 (34%)
6	1XE	L	5201	3	42,53,54	2.47	9 (21%)	44,78,80	2.79	16 (36%)

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
5	SO4	A	815	-	-	0/0/0/0	0/0/0/0
5	SO4	D	816	-	-	0/0/0/0	0/0/0/0
6	1XE	I	5201	3	-	0/42/51/52	0/2/3/3
6	1XE	J	5201	3	-	0/42/51/52	0/2/3/3
6	1XE	K	5201	3	-	0/42/51/52	0/2/3/3
6	1XE	L	5201	3	-	0/42/51/52	0/2/3/3

All (42) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	J	5201	1XE	C1-S1P	-6.58	1.73	1.81
6	K	5201	1XE	C1-S1P	-4.67	1.75	1.81
6	I	5201	1XE	C1-S1P	-3.95	1.76	1.81
6	K	5201	1XE	O3B-C3B	-3.74	1.33	1.41
6	L	5201	1XE	C1-S1P	-3.70	1.76	1.81
6	I	5201	1XE	C1B-N9A	-3.64	1.40	1.46
6	J	5201	1XE	C1B-N9A	-3.58	1.40	1.46
6	L	5201	1XE	C1B-N9A	-3.40	1.40	1.46
6	J	5201	1XE	CDP-CBP	-3.26	1.46	1.53
6	I	5201	1XE	CDP-CBP	-3.08	1.47	1.53
6	L	5201	1XE	CDP-CBP	-3.05	1.47	1.53
6	K	5201	1XE	CDP-CBP	-2.93	1.47	1.53
6	K	5201	1XE	C1B-N9A	-2.92	1.41	1.46
6	I	5201	1XE	O3B-C3B	-2.67	1.35	1.41
6	J	5201	1XE	O3B-C3B	-2.35	1.36	1.41
6	I	5201	1XE	P2A-O4A	2.16	1.59	1.51
6	J	5201	1XE	P2A-O4A	2.21	1.59	1.51
6	I	5201	1XE	O5P-C5P	2.36	1.28	1.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	J	5201	1XE	O2B-C2B	2.98	1.44	1.37
6	I	5201	1XE	O2B-C2B	3.03	1.44	1.37
6	L	5201	1XE	O2B-C2B	3.13	1.44	1.37
6	K	5201	1XE	C3P-N4P	3.16	1.49	1.40
6	K	5201	1XE	O2B-C2B	3.18	1.44	1.37
6	L	5201	1XE	C3P-N4P	3.23	1.49	1.40
6	J	5201	1XE	C6A-N6A	3.24	1.44	1.34
6	I	5201	1XE	C6A-N6A	3.25	1.45	1.34
6	J	5201	1XE	C3P-N4P	3.30	1.49	1.40
6	L	5201	1XE	C6A-N6A	3.31	1.45	1.34
6	K	5201	1XE	C6A-N6A	3.60	1.46	1.34
6	I	5201	1XE	C3P-N4P	3.62	1.50	1.40
6	K	5201	1XE	C5P-N4P	5.38	1.47	1.37
6	J	5201	1XE	C5P-N4P	5.53	1.48	1.37
6	L	5201	1XE	C5P-N4P	5.78	1.48	1.37
6	I	5201	1XE	C5P-N4P	5.80	1.48	1.37
6	I	5201	1XE	C9P-N8P	6.83	1.47	1.33
6	J	5201	1XE	C9P-N8P	7.04	1.48	1.33
6	K	5201	1XE	C9P-N8P	7.07	1.48	1.33
6	L	5201	1XE	C9P-N8P	7.12	1.48	1.33
6	J	5201	1XE	C3P-C2P	7.55	1.49	1.31
6	I	5201	1XE	C3P-C2P	7.93	1.50	1.31
6	K	5201	1XE	C3P-C2P	8.07	1.50	1.31
6	L	5201	1XE	C3P-C2P	8.26	1.50	1.31

All (67) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	J	5201	1XE	N3A-C2A-N1A	-9.00	122.00	128.89
6	I	5201	1XE	N3A-C2A-N1A	-8.94	122.05	128.89
6	L	5201	1XE	N3A-C2A-N1A	-8.54	122.36	128.89
6	I	5201	1XE	C7P-N8P-C9P	-7.03	108.62	122.53
6	K	5201	1XE	N3A-C2A-N1A	-7.00	123.53	128.89
6	J	5201	1XE	C3P-N4P-C5P	-5.83	113.78	123.74
6	K	5201	1XE	P2A-O3A-P1A	-5.36	117.67	132.73
6	I	5201	1XE	P2A-O3A-P1A	-4.61	119.79	132.73
6	J	5201	1XE	P2A-O3A-P1A	-4.35	120.50	132.73
6	J	5201	1XE	C3P-C2P-S1P	-4.35	115.50	124.33
6	K	5201	1XE	C2P-C3P-N4P	-4.15	114.26	124.30
6	K	5201	1XE	C3P-N4P-C5P	-3.88	117.11	123.74
6	L	5201	1XE	C2P-C3P-N4P	-3.74	115.27	124.30
6	I	5201	1XE	C2P-C3P-N4P	-3.57	115.68	124.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	L	5201	1XE	C3P-N4P-C5P	-3.52	117.74	123.74
6	L	5201	1XE	C7P-N8P-C9P	-3.35	115.89	122.53
6	K	5201	1XE	C4A-C5A-N7A	-3.30	106.45	109.48
6	I	5201	1XE	O5P-C5P-N4P	-3.25	115.90	122.54
6	L	5201	1XE	C3P-C2P-S1P	-3.21	117.80	124.33
6	L	5201	1XE	O5P-C5P-N4P	-2.91	116.60	122.54
6	I	5201	1XE	C4A-C5A-N7A	-2.87	106.83	109.48
6	J	5201	1XE	CEP-CBP-CDP	-2.66	103.94	109.28
6	L	5201	1XE	P2A-O3A-P1A	-2.54	125.59	132.73
6	K	5201	1XE	O5P-C5P-N4P	-2.47	117.50	122.54
6	K	5201	1XE	C3P-C2P-S1P	-2.46	119.33	124.33
6	J	5201	1XE	O5P-C5P-N4P	-2.43	117.58	122.54
6	I	5201	1XE	C3P-N4P-C5P	-2.41	119.63	123.74
6	I	5201	1XE	C8A-N9A-C1B	-2.38	122.88	125.39
6	K	5201	1XE	P3B-O3B-C3B	-2.37	115.88	122.97
6	J	5201	1XE	C4A-C5A-N7A	-2.35	107.31	109.48
6	I	5201	1XE	C3P-C2P-S1P	-2.31	119.63	124.33
6	L	5201	1XE	C4A-C5A-N7A	-2.31	107.36	109.48
6	I	5201	1XE	O9P-C9P-N8P	-2.31	118.45	123.08
6	I	5201	1XE	P3B-O3B-C3B	-2.08	116.76	122.97
6	J	5201	1XE	O9P-C9P-N8P	-2.06	118.96	123.08
6	J	5201	1XE	O21-C2-C1	2.09	120.01	110.83
6	L	5201	1XE	O5A-P2A-O3A	2.13	114.77	105.09
6	L	5201	1XE	C2-C1-S1P	2.15	121.57	113.03
6	L	5201	1XE	C7P-C6P-C5P	2.15	115.85	112.31
6	K	5201	1XE	C7P-C6P-C5P	2.27	116.05	112.31
6	I	5201	1XE	CDP-CBP-CCP	2.43	111.65	108.50
6	I	5201	1XE	O3A-P1A-O5B	2.45	109.44	102.94
6	J	5201	1XE	CDP-CBP-CCP	2.62	111.89	108.50
6	I	5201	1XE	CAP-C9P-N8P	2.76	122.58	116.47
6	K	5201	1XE	CDP-CBP-CCP	2.78	112.11	108.50
6	J	5201	1XE	O5B-C5B-C4B	2.93	114.23	109.14
6	J	5201	1XE	CDP-CBP-CAP	3.21	115.20	109.34
6	K	5201	1XE	C6P-C5P-N4P	3.37	122.43	114.99
6	L	5201	1XE	C6P-C5P-N4P	3.69	123.12	114.99
6	I	5201	1XE	C6P-C5P-N4P	3.78	123.32	114.99
6	J	5201	1XE	O3A-P1A-O5B	3.78	112.96	102.94
6	J	5201	1XE	C6P-C5P-N4P	3.85	123.49	114.99
6	I	5201	1XE	O6A-CCP-CBP	3.90	116.82	110.55
6	J	5201	1XE	O6A-CCP-CBP	3.97	116.93	110.55
6	K	5201	1XE	C8A-N9A-C1B	4.19	129.81	125.39
6	J	5201	1XE	C1-S1P-C2P	4.48	107.68	100.33

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Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
6	I	5201	1XE	O5B-C5B-C4B	4.58	117.11	109.14
6	L	5201	1XE	CDP-CBP-CCP	4.81	114.74	108.50
6	K	5201	1XE	O6A-CCP-CBP	5.22	118.94	110.55
6	L	5201	1XE	C6P-C7P-N8P	5.57	124.11	111.88
6	I	5201	1XE	C1-S1P-C2P	5.76	109.80	100.33
6	I	5201	1XE	C6P-C7P-N8P	6.12	125.31	111.88
6	L	5201	1XE	O5B-C5B-C4B	6.58	120.59	109.14
6	K	5201	1XE	C1-S1P-C2P	7.17	112.11	100.33
6	L	5201	1XE	C1-S1P-C2P	7.25	112.24	100.33
6	I	5201	1XE	C7P-C6P-C5P	8.13	125.72	112.31
6	K	5201	1XE	O5B-C5B-C4B	9.26	125.26	109.14

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 17 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	I	5201	1XE	5	0
6	J	5201	1XE	2	0
6	K	5201	1XE	7	0
6	L	5201	1XE	3	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	718/734 (97%)	0.41	42 (5%) 26 20	55, 89, 162, 258	0
1	B	722/734 (98%)	0.71	83 (11%) 6 4	52, 109, 199, 296	0
1	C	717/734 (97%)	0.63	65 (9%) 11 7	52, 104, 191, 257	0
1	D	718/734 (97%)	0.48	63 (8%) 12 8	56, 95, 180, 280	0
2	E	153/156 (98%)	0.43	2 (1%) 79 75	51, 73, 139, 167	0
2	F	153/156 (98%)	0.65	9 (5%) 26 19	58, 104, 168, 207	0
2	G	153/156 (98%)	0.80	10 (6%) 22 16	59, 110, 179, 215	0
2	H	153/156 (98%)	0.42	5 (3%) 50 43	52, 78, 137, 182	0
3	I	4/5 (80%)	0.14	0 100 100	60, 65, 80, 111	0
3	J	4/5 (80%)	0.33	0 100 100	80, 92, 100, 125	0
3	K	4/5 (80%)	0.31	0 100 100	90, 93, 130, 151	0
3	L	4/5 (80%)	0.08	0 100 100	65, 66, 88, 108	0
All	All	3503/3580 (97%)	0.56	279 (7%) 15 10	51, 96, 181, 296	0

All (279) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	731	ALA	17.4
1	C	730	ALA	16.6
1	B	730	ALA	10.9
1	C	370	ASN	10.2
1	A	38	GLU	8.8
1	B	374	GLU	7.9
1	C	351	VAL	7.9
1	B	351	VAL	7.2
1	C	37	LEU	7.1
1	C	371	SER	6.8
1	B	355	ALA	6.6

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Mol	Chain	Res	Type	RSRZ
1	D	730	ALA	6.3
1	B	306	LEU	6.1
1	B	318	TYR	5.9
1	A	730	ALA	5.9
1	A	597	GLY	5.9
1	A	731	ALA	5.8
2	F	66	ASP	5.8
1	C	59	ASN	5.7
1	B	39	ARG	5.7
2	G	66	ASP	5.7
1	C	390	PHE	5.7
1	B	281	TRP	5.5
1	B	370	ASN	5.5
1	C	312	LEU	5.4
1	D	731	ALA	5.4
1	D	59	ASN	5.3
1	D	371	SER	5.2
1	A	42	GLU	5.2
1	D	76	GLY	5.0
1	C	181	PRO	5.0
1	B	69	LEU	5.0
1	B	38	GLU	5.0
1	D	729	ASN	5.0
1	D	179	GLY	4.9
1	C	383	TYR	4.9
1	B	364	PHE	4.7
1	D	71	LEU	4.7
1	C	347	VAL	4.6
2	G	134	ILE	4.6
1	B	347	VAL	4.5
1	B	372	GLN	4.5
1	B	293	PRO	4.4
1	A	370	ASN	4.4
1	C	480	VAL	4.4
1	C	39	ARG	4.3
1	C	306	LEU	4.2
1	A	729	ASN	4.2
1	C	374	GLU	4.2
1	A	369	ASP	4.2
1	C	33	ILE	4.2
1	D	10	GLU	4.1
1	D	182	VAL	4.1

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Mol	Chain	Res	Type	RSRZ
1	B	13	LEU	4.1
1	A	182	VAL	4.1
1	A	373	ILE	4.1
1	D	374	GLU	4.1
1	A	591	PHE	4.1
1	B	305	LYS	4.1
1	B	479	ALA	4.1
1	D	72	ARG	4.0
1	B	368	ASP	4.0
1	C	318	TYR	4.0
1	B	259	TYR	3.9
1	C	13	LEU	3.9
1	C	364	PHE	3.9
1	D	648	LEU	3.9
1	B	729	ASN	3.8
1	A	648	LEU	3.8
1	C	293	PRO	3.8
1	D	409	HIS	3.7
1	B	288	LEU	3.7
1	D	292	TYR	3.7
1	B	390	PHE	3.7
1	A	409	HIS	3.7
1	B	59	ASN	3.6
2	E	1[A]	MET	3.6
1	B	383	TYR	3.6
1	A	39	ARG	3.6
1	C	57	LEU	3.6
1	A	59	ASN	3.6
1	A	480	VAL	3.5
1	C	707	LEU	3.5
1	C	38	GLU	3.5
2	H	66	ASP	3.5
1	B	359	SER	3.5
1	D	363	LYS	3.5
1	C	259	TYR	3.4
1	B	37	LEU	3.4
1	B	58	GLY	3.4
1	B	311	PHE	3.4
1	A	37	LEU	3.4
1	C	368	ASP	3.4
1	A	594	LEU	3.3
1	B	346	VAL	3.3

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Mol	Chain	Res	Type	RSRZ
1	C	649	GLY	3.3
1	C	311	PHE	3.3
1	B	246	TYR	3.3
1	B	312	LEU	3.3
1	C	354	TYR	3.3
1	B	3	LYS	3.3
1	C	479	ALA	3.3
1	D	370	ASN	3.3
2	H	65	LYS	3.2
1	A	694	ASP	3.2
1	C	648	LEU	3.2
1	D	373	ILE	3.2
1	D	177	ASN	3.1
1	B	263	GLN	3.1
1	C	246	TYR	3.1
1	D	81	TRP	3.1
1	B	2	ALA	3.1
1	B	265	ALA	3.1
1	D	728	SER	3.1
1	B	298	PRO	3.0
1	B	338	TYR	3.0
1	B	648	LEU	3.0
1	D	178	GLN	3.0
1	B	313	THR	3.0
1	D	33	ILE	3.0
1	D	233	LEU	3.0
1	D	69	LEU	3.0
1	A	33	ILE	3.0
1	D	480	VAL	2.9
1	D	715	ILE	2.9
1	D	693	PHE	2.9
1	D	42	GLU	2.9
1	B	360	THR	2.9
1	A	293	PRO	2.9
1	D	30	LEU	2.9
1	B	36	LEU	2.9
1	C	369	ASP	2.9
1	A	371	SER	2.8
1	B	242	LYS	2.8
1	D	369	ASP	2.8
2	F	146	TYR	2.8
1	A	57	LEU	2.8

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Mol	Chain	Res	Type	RSRZ
1	B	181	PRO	2.8
1	C	627	GLU	2.8
1	B	303	LEU	2.8
1	A	576	LEU	2.8
1	B	319	LEU	2.8
1	D	53	LEU	2.8
1	B	603	GLU	2.8
2	G	1	MET	2.8
2	G	146	TYR	2.8
2	G	153	SER	2.8
2	G	135	GLU	2.7
1	A	686	LEU	2.7
1	B	354	TYR	2.7
1	C	338	TYR	2.7
1	B	649	GLY	2.7
1	D	721	TYR	2.7
1	B	280	GLU	2.7
1	B	337	LEU	2.7
1	B	396	LEU	2.7
1	C	282	LEU	2.7
1	A	290	LYS	2.7
1	D	279	ALA	2.7
1	A	233	LEU	2.7
1	A	707	LEU	2.6
1	B	30	LEU	2.6
1	A	683	ALA	2.6
1	D	364	PHE	2.6
1	A	328	PRO	2.6
1	C	69	LEU	2.6
1	B	597	GLY	2.6
1	C	647	PRO	2.6
1	D	17	ALA	2.6
1	A	314	HIS	2.6
1	C	285	TYR	2.5
1	D	293	PRO	2.5
1	B	33	ILE	2.5
2	H	121	HIS	2.5
1	C	32	ALA	2.5
1	A	479	ALA	2.5
1	D	267	GLY	2.5
1	C	224	PHE	2.5
2	F	112	VAL	2.5

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Mol	Chain	Res	Type	RSRZ
1	B	707	LEU	2.5
1	A	292	TYR	2.5
2	G	123	TYR	2.5
1	C	281	TRP	2.5
1	D	115	LEU	2.5
1	D	329	SER	2.5
1	D	725	LYS	2.4
1	A	54	LEU	2.4
1	B	373	ILE	2.4
2	F	123	TYR	2.4
1	B	385	PHE	2.4
1	D	700	LEU	2.4
1	B	302	PRO	2.4
1	C	319	LEU	2.4
1	D	360	THR	2.4
1	C	373	ILE	2.4
1	A	69	LEU	2.4
2	F	85	LEU	2.4
1	C	355	ALA	2.4
1	B	297	CYS	2.4
1	D	720	PHE	2.4
1	B	317	LEU	2.4
2	F	86	GLY	2.3
1	D	692	ASN	2.3
1	B	285	TYR	2.3
1	D	351	VAL	2.3
1	A	360	THR	2.3
1	C	315	VAL	2.3
1	B	339	LYS	2.3
1	C	317	LEU	2.3
1	C	372	GLN	2.3
1	B	334	VAL	2.3
1	D	180	VAL	2.3
1	B	728	SER	2.3
1	B	384	TYR	2.3
1	D	67	VAL	2.3
1	B	14	PHE	2.2
2	F	117	ARG	2.2
2	H	1	MET	2.2
1	B	309	ASP	2.2
1	A	708	GLY	2.2
1	B	341	THR	2.2

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	A	644	ASP	2.2
1	C	309	ASP	2.2
1	C	710	ASN	2.2
1	A	179	GLY	2.2
2	H	17	CYS	2.2
1	D	110	ASN	2.2
2	E	66	ASP	2.2
1	B	389	HIS	2.2
1	C	211	LEU	2.2
2	G	122	LEU	2.2
1	D	173	GLU	2.2
1	B	454	CYS	2.2
1	C	344	CYS	2.2
1	D	479	ALA	2.2
2	G	137	LYS	2.2
1	D	416	LEU	2.2
1	A	367	ASP	2.2
1	D	714	VAL	2.2
1	C	727	GLN	2.2
1	A	62	GLU	2.2
1	B	601	GLU	2.2
1	B	627	GLU	2.2
1	C	288	LEU	2.2
1	C	35	PRO	2.2
1	D	8	PRO	2.2
1	D	238	MET	2.1
1	C	305	LYS	2.1
1	C	53	LEU	2.1
1	D	686	LEU	2.1
1	D	707	LEU	2.1
1	C	265	ALA	2.1
1	C	398	LYS	2.1
1	C	36	LEU	2.1
1	B	647	PRO	2.1
1	A	50	LYS	2.1
1	B	386	LEU	2.1
1	C	417	PHE	2.1
1	C	360	THR	2.1
2	F	13	GLY	2.1
1	D	703	ALA	2.1
1	B	344	CYS	2.1
1	C	445	LEU	2.1

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Mol	Chain	Res	Type	RSRZ
1	C	365	SER	2.1
1	D	39	ARG	2.0
2	G	105	ALA	2.0
1	D	38	GLU	2.0
1	B	343	LYS	2.0
1	B	35	PRO	2.0
1	C	298	PRO	2.0
1	D	35	PRO	2.0
1	B	393	VAL	2.0
1	D	118	LEU	2.0
1	B	365	SER	2.0
1	B	72	ARG	2.0
2	F	63	GLU	2.0
1	B	403	VAL	2.0
1	C	178	GLN	2.0
1	D	722	ASN	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(Å <sup>2</sup> )	Q<0.9
4	CL	C	812	1/1	0.82	0.74	17.95	126,126,126,126	0
4	CL	D	814	1/1	0.95	0.54	15.42	110,110,110,110	0
4	CL	D	805	1/1	0.12	1.50	12.87	288,288,288,288	0
4	CL	A	801	1/1	0.94	0.49	11.12	96,96,96,96	0
4	CL	B	802	1/1	0.99	0.33	5.97	96,96,96,96	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
4	CL	B	804	1/1	0.81	0.41	4.94	107,107,107,107	0
4	CL	C	802	1/1	0.91	0.32	4.54	106,106,106,106	0
4	CL	B	805	1/1	0.83	0.24	3.21	108,108,108,108	0
4	CL	D	815	1/1	0.87	0.27	1.46	105,105,105,105	0
4	CL	C	811	1/1	0.95	0.19	0.51	94,94,94,94	0
6	1XE	K	5201	51/52	0.89	0.21	0.35	53,128,279,303	0
6	1XE	I	5201	51/52	0.93	0.22	0.20	49,92,190,217	0
6	1XE	L	5201	51/52	0.94	0.21	0.05	49,92,179,181	0
6	1XE	J	5201	51/52	0.89	0.20	-0.12	67,142,228,241	0
5	SO4	D	816	5/5	0.92	0.13	-1.30	80,110,119,124	0
4	CL	D	801	1/1	0.91	0.11	-2.29	93,93,93,93	0
5	SO4	A	815	5/5	0.98	0.11	-2.42	88,104,110,121	0
4	CL	D	812	1/1	0.75	0.22	-	138,138,138,138	0
4	CL	A	808	1/1	0.78	0.36	-	113,113,113,113	0
4	CL	D	807	1/1	0.74	0.28	-	173,173,173,173	0
4	CL	D	809	1/1	0.78	0.25	-	127,127,127,127	0
4	CL	D	802	1/1	0.70	0.18	-	149,149,149,149	0
4	CL	A	807	1/1	0.57	0.29	-	148,148,148,148	0
4	CL	D	806	1/1	0.63	0.49	-	139,139,139,139	0
4	CL	E	202	1/1	0.62	0.31	-	102,102,102,102	0
4	CL	C	810	1/1	0.95	0.35	-	97,97,97,97	0
4	CL	A	803	1/1	0.93	0.08	-	99,99,99,99	0
4	CL	B	806	1/1	0.59	0.61	-	151,151,151,151	0
4	CL	A	804	1/1	0.58	0.08	-	143,143,143,143	0
4	CL	B	811	1/1	0.98	0.37	-	99,99,99,99	0
4	CL	D	808	1/1	0.89	0.39	-	131,131,131,131	0
4	CL	B	814	1/1	0.87	0.18	-	141,141,141,141	0
4	CL	B	810	1/1	0.90	0.30	-	99,99,99,99	0
4	CL	A	802	1/1	0.97	0.19	-	93,93,93,93	0
4	CL	C	808	1/1	0.84	0.26	-	110,110,110,110	0
4	CL	D	813	1/1	0.77	0.41	-	130,130,130,130	0
4	CL	C	806	1/1	0.83	0.12	-	117,117,117,117	0
4	CL	A	806	1/1	0.88	0.17	-	145,145,145,145	0
4	CL	B	808	1/1	-0.39	0.18	-	161,161,161,161	0
4	CL	C	809	1/1	0.84	0.10	-	151,151,151,151	0
4	CL	A	811	1/1	0.82	0.65	-	188,188,188,188	0
4	CL	B	801	1/1	0.79	0.14	-	127,127,127,127	0
4	CL	A	814	1/1	0.90	0.10	-	120,120,120,120	0
4	CL	B	816	1/1	0.82	0.11	-	107,107,107,107	0
4	CL	B	812	1/1	0.88	0.34	-	112,112,112,112	0
4	CL	G	201	1/1	0.79	0.13	-	133,133,133,133	0
4	CL	C	804	1/1	0.72	0.22	-	118,118,118,118	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
4	CL	C	807	1/1	0.66	0.41	-	125,125,125,125	0
4	CL	C	805	1/1	0.85	0.10	-	119,119,119,119	0
4	CL	D	803	1/1	0.28	0.43	-	118,118,118,118	0
4	CL	A	812	1/1	0.12	0.26	-	141,141,141,141	0
4	CL	A	805	1/1	0.91	0.23	-	138,138,138,138	0
4	CL	D	804	1/1	0.62	0.21	-	132,132,132,132	0
4	CL	D	811	1/1	0.98	0.24	-	73,73,73,73	0
4	CL	A	809	1/1	0.77	0.15	-	125,125,125,125	0
4	CL	A	813	1/1	0.96	0.18	-	124,124,124,124	0
4	CL	B	813	1/1	0.63	0.86	-	145,145,145,145	0
4	CL	B	809	1/1	0.89	0.19	-	109,109,109,109	0
4	CL	C	803	1/1	0.41	0.18	-	129,129,129,129	0
4	CL	C	813	1/1	0.10	0.23	-	137,137,137,137	0
4	CL	A	810	1/1	0.86	0.41	-	86,86,86,86	0
4	CL	E	201	1/1	0.97	0.27	-	79,79,79,79	0
4	CL	B	815	1/1	0.78	0.26	-	192,192,192,192	0
4	CL	E	203	1/1	0.87	0.14	-	110,110,110,110	0
4	CL	B	807	1/1	0.59	0.68	-	140,140,140,140	0
4	CL	D	810	1/1	0.71	0.30	-	157,157,157,157	0
4	CL	B	803	1/1	0.91	0.12	-	99,99,99,99	0
4	CL	C	801	1/1	0.81	0.09	-	111,111,111,111	0
4	CL	H	201	1/1	0.95	0.27	-	84,84,84,84	0
4	CL	F	201	1/1	0.56	0.91	-	148,148,148,148	0

## 6.5 Other polymers

There are no such residues in this entry.