



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 15, 2017 – 05:37 am GMT

PDB ID : 5EUY  
Title : Thermostable aldehyde dehydrogenase from *Pyrobaculum* sp.1860 complexed with NADP+  
Authors : Petrova, T.; Bezsudnova, E.Y.; Boyko, K.M.; Nikolaeva, A.Y.; Rakitina, T.V.; Popov, V.O.  
Deposited on : 2015-11-19  
Resolution : 2.06 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.

---

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.7.2 (RC1), CSD as538be (2017)  
Xtriage (Phenix) : 1.9-1692  
EDS : trunk28620  
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)  
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) : recalc28949

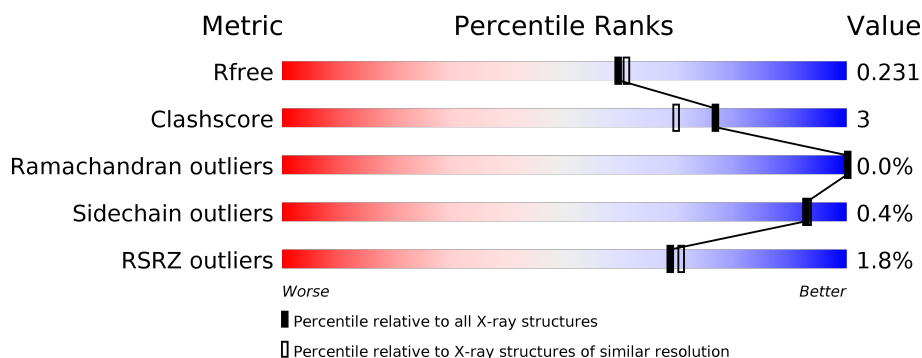
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.06 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.



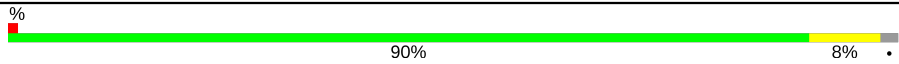
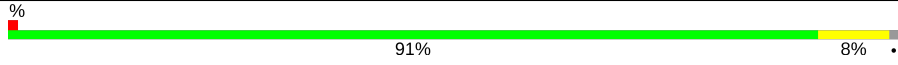
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	100719	2028 (2.08-2.04)
Clashscore	112137	2143 (2.08-2.04)
Ramachandran outliers	110173	2126 (2.08-2.04)
Sidechain outliers	110143	2126 (2.08-2.04)
RSRZ outliers	101464	2035 (2.08-2.04)

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	491	<div> <div>2%</div> <div> <div></div> <div>91%</div> <div>8%</div> </div> </div>
1	B	491	<div> <div>%</div> <div> <div></div> <div>92%</div> <div>7%</div> </div> </div>
1	C	491	<div> <div>3%</div> <div> <div></div> <div>90%</div> <div>9%</div> </div> </div>
1	D	491	<div> <div>%</div> <div> <div></div> <div>90%</div> <div>9%</div> </div> </div>
1	E	491	<div> <div>3%</div> <div> <div></div> <div>92%</div> <div>8%</div> </div> </div>
1	F	491	<div> <div>2%</div> <div> <div></div> <div>87%</div> <div>11%</div> </div> </div>

Continued on next page...

*Continued from previous page...*

Mol	Chain	Length	Quality of chain
1	G	491	 90% 8%
1	H	491	 91% 8%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	NAP	B	500[B]	-	-	-	X
2	NAP	D	500[A]	-	-	-	X
2	NAP	D	500[B]	-	-	-	X

## 2 Entry composition

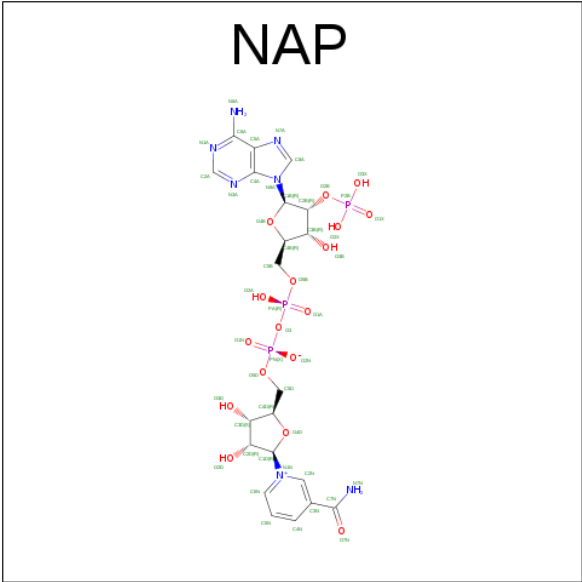
There are 3 unique types of molecules in this entry. The entry contains 33662 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Aldehyde dehydrogenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	485	Total	C	N	O	S	0	8	1
			3789	2416	661	699	13			
1	B	488	Total	C	N	O	S	0	7	1
			3812	2429	663	708	12			
1	C	485	Total	C	N	O	S	0	10	1
			3811	2425	664	709	13			
1	D	483	Total	C	N	O	S	0	7	0
			3769	2401	656	700	12			
1	E	490	Total	C	N	O	S	0	8	0
			3821	2433	667	708	13			
1	F	485	Total	C	N	O	S	0	6	0
			3793	2419	660	701	13			
1	G	482	Total	C	N	O	S	0	10	0
			3775	2407	654	702	12			
1	H	485	Total	C	N	O	S	0	6	1
			3784	2410	660	701	13			

- Molecule 2 is NADP NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (three-letter code: NAP) (formula: C<sub>21</sub>H<sub>28</sub>N<sub>7</sub>O<sub>17</sub>P<sub>3</sub>).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	1
			51	20	5	22	4		
2	B	1	Total	C	N	O	P	0	1
			51	20	5	22	4		
2	C	1	Total	C	N	O	P	0	1
			51	20	5	22	4		
2	D	1	Total	C	N	O	P	0	1
			51	20	5	22	4		
2	E	1	Total	C	N	O	P	0	1
			51	20	5	22	4		
2	F	1	Total	C	N	O	P	0	1
			51	20	5	22	4		
2	G	1	Total	C	N	O	P	0	1
			51	20	5	22	4		
2	H	1	Total	C	N	O	P	0	1
			51	20	5	22	4		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	403	Total	O	0	0
			403	403		
3	B	395	Total	O	0	0
			395	395		
3	C	323	Total	O	0	0
			323	323		
3	D	372	Total	O	0	0
			372	372		

Continued on next page...

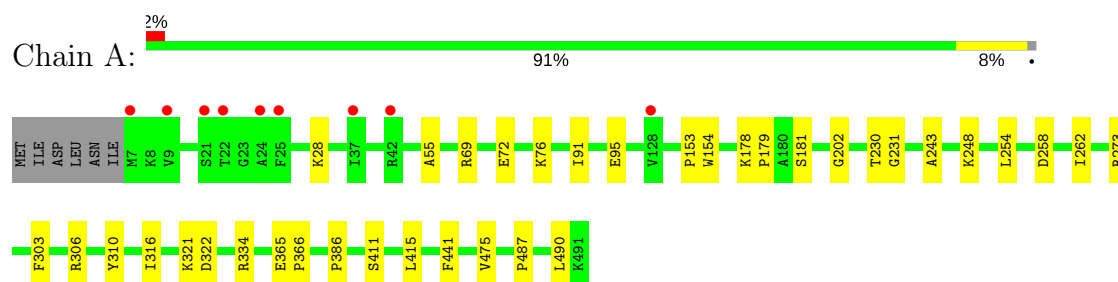
*Continued from previous page...*

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	E	342	Total 342	O 342	0	0
3	F	329	Total 329	O 329	0	0
3	G	382	Total 382	O 382	0	0
3	H	354	Total 354	O 354	0	0

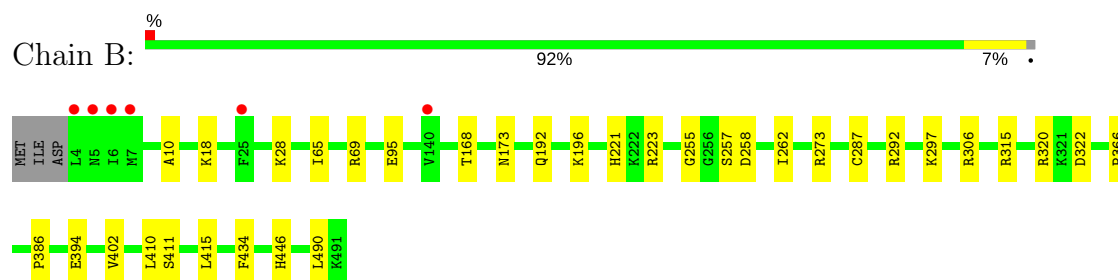
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes 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.

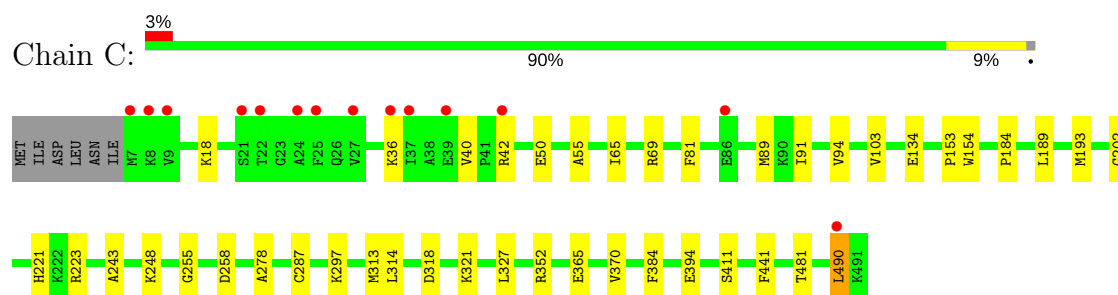
- Molecule 1: Aldehyde dehydrogenase



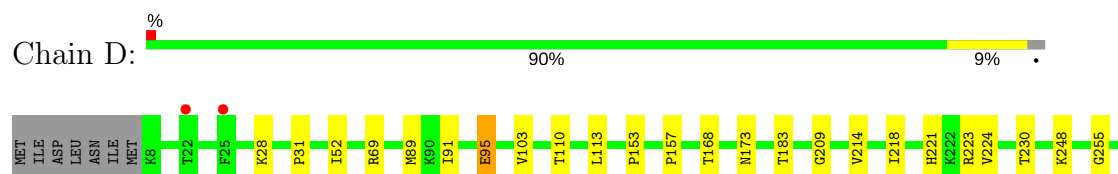
- Molecule 1: Aldehyde dehydrogenase



- Molecule 1: Aldehyde dehydrogenase



- Molecule 1: Aldehyde dehydrogenase

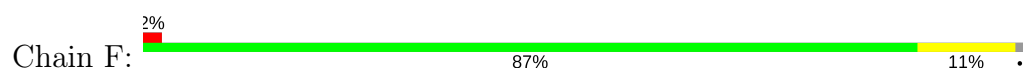




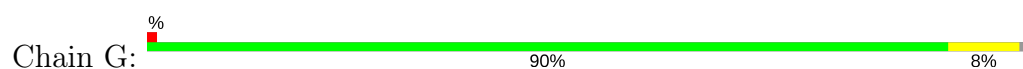
● Molecule 1: Aldehyde dehydrogenase



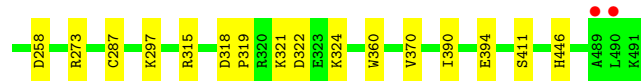
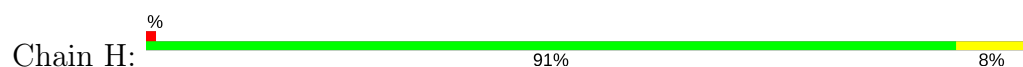
● Molecule 1: Aldehyde dehydrogenase



● Molecule 1: Aldehyde dehydrogenase



● Molecule 1: Aldehyde dehydrogenase





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	184.77Å 208.05Å 165.40Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	59.06 – 2.06 59.06 – 2.06	Depositor EDS
% Data completeness (in resolution range)	99.3 (59.06-2.06) 99.4 (59.06-2.06)	Depositor EDS
$R_{merge}$	0.10	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.01 (at 2.07Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.4_1496)	Depositor
R, $R_{free}$	0.196 , 0.233 0.195 , 0.231	Depositor DCC
$R_{free}$ test set	2016 reflections (0.52%)	DCC
Wilson B-factor (Å <sup>2</sup> )	35.3	Xtriage
Anisotropy	0.025	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 47.8	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	33662	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	37.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 45.30 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 1.3478e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<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, 0.333 respectively for untwinned datasets, and 0.375, 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: NAP

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	0.41	0/3896	0.52	0/5280
1	B	0.41	0/3913	0.53	0/5305
1	C	0.39	0/3918	0.51	0/5313
1	D	0.42	0/3873	0.53	0/5253
1	E	0.39	0/3922	0.52	0/5317
1	F	0.40	0/3894	0.53	0/5278
1	G	0.41	0/3888	0.52	1/5274 (0.0%)
1	H	0.40	0/3885	0.51	0/5266
All	All	0.40	0/31189	0.52	1/42286 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	292	ARG	NE-CZ-NH2	-5.21	117.69	120.30

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	3789	0	3785	28	0
1	B	3812	0	3798	20	0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	3811	0	3789	26	0
1	D	3769	0	3743	29	0
1	E	3821	0	3806	29	0
1	F	3793	0	3796	34	0
1	G	3775	0	3755	30	0
1	H	3784	0	3771	27	0
2	A	51	0	12	4	0
2	B	51	0	12	1	0
2	C	51	0	12	3	0
2	D	51	0	12	2	0
2	E	51	0	12	5	0
2	F	51	0	12	4	0
2	G	51	0	12	5	0
2	H	51	0	11	3	0
3	A	403	0	0	1	0
3	B	395	0	0	0	1
3	C	323	0	0	2	0
3	D	372	0	0	2	1
3	E	342	0	0	2	0
3	F	329	0	0	1	0
3	G	382	0	0	0	0
3	H	354	0	0	2	0
All	All	33662	0	30338	214	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 3.

All (214) 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:334:ARG:HE	2:A:500[B]:NAP:H2D	1.48	0.78
1:H:297:LYS:HE2	1:H:394:GLU:HG2	1.65	0.76
1:F:315:ARG:NH2	1:F:322:ASP:OD2	2.21	0.74
1:F:28:LYS:HE2	1:F:95:GLU:HG3	1.69	0.72
1:F:233:SER:HA	1:F:254:LEU:HG	1.75	0.69
1:F:154:TRP:HE1	2:F:500[B]:NAP:H4D	1.56	0.68
1:E:221:HIS:HE1	1:E:223:ARG:HG3	1.59	0.66
1:B:297:LYS:HD3	1:B:394:GLU:HG2	1.78	0.66
1:C:154:TRP:HE1	2:C:500[B]:NAP:H4D	1.60	0.65
1:H:255[B]:GLY:HA2	1:H:287[B]:CYS:HB3	1.77	0.64
1:B:315:ARG:NH2	1:B:322:ASP:OD1	2.24	0.63

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:154:TRP:HE1	2:H:500[B]:NAP:H4D	1.63	0.63
1:A:316:ILE:HD12	1:A:365:GLU:HG2	1.80	0.62
1:A:178:LYS:NZ	1:A:179:PRO:O	2.32	0.61
1:A:154:TRP:HE1	2:A:500[B]:NAP:H4D	1.65	0.61
1:A:487:PRO:HD2	1:A:490:LEU:HD12	1.81	0.61
1:E:28:LYS:HE2	1:E:95:GLU:HG3	1.83	0.61
1:A:28[B]:LYS:HE2	1:A:95:GLU:HG3	1.83	0.60
1:D:69[A]:ARG:NH2	3:D:601:HOH:O	2.30	0.59
1:B:258:ASP:OD2	1:B:411:SER:HB3	2.03	0.58
1:H:315:ARG:NH2	1:H:322:ASP:OD2	2.25	0.58
1:B:221:HIS:HE1	1:B:223:ARG:HG3	1.69	0.58
1:F:154:TRP:NE1	2:F:500[B]:NAP:H4D	2.19	0.57
1:C:313:MET:HE1	1:D:490:LEU:HD13	1.87	0.57
1:G:318:ASP:HB3	1:G:321:LYS:HG3	1.86	0.57
1:A:490:LEU:HD13	1:B:273:ARG:NH1	2.20	0.57
1:B:28:LYS:HE2	1:B:95:GLU:HG3	1.87	0.57
1:E:315:ARG:NH2	1:E:322:ASP:OD2	2.34	0.57
1:G:315:ARG:NH2	1:G:322:ASP:OD2	2.36	0.57
1:C:255[B]:GLY:HA2	1:C:287[B]:CYS:HB3	1.85	0.57
1:F:334:ARG:HH11	2:F:500[B]:NAP:H2D	1.68	0.57
1:E:154:TRP:HE1	2:E:500[B]:NAP:H4D	1.70	0.56
1:G:221:HIS:HE1	1:G:223:ARG:HG3	1.70	0.56
1:H:221:HIS:HE1	1:H:223:ARG:HG3	1.69	0.56
1:G:292:ARG:NH2	1:G:402:VAL:O	2.38	0.56
1:E:223:ARG:HD3	3:E:841:HOH:O	2.04	0.56
1:G:130:GLN:O	1:H:446:HIS:HE1	1.90	0.55
1:D:305:GLU:OE1	1:D:306:ARG:NH1	2.40	0.55
1:G:27:VAL:HG11	1:G:36:LYS:HG3	1.87	0.55
1:E:154:TRP:NE1	2:E:500[B]:NAP:H4D	2.22	0.55
1:G:28:LYS:HE2	1:G:95:GLU:HG3	1.89	0.55
1:C:91:ILE:HA	1:C:94:VAL:HG12	1.90	0.54
1:H:154:TRP:NE1	2:H:500[B]:NAP:H4D	2.22	0.54
1:E:305:GLU:OE2	1:E:306:ARG:NH1	2.40	0.54
1:G:384:PHE:CE1	2:G:500[A]:NAP:H2D	2.42	0.54
1:C:490:LEU:HD11	1:D:310:TYR:CE1	2.43	0.54
1:G:68:ILE:HG23	1:G:69:ARG:HH11	1.73	0.54
1:G:243:ALA:HB1	1:G:248:LYS:HG3	1.89	0.54
1:A:154:TRP:NE1	2:A:500[B]:NAP:H4D	2.23	0.53
1:C:154:TRP:NE1	2:C:500[B]:NAP:H4D	2.23	0.53
1:G:318:ASP:OD1	1:G:320:ARG:HD3	2.08	0.53
1:A:262:ILE:HG12	1:A:415:LEU:HD12	1.91	0.53

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:178:LYS:NZ	1:E:179:PRO:O	2.41	0.53
1:E:221:HIS:CE1	1:E:223:ARG:HG3	2.40	0.53
1:C:65:ILE:HD12	1:C:69[B]:ARG:HB3	1.90	0.53
1:D:31:PRO:HB3	1:D:331:ILE:O	2.09	0.53
1:E:255[A]:GLY:HA2	2:E:500[A]:NAP:O2D	2.09	0.53
1:C:89:MET:HE3	1:C:103:VAL:HG23	1.91	0.52
1:B:262:ILE:HG12	1:B:415:LEU:HD12	1.90	0.52
1:D:224:VAL:O	1:D:248:LYS:HE3	2.09	0.52
1:E:258:ASP:OD2	1:E:411:SER:HB3	2.09	0.52
1:E:91:ILE:O	1:E:95:GLU:HB3	2.10	0.52
1:F:65:ILE:HD12	1:F:69:ARG:HB3	1.92	0.52
1:G:490:LEU:HD13	1:H:273:ARG:NH1	2.24	0.52
1:F:243:ALA:HB1	1:F:248:LYS:HG3	1.92	0.52
1:E:472:ASP:OD2	1:F:464:TRP:NE1	2.39	0.51
1:F:122:ARG:NH2	1:H:446:HIS:CD2	2.78	0.51
1:G:312:LYS:HG3	1:G:355:ILE:HD11	1.93	0.51
1:H:49:ARG:NH2	3:H:601:HOH:O	2.29	0.51
1:D:258:ASP:OD2	1:D:411:SER:HB3	2.11	0.51
1:G:154:TRP:HE1	2:G:500[B]:NAP:H4D	1.75	0.51
1:A:273:ARG:NH1	1:B:490:LEU:HD13	2.25	0.51
1:H:76:LYS:NZ	3:H:604:HOH:O	2.45	0.50
1:D:168:THR:HG22	1:D:173:ASN:HB2	1.92	0.50
1:D:209:GLY:HA3	1:D:214:VAL:HG21	1.94	0.50
1:A:321:LYS:HG2	1:A:322:ASP:OD2	2.12	0.50
1:F:316:ILE:HD12	1:F:365:GLU:HG2	1.94	0.50
1:E:255[B]:GLY:HA2	1:E:287[B]:CYS:HB3	1.94	0.50
1:A:334:ARG:HH21	2:A:500[B]:NAP:C1D	2.25	0.49
1:D:221:HIS:HE1	1:D:223:ARG:HG3	1.77	0.48
1:H:221:HIS:CE1	1:H:223:ARG:HG3	2.48	0.48
1:G:255[A]:GLY:HA2	2:G:500[A]:NAP:O2D	2.12	0.48
1:C:55:ALA:HA	1:C:202:GLY:O	2.13	0.48
1:D:263:LEU:HD12	1:D:416:THR:HB	1.95	0.48
1:C:314:LEU:HD13	1:C:327:LEU:HD11	1.96	0.48
1:D:315:ARG:NH2	1:D:322:ASP:OD2	2.36	0.48
1:A:310:TYR:CE1	1:B:490:LEU:HD11	2.48	0.48
1:C:243:ALA:HB1	1:C:248:LYS:HG3	1.96	0.48
1:C:297:LYS:HD3	1:C:394:GLU:HG2	1.95	0.47
1:F:184:PRO:HB2	1:F:208:ILE:HD13	1.95	0.47
1:E:384:PHE:CE1	2:E:500[A]:NAP:H2D	2.50	0.47
1:H:318:ASP:HB3	1:H:321:LYS:HG3	1.96	0.47
1:B:255[B]:GLY:HA2	1:B:287[B]:CYS:HB3	1.97	0.47

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:287[A]:CYS:SG	3:D:788:HOH:O	2.60	0.47
1:A:231:GLY:O	1:A:254[A]:LEU:HA	2.15	0.47
1:C:221:HIS:HE1	1:C:223:ARG:HG3	1.78	0.47
1:D:28:LYS:HE2	1:D:95:GLU:HG3	1.96	0.47
1:A:306:ARG:HA	1:A:306:ARG:HD3	1.70	0.47
1:H:258:ASP:OD2	1:H:411:SER:HB3	2.15	0.47
1:C:318:ASP:HB3	1:C:321:LYS:HG3	1.97	0.47
1:D:110:THR:HA	1:D:113:LEU:HD12	1.96	0.47
1:D:370:VAL:HG12	1:D:390:ILE:HB	1.96	0.47
1:E:269:ASP:OD1	1:E:310:TYR:OH	2.28	0.47
1:E:334:ARG:HD2	2:E:500[B]:NAP:H2D	1.96	0.47
1:H:55:ALA:HA	1:H:202:GLY:O	2.15	0.47
1:E:42:ARG:NH1	1:E:42:ARG:HG2	2.30	0.46
1:F:224:VAL:O	1:F:248:LYS:HE3	2.15	0.46
1:D:306:ARG:HA	1:D:306:ARG:HD3	1.60	0.46
1:A:91:ILE:O	1:A:95:GLU:HB3	2.16	0.46
1:H:324:LYS:HE3	1:H:324:LYS:HB3	1.71	0.46
1:F:318:ASP:O	1:F:321:LYS:HG3	2.15	0.46
1:F:254:LEU:HD22	1:F:456:GLY:HA2	1.97	0.46
1:C:278:ALA:HA	1:C:441:PHE:CE2	2.50	0.46
1:D:384:PHE:CE1	2:D:500[A]:NAP:H2D	2.51	0.46
1:F:269:ASP:HA	1:F:306:ARG:HG2	1.98	0.46
1:C:481:THR:HB	1:D:270:TYR:CE1	2.51	0.46
1:E:243:ALA:HB1	1:E:248:LYS:HG3	1.98	0.45
1:G:221:HIS:CE1	1:G:223:ARG:HG3	2.49	0.45
1:H:76:LYS:HE3	1:H:197:ALA:HA	1.98	0.45
1:G:154:TRP:NE1	2:G:500[B]:NAP:H4D	2.32	0.45
1:G:305:GLU:OE1	1:G:306:ARG:NH1	2.50	0.45
1:D:333:GLU:HG2	1:D:334:ARG:N	2.31	0.45
1:E:45:ARG:NH1	3:E:610:HOH:O	2.50	0.45
1:F:89:MET:HG3	1:F:107:VAL:HG21	1.98	0.45
1:G:331:ILE:HG22	1:G:335:GLN:HG3	1.99	0.45
1:F:424[B]:ARG:HD2	3:F:761:HOH:O	2.16	0.45
1:B:306:ARG:HD3	1:B:306:ARG:HA	1.63	0.44
1:F:423:PHE:HZ	1:G:423:PHE:HZ	1.65	0.44
1:G:231:GLY:O	1:G:254[A]:LEU:HA	2.17	0.44
1:A:55:ALA:HA	1:A:202:GLY:O	2.18	0.44
1:B:65:ILE:HD12	1:B:69[B]:ARG:HB3	2.00	0.44
1:E:168:THR:HG22	1:E:173:ASN:HB2	2.00	0.44
1:G:20:PRO:HD3	1:G:41:PRO:HB3	1.99	0.44
1:F:302:LYS:HE2	1:F:302:LYS:HB3	1.75	0.44

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:42:ARG:HG2	1:E:42:ARG:HH11	1.82	0.44
1:B:168:THR:HG22	1:B:173:ASN:HB2	2.00	0.44
1:F:258:ASP:OD2	1:F:411:SER:HB3	2.17	0.44
1:H:93:THR:HG23	1:H:319:PRO:HB2	1.99	0.44
1:C:40:VAL:HG11	1:C:184:PRO:HG2	1.98	0.44
1:D:255[B]:GLY:HA2	1:D:287[B]:CYS:HB3	2.00	0.44
1:H:115:GLN:O	1:H:119:GLU:HG3	2.17	0.44
1:C:352:ARG:HB3	1:C:370:VAL:HG23	2.00	0.43
1:F:337:ALA:O	1:F:341:GLU:HG3	2.18	0.43
1:F:76:LYS:HD2	1:F:197:ALA:O	2.18	0.43
1:E:13:ILE:HG23	1:E:51:ALA:HA	1.99	0.43
1:G:255[B]:GLY:HA2	1:G:287[B]:CYS:HB3	2.00	0.43
1:G:321:LYS:HE3	1:G:321:LYS:HB3	1.78	0.43
1:D:153:PRO:HG3	1:D:230:THR:HG22	2.00	0.43
1:F:221:HIS:HE1	1:F:223:ARG:HG3	1.83	0.43
1:C:384:PHE:CE1	2:C:500[A]:NAP:H2D	2.54	0.43
1:A:475:VAL:HA	1:B:434:PHE:O	2.19	0.43
1:F:255:GLY:HA2	2:F:500[A]:NAP:O2D	2.19	0.43
1:E:143:ARG:HB3	1:E:143:ARG:HE	1.59	0.42
1:F:356:GLY:HA3	1:F:366:PRO:O	2.20	0.42
1:H:20:PRO:HD3	1:H:41:PRO:HB3	2.00	0.42
1:H:224:VAL:O	1:H:248:LYS:HE3	2.19	0.42
1:A:258:ASP:OD2	1:A:411:SER:HB3	2.19	0.42
1:H:13:ILE:HG21	1:H:50:GLU:HG2	2.02	0.42
1:D:157:PRO:HG3	1:D:183:THR:HG21	2.01	0.42
1:E:366:PRO:HA	1:E:386:PRO:O	2.20	0.42
1:A:28[A]:LYS:HE2	1:A:181:SER:O	2.20	0.42
1:E:420:ASN:O	1:E:424:ARG:HB2	2.19	0.42
1:B:257:SER:OG	1:B:292:ARG:HD2	2.19	0.42
1:C:91:ILE:HG13	1:C:189:LEU:HD11	2.01	0.42
1:D:91:ILE:O	1:D:95:GLU:HB3	2.19	0.42
1:H:231:GLY:O	1:H:254[A]:LEU:HA	2.20	0.42
1:H:28:LYS:HE2	1:H:95:GLU:HG3	2.01	0.42
1:F:153:PRO:HD3	1:F:230:THR:HB	2.01	0.42
1:C:134:GLU:HG3	3:C:745:HOH:O	2.19	0.42
1:C:69[B]:ARG:HA	1:C:69[B]:ARG:HD3	1.80	0.42
1:D:89:MET:HE3	1:D:103:VAL:HG23	2.02	0.42
1:F:31:PRO:HD2	1:F:94:VAL:O	2.20	0.42
1:D:52:ILE:HD11	1:D:218:ILE:HA	2.02	0.41
1:H:91:ILE:O	1:H:95:GLU:HB3	2.20	0.41
1:A:28[A]:LYS:HE3	3:A:796:HOH:O	2.19	0.41

*Continued on next page...*



Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:366:PRO:HA	1:B:386:PRO:HB2	2.02	0.41
1:C:258:ASP:OD2	1:C:411:SER:HB3	2.21	0.41
1:F:210:PRO:HG2	1:F:213:VAL:HB	2.01	0.41
1:F:55:ALA:HA	1:F:202:GLY:O	2.20	0.41
1:C:365[B]:GLU:HG2	3:C:667:HOH:O	2.19	0.41
1:D:153:PRO:HD3	1:D:230:THR:HB	2.03	0.41
1:G:178:LYS:NZ	1:G:179:PRO:O	2.33	0.41
1:A:153:PRO:HG3	1:A:230:THR:HG22	2.02	0.41
1:A:76:LYS:HD2	1:A:76:LYS:HA	1.72	0.41
1:B:10:ALA:HB1	1:B:18:LYS:O	2.20	0.41
1:A:366:PRO:HA	1:A:386:PRO:O	2.20	0.41
1:G:217:GLU:O	1:G:221:HIS:HB2	2.20	0.41
1:G:360:TRP:HZ3	1:G:365[B]:GLU:HG3	1.85	0.41
1:G:91:ILE:O	1:G:95:GLU:HB3	2.21	0.41
1:A:243:ALA:HB1	1:A:248:LYS:HG3	2.03	0.41
1:B:192:GLN:O	1:B:196:LYS:HG3	2.21	0.41
1:F:91:ILE:O	1:F:95:GLU:HB3	2.21	0.41
1:C:81:PHE:HB2	1:C:193:MET:SD	2.61	0.41
1:D:490:LEU:HD12	1:D:490:LEU:HA	1.88	0.41
1:A:262:ILE:HD13	1:A:303:PHE:CE1	2.55	0.41
1:F:46:GLU:OE1	1:F:49:ARG:NH1	2.53	0.41
1:G:485:PRO:HB2	1:H:101:ARG:HG2	2.02	0.41
1:D:315:ARG:HH22	1:D:322:ASP:CG	2.22	0.40
1:F:393:VAL:HB	1:F:398[A]:GLN:HB3	2.03	0.40
1:H:370:VAL:HG12	1:H:390:ILE:HB	2.04	0.40
1:C:18:LYS:NZ	1:C:50:GLU:OE2	2.35	0.40
1:B:410:LEU:HA	1:B:410:LEU:HD12	1.90	0.40
1:E:339:MET:SD	1:E:385:GLY:HA3	2.61	0.40
1:F:448:PRO:HB3	1:F:464:TRP:CG	2.57	0.40
1:G:315:ARG:HH22	1:G:322:ASP:CG	2.22	0.40
1:E:55:ALA:HA	1:E:202:GLY:O	2.22	0.40
1:A:231:GLY:O	1:A:254[B]:LEU:HA	2.22	0.40
1:A:69[B]:ARG:NH1	1:A:72:GLU:HB2	2.37	0.40
1:B:292:ARG:NH2	1:B:402:VAL:O	2.54	0.40
1:E:178:LYS:HE2	1:E:209:GLY:O	2.21	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)
3:B:962:HOH:O	3:D:907:HOH:O[4_456]	2.14	0.06



## 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	491/491 (100%)	476 (97%)	15 (3%)	0	100	100
1	B	493/491 (100%)	479 (97%)	14 (3%)	0	100	100
1	C	493/491 (100%)	480 (97%)	12 (2%)	1 (0%)	51	42
1	D	488/491 (99%)	479 (98%)	9 (2%)	0	100	100
1	E	494/491 (101%)	481 (97%)	13 (3%)	0	100	100
1	F	489/491 (100%)	472 (96%)	17 (4%)	0	100	100
1	G	490/491 (100%)	475 (97%)	15 (3%)	0	100	100
1	H	489/491 (100%)	471 (96%)	18 (4%)	0	100	100
All	All	3927/3928 (100%)	3813 (97%)	113 (3%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	153	PRO

### 5.3.2 Protein sidechains

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	401/408 (98%)	400 (100%)	1 (0%)	94	95
1	B	404/408 (99%)	402 (100%)	2 (0%)	91	91
1	C	404/408 (99%)	401 (99%)	3 (1%)	87	87
1	D	398/408 (98%)	396 (100%)	2 (0%)	91	91

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	E	405/408 (99%)	405 (100%)	0	100	100
1	F	402/408 (98%)	399 (99%)	3 (1%)	87	87
1	G	400/408 (98%)	400 (100%)	0	100	100
1	H	401/408 (98%)	399 (100%)	2 (0%)	91	91
All	All	3215/3264 (98%)	3202 (100%)	13 (0%)	93	93

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	441	PHE
1	B	320	ARG
1	B	446	HIS
1	C	36	LYS
1	C	42	ARG
1	C	490	LEU
1	D	95	GLU
1	D	360	TRP
1	F	171	VAL
1	F	254	LEU
1	F	370	VAL
1	H	95	GLU
1	H	360	TRP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	F	335	GLN
1	H	446	HIS

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

16 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z  > 2$	Counts	RMSZ	# $ Z  > 2$
2	NAP	A	500[A]	-	36,42,52	1.98	8 (22%)	40,65,80	1.95	6 (15%)
2	NAP	A	500[B]	-	36,42,52	1.86	8 (22%)	40,65,80	1.84	4 (10%)
2	NAP	B	500[A]	-	36,42,52	1.87	8 (22%)	40,65,80	1.76	5 (12%)
2	NAP	B	500[B]	-	36,42,52	1.88	8 (22%)	40,65,80	1.78	4 (10%)
2	NAP	C	500[A]	-	36,42,52	1.90	8 (22%)	40,65,80	1.78	4 (10%)
2	NAP	C	500[B]	-	36,42,52	1.84	9 (25%)	40,65,80	1.86	3 (7%)
2	NAP	D	500[A]	-	36,42,52	1.87	9 (25%)	40,65,80	1.71	5 (12%)
2	NAP	D	500[B]	-	36,42,52	1.85	9 (25%)	40,65,80	1.67	4 (10%)
2	NAP	E	500[A]	-	36,42,52	1.87	8 (22%)	40,65,80	2.01	4 (10%)
2	NAP	E	500[B]	-	36,42,52	1.84	8 (22%)	40,65,80	2.01	5 (12%)
2	NAP	F	500[A]	-	36,42,52	1.86	8 (22%)	40,65,80	1.77	5 (12%)
2	NAP	F	500[B]	-	36,42,52	1.93	8 (22%)	40,65,80	1.80	5 (12%)
2	NAP	G	500[A]	-	36,42,52	1.93	9 (25%)	40,65,80	1.82	9 (22%)
2	NAP	G	500[B]	-	36,42,52	1.90	9 (25%)	40,65,80	1.76	5 (12%)
2	NAP	H	500[A]	-	36,42,52	1.95	9 (25%)	40,65,80	2.00	6 (15%)
2	NAP	H	500[B]	-	36,42,52	1.86	9 (25%)	40,65,80	1.84	4 (10%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAP	A	500[A]	-	-	0/23/56/67	0/4/4/5
2	NAP	A	500[B]	-	-	0/23/56/67	0/4/4/5
2	NAP	B	500[A]	-	-	0/23/56/67	0/4/4/5
2	NAP	B	500[B]	-	-	0/23/56/67	0/4/4/5
2	NAP	C	500[A]	-	-	0/23/56/67	0/4/4/5
2	NAP	C	500[B]	-	-	0/23/56/67	0/4/4/5
2	NAP	D	500[A]	-	-	0/23/56/67	0/4/4/5
2	NAP	D	500[B]	-	-	0/23/56/67	0/4/4/5
2	NAP	E	500[A]	-	-	0/23/56/67	0/4/4/5
2	NAP	E	500[B]	-	-	0/23/56/67	0/4/4/5
2	NAP	F	500[A]	-	-	0/23/56/67	0/4/4/5
2	NAP	F	500[B]	-	-	0/23/56/67	0/4/4/5
2	NAP	G	500[A]	-	-	0/23/56/67	0/4/4/5
2	NAP	G	500[B]	-	-	0/23/56/67	0/4/4/5
2	NAP	H	500[A]	-	-	0/23/56/67	0/4/4/5
2	NAP	H	500[B]	-	-	0/23/56/67	0/4/4/5

All (135) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	500[A]	NAP	C2D-C3D	-5.42	1.45	1.53
2	H	500[A]	NAP	C2D-C3D	-5.39	1.45	1.53
2	F	500[A]	NAP	C3B-C2B	-5.37	1.41	1.53
2	F	500[B]	NAP	C3B-C2B	-5.37	1.41	1.53
2	B	500[A]	NAP	C3B-C2B	-5.23	1.41	1.53
2	B	500[B]	NAP	C3B-C2B	-5.23	1.41	1.53
2	C	500[A]	NAP	C3B-C2B	-5.18	1.41	1.53
2	C	500[B]	NAP	C3B-C2B	-5.18	1.41	1.53
2	A	500[B]	NAP	C3B-C2B	-5.15	1.41	1.53
2	A	500[A]	NAP	C3B-C2B	-5.15	1.41	1.53
2	E	500[A]	NAP	C3B-C2B	-5.15	1.41	1.53
2	E	500[B]	NAP	C3B-C2B	-5.15	1.41	1.53
2	G	500[B]	NAP	C3B-C2B	-5.12	1.41	1.53
2	G	500[A]	NAP	C3B-C2B	-5.12	1.41	1.53
2	G	500[A]	NAP	C2D-C3D	-4.98	1.45	1.53
2	D	500[B]	NAP	C3B-C2B	-4.78	1.42	1.53
2	D	500[A]	NAP	C3B-C2B	-4.78	1.42	1.53
2	H	500[A]	NAP	C3B-C2B	-4.74	1.42	1.53
2	H	500[B]	NAP	C3B-C2B	-4.74	1.42	1.53
2	F	500[B]	NAP	C2D-C3D	-4.67	1.46	1.53
2	D	500[A]	NAP	C2D-C3D	-4.60	1.46	1.53
2	C	500[A]	NAP	C2D-C3D	-4.56	1.46	1.53
2	D	500[B]	NAP	C2D-C3D	-4.53	1.46	1.53

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	500[A]	NAP	C2D-C3D	-4.49	1.46	1.53
2	E	500[A]	NAP	C2D-C3D	-4.47	1.46	1.53
2	B	500[B]	NAP	C2D-C3D	-4.46	1.46	1.53
2	G	500[B]	NAP	C2D-C3D	-4.40	1.46	1.53
2	F	500[A]	NAP	C2D-C3D	-4.30	1.46	1.53
2	H	500[B]	NAP	C2D-C3D	-4.25	1.46	1.53
2	A	500[B]	NAP	C2D-C3D	-4.07	1.47	1.53
2	E	500[B]	NAP	C2D-C3D	-3.96	1.47	1.53
2	C	500[B]	NAP	C2D-C3D	-3.95	1.47	1.53
2	G	500[A]	NAP	O3D-C3D	-3.85	1.34	1.43
2	H	500[A]	NAP	O3D-C3D	-3.83	1.34	1.43
2	F	500[A]	NAP	O3D-C3D	-3.74	1.34	1.43
2	C	500[A]	NAP	O3D-C3D	-3.72	1.34	1.43
2	D	500[A]	NAP	O3D-C3D	-3.66	1.34	1.43
2	A	500[A]	NAP	O3D-C3D	-3.65	1.34	1.43
2	F	500[B]	NAP	O3D-C3D	-3.55	1.34	1.43
2	H	500[B]	NAP	O3D-C3D	-3.52	1.34	1.43
2	B	500[A]	NAP	O3D-C3D	-3.52	1.34	1.43
2	D	500[B]	NAP	O3D-C3D	-3.50	1.34	1.43
2	B	500[B]	NAP	O3D-C3D	-3.48	1.34	1.43
2	E	500[A]	NAP	O3D-C3D	-3.48	1.34	1.43
2	E	500[B]	NAP	O3D-C3D	-3.42	1.35	1.43
2	C	500[B]	NAP	O3D-C3D	-3.35	1.35	1.43
2	A	500[B]	NAP	O3D-C3D	-3.35	1.35	1.43
2	G	500[B]	NAP	O3D-C3D	-3.30	1.35	1.43
2	C	500[B]	NAP	C5D-C4D	-3.03	1.42	1.51
2	G	500[B]	NAP	C5D-C4D	-2.99	1.42	1.51
2	F	500[B]	NAP	C5D-C4D	-2.97	1.42	1.51
2	H	500[A]	NAP	O2D-C2D	-2.97	1.36	1.43
2	B	500[B]	NAP	C5D-C4D	-2.91	1.42	1.51
2	A	500[B]	NAP	C5D-C4D	-2.90	1.42	1.51
2	E	500[B]	NAP	C5D-C4D	-2.88	1.42	1.51
2	H	500[B]	NAP	C5D-C4D	-2.85	1.42	1.51
2	C	500[A]	NAP	O2D-C2D	-2.78	1.37	1.43
2	D	500[B]	NAP	C5D-C4D	-2.78	1.42	1.51
2	A	500[A]	NAP	C3D-C4D	-2.75	1.45	1.53
2	A	500[A]	NAP	C5D-C4D	-2.74	1.42	1.51
2	G	500[B]	NAP	C3D-C4D	-2.72	1.45	1.53
2	B	500[B]	NAP	C3D-C4D	-2.70	1.46	1.53
2	E	500[A]	NAP	O2D-C2D	-2.69	1.37	1.43
2	H	500[B]	NAP	C3D-C4D	-2.69	1.46	1.53
2	C	500[B]	NAP	C3D-C4D	-2.67	1.46	1.53

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	500[A]	NAP	O2D-C2D	-2.65	1.37	1.43
2	H	500[A]	NAP	C3D-C4D	-2.64	1.46	1.53
2	F	500[B]	NAP	C3D-C4D	-2.62	1.46	1.53
2	A	500[A]	NAP	O2D-C2D	-2.59	1.37	1.43
2	E	500[B]	NAP	C3D-C4D	-2.59	1.46	1.53
2	B	500[B]	NAP	O2D-C2D	-2.57	1.37	1.43
2	G	500[B]	NAP	O2D-C2D	-2.56	1.37	1.43
2	G	500[A]	NAP	O2D-C2D	-2.55	1.37	1.43
2	B	500[A]	NAP	O2D-C2D	-2.54	1.37	1.43
2	F	500[B]	NAP	O2D-C2D	-2.51	1.37	1.43
2	A	500[B]	NAP	C3D-C4D	-2.51	1.46	1.53
2	E	500[A]	NAP	C5D-C4D	-2.50	1.43	1.51
2	D	500[B]	NAP	C3D-C4D	-2.50	1.46	1.53
2	E	500[B]	NAP	O2D-C2D	-2.46	1.38	1.43
2	H	500[B]	NAP	O2D-C2D	-2.45	1.38	1.43
2	G	500[B]	NAP	O4B-C4B	-2.45	1.39	1.45
2	G	500[A]	NAP	O4B-C4B	-2.45	1.39	1.45
2	H	500[A]	NAP	C5D-C4D	-2.44	1.43	1.51
2	C	500[A]	NAP	C5D-C4D	-2.42	1.44	1.51
2	G	500[A]	NAP	C5D-C4D	-2.41	1.44	1.51
2	F	500[A]	NAP	O2D-C2D	-2.34	1.38	1.43
2	B	500[A]	NAP	C5D-C4D	-2.33	1.44	1.51
2	A	500[B]	NAP	O4B-C4B	-2.32	1.39	1.45
2	A	500[A]	NAP	O4B-C4B	-2.32	1.39	1.45
2	A	500[B]	NAP	O2D-C2D	-2.30	1.38	1.43
2	D	500[A]	NAP	C5D-C4D	-2.29	1.44	1.51
2	B	500[A]	NAP	O4B-C4B	-2.28	1.39	1.45
2	B	500[B]	NAP	O4B-C4B	-2.28	1.39	1.45
2	H	500[A]	NAP	O4B-C4B	-2.27	1.39	1.45
2	H	500[B]	NAP	O4B-C4B	-2.27	1.39	1.45
2	C	500[B]	NAP	O2D-C2D	-2.25	1.38	1.43
2	D	500[B]	NAP	O4B-C4B	-2.25	1.39	1.45
2	D	500[A]	NAP	O4B-C4B	-2.25	1.39	1.45
2	F	500[A]	NAP	C5D-C4D	-2.22	1.44	1.51
2	H	500[A]	NAP	P2B-O2X	-2.20	1.45	1.54
2	H	500[B]	NAP	P2B-O2X	-2.20	1.45	1.54
2	E	500[A]	NAP	C3D-C4D	-2.19	1.47	1.53
2	C	500[A]	NAP	C3D-C4D	-2.17	1.47	1.53
2	F	500[A]	NAP	O4B-C4B	-2.11	1.40	1.45
2	F	500[B]	NAP	O4B-C4B	-2.11	1.40	1.45
2	C	500[A]	NAP	O4B-C4B	-2.11	1.40	1.45
2	C	500[B]	NAP	O4B-C4B	-2.11	1.40	1.45

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	500[A]	NAP	C3D-C4D	-2.11	1.47	1.53
2	D	500[B]	NAP	O2D-C2D	-2.10	1.38	1.43
2	D	500[B]	NAP	O5D-C5D	-2.09	1.36	1.44
2	G	500[A]	NAP	C1D-C2D	-2.07	1.48	1.51
2	D	500[A]	NAP	C3D-C4D	-2.07	1.47	1.53
2	G	500[A]	NAP	C3D-C4D	-2.07	1.47	1.53
2	G	500[B]	NAP	O4D-C1D	-2.05	1.39	1.43
2	D	500[A]	NAP	C1D-C2D	-2.03	1.48	1.51
2	F	500[A]	NAP	C3D-C4D	-2.02	1.47	1.53
2	E	500[A]	NAP	O4B-C4B	-2.02	1.40	1.45
2	E	500[B]	NAP	O4B-C4B	-2.02	1.40	1.45
2	C	500[B]	NAP	O5D-C5D	-2.00	1.36	1.44
2	B	500[A]	NAP	C6A-N6A	3.47	1.48	1.34
2	B	500[B]	NAP	C6A-N6A	3.47	1.48	1.34
2	E	500[A]	NAP	C6A-N6A	3.60	1.48	1.34
2	E	500[B]	NAP	C6A-N6A	3.60	1.48	1.34
2	A	500[B]	NAP	C6A-N6A	3.70	1.49	1.34
2	A	500[A]	NAP	C6A-N6A	3.70	1.49	1.34
2	C	500[A]	NAP	C6A-N6A	3.79	1.49	1.34
2	C	500[B]	NAP	C6A-N6A	3.79	1.49	1.34
2	H	500[A]	NAP	C6A-N6A	3.79	1.49	1.34
2	H	500[B]	NAP	C6A-N6A	3.79	1.49	1.34
2	G	500[B]	NAP	C6A-N6A	3.80	1.49	1.34
2	G	500[A]	NAP	C6A-N6A	3.80	1.49	1.34
2	F	500[A]	NAP	C6A-N6A	3.83	1.49	1.34
2	F	500[B]	NAP	C6A-N6A	3.83	1.49	1.34
2	D	500[B]	NAP	C6A-N6A	3.90	1.50	1.34
2	D	500[A]	NAP	C6A-N6A	3.90	1.50	1.34

All (78) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	500[A]	NAP	N3A-C2A-N1A	-8.28	121.64	128.86
2	E	500[B]	NAP	N3A-C2A-N1A	-8.28	121.64	128.86
2	A	500[B]	NAP	N3A-C2A-N1A	-7.59	122.25	128.86
2	A	500[A]	NAP	N3A-C2A-N1A	-7.59	122.25	128.86
2	B	500[A]	NAP	N3A-C2A-N1A	-7.46	122.36	128.86
2	B	500[B]	NAP	N3A-C2A-N1A	-7.46	122.36	128.86
2	H	500[A]	NAP	N3A-C2A-N1A	-7.36	122.44	128.86
2	H	500[B]	NAP	N3A-C2A-N1A	-7.36	122.44	128.86
2	E	500[A]	NAP	C1B-N9A-C4A	-6.86	114.78	126.64
2	E	500[B]	NAP	C1B-N9A-C4A	-6.86	114.78	126.64

*Continued on next page...*



*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	500[A]	NAP	N3A-C2A-N1A	-6.86	122.89	128.86
2	C	500[B]	NAP	N3A-C2A-N1A	-6.86	122.89	128.86
2	F	500[A]	NAP	N3A-C2A-N1A	-6.69	123.03	128.86
2	F	500[B]	NAP	N3A-C2A-N1A	-6.69	123.03	128.86
2	D	500[B]	NAP	N3A-C2A-N1A	-6.54	123.17	128.86
2	D	500[A]	NAP	N3A-C2A-N1A	-6.54	123.17	128.86
2	G	500[B]	NAP	N3A-C2A-N1A	-6.48	123.22	128.86
2	G	500[A]	NAP	N3A-C2A-N1A	-6.48	123.22	128.86
2	H	500[A]	NAP	C1B-N9A-C4A	-5.93	116.39	126.64
2	H	500[B]	NAP	C1B-N9A-C4A	-5.93	116.39	126.64
2	A	500[B]	NAP	C1B-N9A-C4A	-5.88	116.47	126.64
2	A	500[A]	NAP	C1B-N9A-C4A	-5.88	116.47	126.64
2	C	500[A]	NAP	C1B-N9A-C4A	-5.77	116.66	126.64
2	C	500[B]	NAP	C1B-N9A-C4A	-5.77	116.66	126.64
2	D	500[B]	NAP	C1B-N9A-C4A	-5.63	116.91	126.64
2	D	500[A]	NAP	C1B-N9A-C4A	-5.63	116.91	126.64
2	F	500[A]	NAP	C1B-N9A-C4A	-5.62	116.92	126.64
2	F	500[B]	NAP	C1B-N9A-C4A	-5.62	116.92	126.64
2	G	500[B]	NAP	C1B-N9A-C4A	-5.43	117.25	126.64
2	G	500[A]	NAP	C1B-N9A-C4A	-5.43	117.25	126.64
2	B	500[A]	NAP	C1B-N9A-C4A	-5.21	117.63	126.64
2	B	500[B]	NAP	C1B-N9A-C4A	-5.21	117.63	126.64
2	C	500[B]	NAP	C1D-O4D-C4D	-4.98	96.28	108.15
2	H	500[A]	NAP	O2D-C2D-C3D	-4.56	102.60	111.28
2	A	500[A]	NAP	O2D-C2D-C3D	-4.22	103.25	111.28
2	H	500[B]	NAP	C1D-O4D-C4D	-4.04	98.51	108.15
2	G	500[B]	NAP	C1D-O4D-C4D	-3.97	98.70	108.15
2	F	500[B]	NAP	C1D-O4D-C4D	-3.93	98.78	108.15
2	E	500[B]	NAP	C1D-O4D-C4D	-3.60	99.57	108.15
2	G	500[A]	NAP	O3D-C3D-C2D	-3.44	103.67	111.91
2	A	500[B]	NAP	C1D-O4D-C4D	-3.31	100.25	108.15
2	D	500[A]	NAP	O3D-C3D-C2D	-2.74	105.36	111.91
2	B	500[B]	NAP	C1D-O4D-C4D	-2.37	102.49	108.15
2	G	500[B]	NAP	C4A-C5A-N7A	-2.29	107.19	109.41
2	G	500[A]	NAP	C4A-C5A-N7A	-2.29	107.19	109.41
2	D	500[B]	NAP	C1D-O4D-C4D	-2.28	102.72	108.15
2	G	500[A]	NAP	O4D-C1D-C2D	-2.25	101.50	106.00
2	G	500[A]	NAP	O2D-C2D-C3D	-2.14	107.20	111.28
2	H	500[A]	NAP	O3D-C3D-C2D	-2.13	106.81	111.91
2	F	500[A]	NAP	C4B-O4B-C1B	-2.13	107.51	109.77
2	F	500[B]	NAP	C4B-O4B-C1B	-2.13	107.51	109.77
2	G	500[B]	NAP	O4B-C1B-C2B	-2.11	102.89	106.59

*Continued on next page...*



*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	G	500[A]	NAP	O4B-C1B-C2B	-2.11	102.89	106.59
2	B	500[A]	NAP	O3D-C3D-C2D	-2.03	107.05	111.91
2	A	500[A]	NAP	C5D-C4D-C3D	-2.01	107.61	115.29
2	E	500[B]	NAP	C1D-C2D-C3D	2.02	104.77	101.67
2	D	500[A]	NAP	C1D-C2D-C3D	2.05	104.81	101.67
2	A	500[B]	NAP	C1D-C2D-C3D	2.15	104.97	101.67
2	E	500[B]	NAP	O5D-C5D-C4D	2.18	116.74	109.00
2	E	500[A]	NAP	O5D-C5D-C4D	2.34	117.31	109.00
2	H	500[B]	NAP	C1D-C2D-C3D	2.39	105.34	101.67
2	B	500[A]	NAP	C1D-C2D-C3D	2.39	105.34	101.67
2	A	500[A]	NAP	C1D-C2D-C3D	2.57	105.62	101.67
2	F	500[B]	NAP	C1D-C2D-C3D	2.59	105.65	101.67
2	G	500[A]	NAP	C1D-C2D-C3D	2.68	105.78	101.67
2	D	500[B]	NAP	C1D-C2D-C3D	2.72	105.85	101.67
2	B	500[B]	NAP	C1D-C2D-C3D	2.76	105.91	101.67
2	F	500[A]	NAP	O5D-C5D-C4D	2.81	118.96	109.00
2	C	500[A]	NAP	C1D-C2D-C3D	2.83	106.02	101.67
2	B	500[A]	NAP	O5D-C5D-C4D	2.84	119.06	109.00
2	G	500[A]	NAP	O5D-C5D-C4D	2.88	119.23	109.00
2	H	500[A]	NAP	C1D-C2D-C3D	2.89	106.11	101.67
2	C	500[A]	NAP	O5D-C5D-C4D	2.90	119.27	109.00
2	F	500[A]	NAP	C1D-C2D-C3D	2.93	106.17	101.67
2	A	500[A]	NAP	O5D-C5D-C4D	2.94	119.41	109.00
2	D	500[A]	NAP	O5D-C5D-C4D	2.95	119.47	109.00
2	E	500[A]	NAP	C1D-C2D-C3D	3.28	106.72	101.67
2	H	500[A]	NAP	O5D-C5D-C4D	3.50	121.42	109.00

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

13 monomers are involved in 27 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	500[B]	NAP	4	0
2	B	500[B]	NAP	1	0
2	C	500[A]	NAP	1	0
2	C	500[B]	NAP	2	0
2	D	500[A]	NAP	1	0
2	D	500[B]	NAP	1	0
2	E	500[A]	NAP	2	0
2	E	500[B]	NAP	3	0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	F	500[A]	NAP	1	0
2	F	500[B]	NAP	3	0
2	G	500[A]	NAP	2	0
2	G	500[B]	NAP	3	0
2	H	500[B]	NAP	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	485/491 (98%)	-0.05	9 (1%) 67 69	24, 33, 49, 63	0
1	B	488/491 (99%)	-0.11	6 (1%) 79 80	23, 33, 48, 77	0
1	C	485/491 (98%)	0.09	14 (2%) 52 56	22, 37, 55, 75	0
1	D	483/491 (98%)	-0.07	3 (0%) 89 90	24, 34, 48, 63	0
1	E	490/491 (99%)	0.06	16 (3%) 47 50	24, 36, 54, 75	2 (0%)
1	F	485/491 (98%)	-0.02	9 (1%) 67 69	24, 36, 54, 76	0
1	G	482/491 (98%)	-0.03	5 (1%) 82 84	23, 34, 53, 68	0
1	H	485/491 (98%)	-0.09	6 (1%) 79 80	23, 35, 50, 64	0
All	All	3883/3928 (98%)	-0.03	68 (1%) 69 71	22, 35, 52, 77	2 (0%)

All (68) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	25	PHE	5.3
1	C	25	PHE	5.1
1	E	5	ASN	4.9
1	B	5	ASN	4.8
1	E	4	LEU	4.6
1	F	25	PHE	4.6
1	A	25	PHE	4.6
1	E	6	ILE	4.5
1	G	25	PHE	4.4
1	D	490	LEU	4.2
1	C	7	MET	4.2
1	F	490	LEU	4.1
1	B	6	ILE	4.1
1	B	7	MET	4.0
1	C	490	LEU	4.0
1	F	7	MET	3.8

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	RSRZ
1	B	4	LEU	3.7
1	H	25	PHE	3.7
1	C	22	THR	3.6
1	C	27	VAL	3.5
1	H	489	ALA	3.5
1	B	25	PHE	3.4
1	F	491	LYS	3.4
1	F	21	SER	3.3
1	D	25	PHE	3.3
1	H	490	LEU	3.2
1	E	7	MET	3.1
1	A	24	ALA	3.0
1	F	22	THR	3.0
1	A	22	THR	2.9
1	D	22	THR	2.8
1	E	2[A]	ILE	2.7
1	C	24	ALA	2.6
1	A	42	ARG	2.6
1	A	9	VAL	2.6
1	G	34	GLY	2.5
1	C	42	ARG	2.5
1	E	32	VAL	2.4
1	G	24	ALA	2.4
1	E	3[A]	ASP	2.4
1	E	42	ARG	2.3
1	C	37	ILE	2.3
1	E	22	THR	2.3
1	G	42	ARG	2.3
1	C	86	GLU	2.3
1	C	39	GLU	2.3
1	C	8	LYS	2.2
1	E	287[A]	CYS	2.2
1	B	140	VAL	2.2
1	A	128	VAL	2.2
1	C	9	VAL	2.2
1	H	140	VAL	2.2
1	E	21	SER	2.2
1	F	37	ILE	2.2
1	E	490	LEU	2.2
1	A	7	MET	2.2
1	G	489	ALA	2.2
1	C	36	LYS	2.1

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	RSRZ
1	E	24	ALA	2.1
1	A	37	ILE	2.1
1	F	23	GLY	2.1
1	A	21	SER	2.1
1	H	126	GLY	2.1
1	H	128	VAL	2.0
1	E	23	GLY	2.0
1	F	287[A]	CYS	2.0
1	E	128	VAL	2.0
1	C	21	SER	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
2	NAP	D	500[A]	39/48	0.95	0.14	2.13	30,35,41,45	12
2	NAP	B	500[B]	39/48	0.95	0.14	1.71	27,33,42,47	12
2	NAP	B	500[A]	39/48	0.95	0.14	1.71	27,32,37,47	12
2	NAP	E	500[B]	39/48	0.95	0.14	1.61	27,38,44,47	12
2	NAP	E	500[A]	39/48	0.95	0.14	1.61	27,37,43,47	12
2	NAP	C	500[A]	39/48	0.94	0.14	1.50	32,37,44,45	12
2	NAP	H	500[A]	39/48	0.96	0.14	1.50	27,33,38,44	12
2	NAP	F	500[A]	39/48	0.94	0.13	1.46	30,37,41,42	12
2	NAP	C	500[B]	39/48	0.94	0.14	1.40	32,38,44,45	12
2	NAP	H	500[B]	39/48	0.96	0.14	1.32	27,33,44,44	12
2	NAP	D	500[B]	39/48	0.95	0.14	1.14	30,36,41,45	12

*Continued on next page...*

*Continued from previous page...*

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
2	NAP	G	500[B]	39/48	0.94	0.14	1.12	29,36,42,45	12
2	NAP	F	500[B]	39/48	0.94	0.13	1.02	33,38,42,43	12
2	NAP	A	500[B]	39/48	0.95	0.13	0.73	28,33,38,39	12
2	NAP	G	500[A]	39/48	0.94	0.14	0.21	29,35,41,45	12
2	NAP	A	500[A]	39/48	0.95	0.13	-0.13	28,32,38,40	12

## 6.5 Other polymers [i](#)

There are no such residues in this entry.