



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 10:13 PM GMT

PDB ID : 4X1Y  
Title : Discovery of cytotoxic Dolastatin 10 analogs with N-terminal modifications  
Authors : Parris, K.D.  
Deposited on : 2014-11-25  
Resolution : 3.19 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

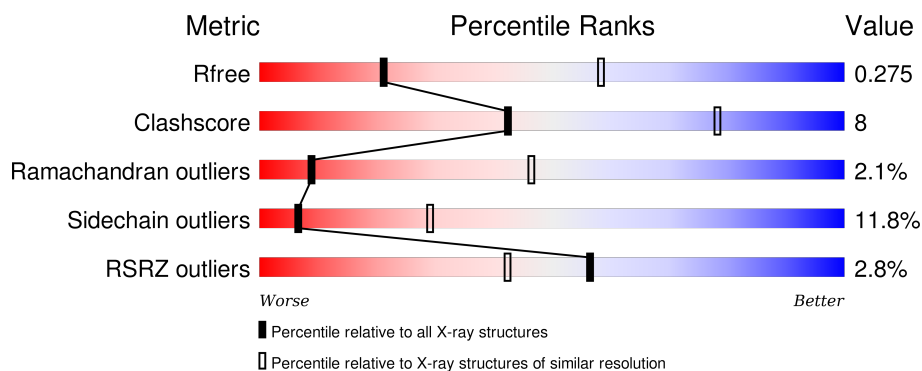
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 3.19 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	1124 (3.24-3.16)
Clashscore	102246	1024 (3.22-3.18)
Ramachandran outliers	100387	1004 (3.22-3.18)
Sidechain outliers	100360	1003 (3.22-3.18)
RSRZ outliers	91569	1129 (3.24-3.16)

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	451	 5% 69% 24% • 5%
1	C	451	 % 71% 21% • 5%
2	B	445	 % 67% 26% • •
2	D	445	 2% 71% 23% • •
3	E	142	 8% 65% 18% • 13%

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	MG	C	601	-	-	-	X

## 2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 14715 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 Tubulin alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	429	Total	C	N	O	S	0	0	0
			3363	2132	572	638	21			
1	C	430	Total	C	N	O	S	0	2	0
			3351	2124	569	635	23			

- Molecule 2 is a protein called Tubulin beta chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	428	Total	C	N	O	S	0	0	0
			3342	2100	568	649	25			
2	D	430	Total	C	N	O	S	0	1	0
			3369	2112	578	655	24			

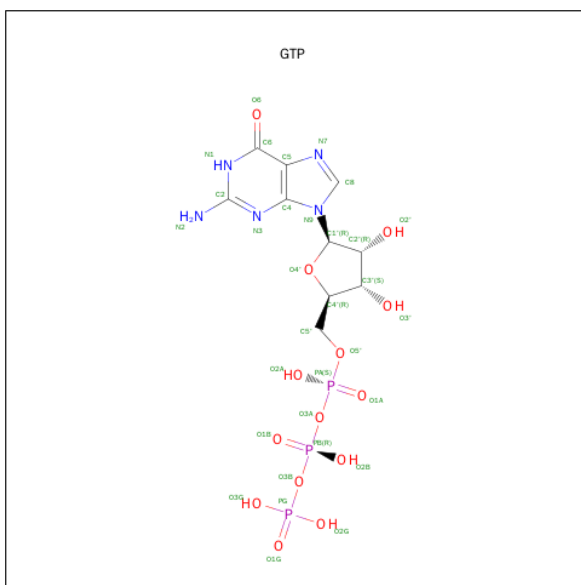
- Molecule 3 is a protein called Stathmin-4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	E	123	Total	C	N	O	S	0	0	0
			1008	626	184	195	3			

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	4	ALA	-	expression tag	UNP P63043
E	14	ALA	CYS	engineered mutation	UNP P63043
E	20	TRP	PHE	engineered mutation	UNP P63043

- Molecule 4 is GUANOSINE-5'-TRIPHOSPHATE (three-letter code: GTP) (formula: C<sub>10</sub>H<sub>16</sub>N<sub>5</sub>O<sub>14</sub>P<sub>3</sub>).

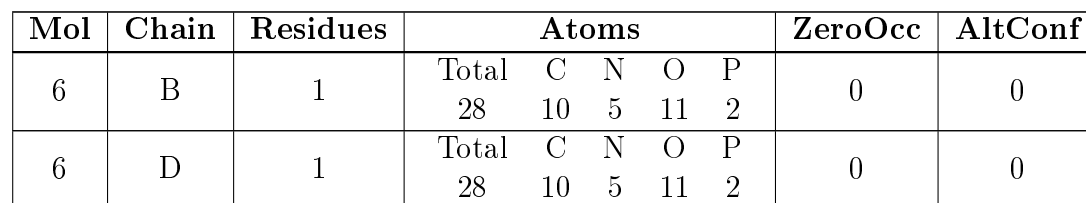


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total 32	C 10	N 5	O 14	P 3	0	0
4	C	1	Total 32	C 10	N 5	O 14	P 3	0	0

- Molecule 5 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total Mg 1 1	0	0
5	C	1	Total Mg 1 1	0	0

- Molecule 6 is GUANOSINE-5'-DIPHOSPHATE (three-letter code: GDP) (formula:  $\text{C}_{10}\text{H}_{15}\text{N}_5\text{O}_{11}\text{P}_2$ ).



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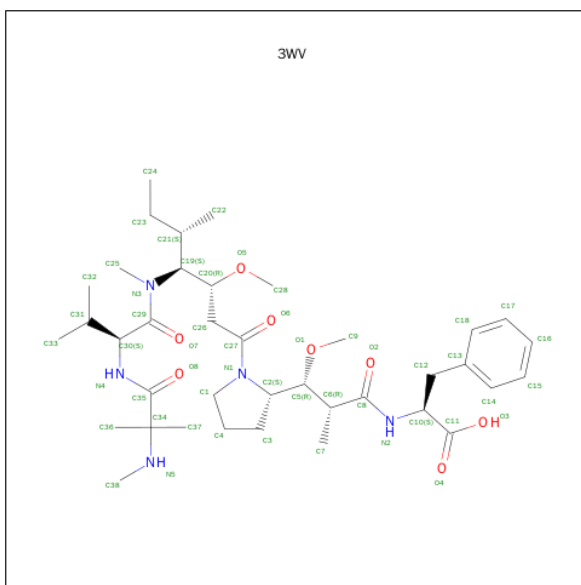
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	B	1	Total	C	N	O	0	0
			29	22	1	6		



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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	D	1	Total	C	N	O	0	0
			29	22	1	6		

- Molecule 8 is N,2-dimethyl-L-alanyl-N-[(3R,4S,5S)-1-{(2S)-2-[(1R,2R)-3-{[(1S)-1-carboxy-2-phenylethyl]amino}-1-methoxy-2-methyl-3-oxopropyl]pyrrolidin-1-yl}-3-methoxy-5-methyl-1-oxoheptan-4-yl]-N-methyl-L-valinamide (three-letter code: 3WV) (formula: C<sub>38</sub>H<sub>63</sub>N<sub>5</sub>O<sub>8</sub>).

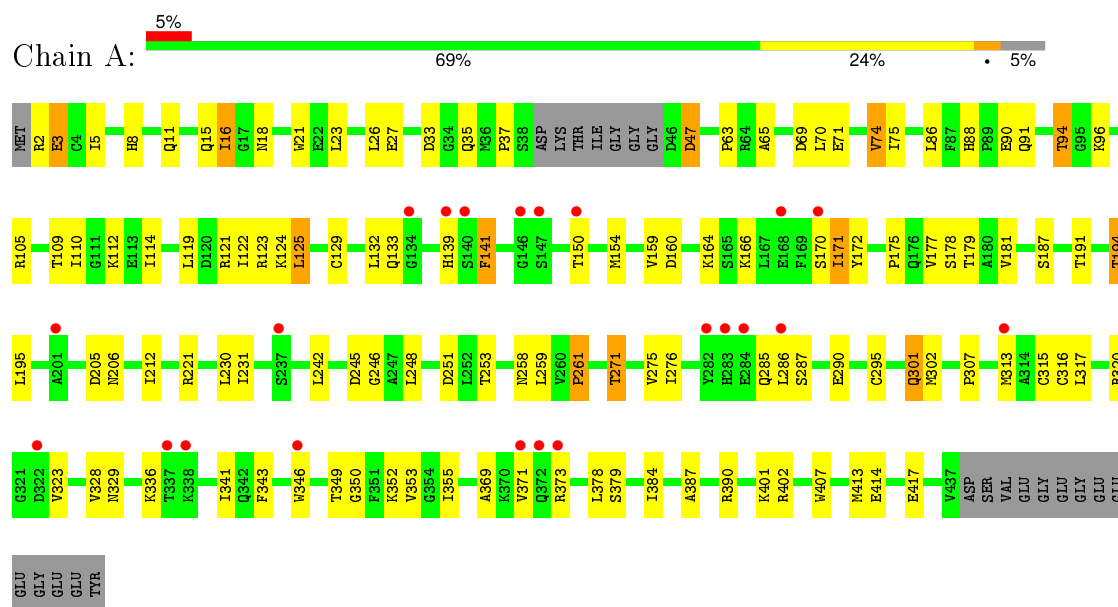


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
8	B	1	Total	C	N	O	0	0
			51	38	5	8		
8	D	1	Total	C	N	O	0	0
			51	38	5	8		

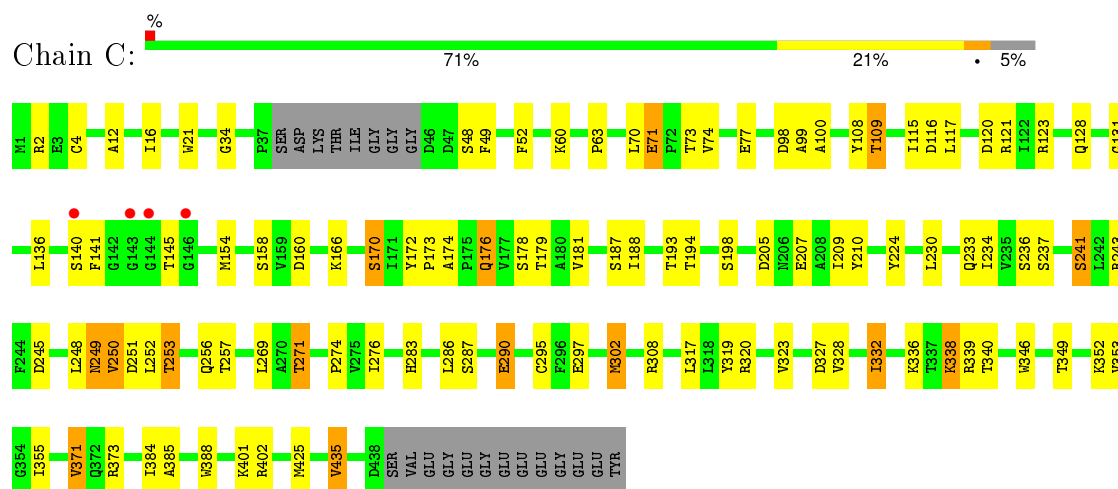
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ( $RSRZ > 2$ ). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

#### • Molecule 1: Tubulin alpha chain



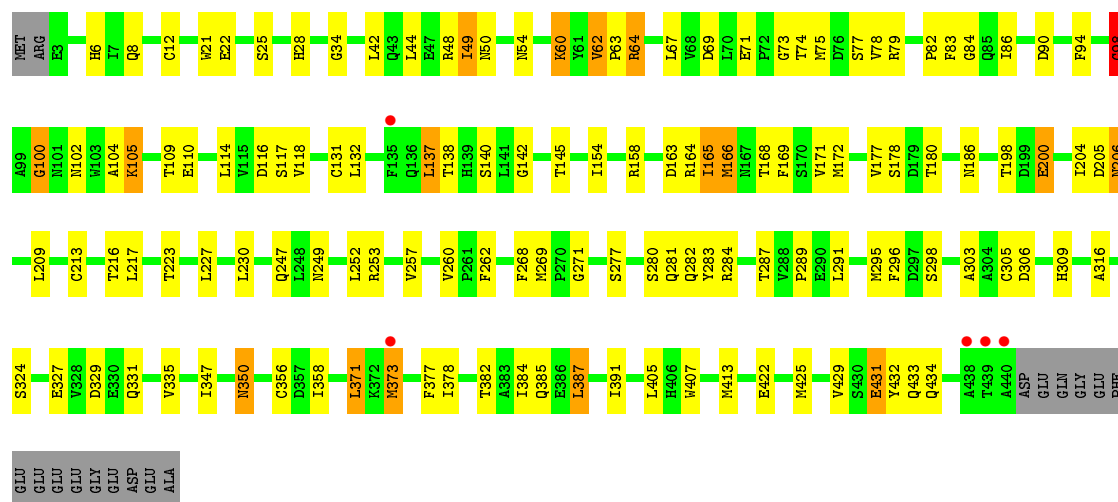
#### • Molecule 1: Tubulin alpha chain



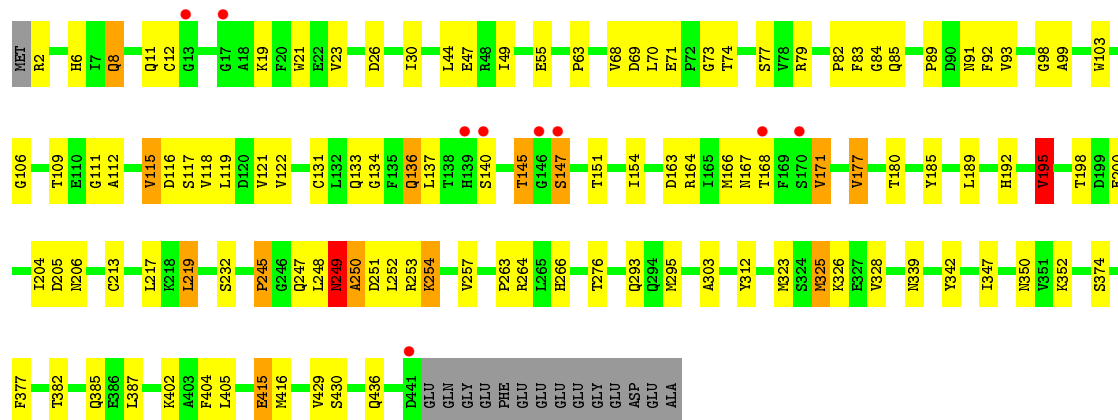
#### • Molecule 2: Tubulin beta chain



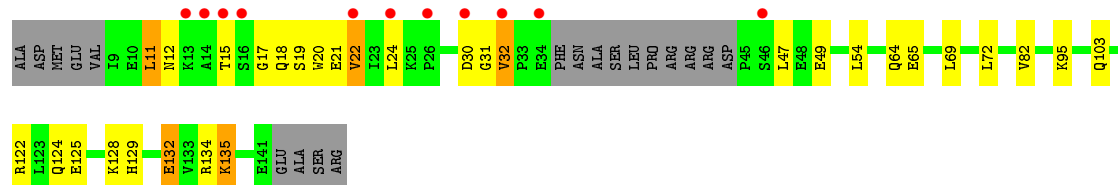




• Molecule 2: Tubulin beta chain



• Molecule 3: Stathmin-4



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	66.61Å 127.86Å 255.04Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.59 – 3.19 28.82 – 2.89	Depositor EDS
% Data completeness (in resolution range)	97.2 (30.59-3.19) 91.4 (28.82-2.89)	Depositor EDS
$R_{merge}$	0.10	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.14 (at 2.90Å)	Xtriage
Refinement program	BUSTER 2.11.5	Depositor
R, $R_{free}$	0.188 , 0.273 0.207 , 0.275	Depositor DCC
$R_{free}$ test set	1870 reflections (5.35%)	DCC
Wilson B-factor (Å <sup>2</sup> )	95.4	Xtriage
Anisotropy	0.535	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.26 , 85.6	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.30$	Xtriage
Outliers	4 of 45392 reflections (0.009%)	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	14715	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	128.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.26% of the height of the origin peak. No significant pseudotranslation is detected.*

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

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

## 5 Model quality [i](#)

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

Bond lengths and bond angles in the following residue types are not validated in this section: GTP, LOC, MG, GDP, 3WV

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	0.51	0/3440	0.74	0/4671
1	C	0.53	0/3432	0.78	0/4662
2	B	0.54	0/3417	0.81	1/4634 (0.0%)
2	D	0.53	0/3446	0.77	2/4670 (0.0%)
3	E	0.50	0/1019	0.72	0/1355
All	All	0.53	0/14754	0.77	3/19992 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	248	LEU	C-N-CA	6.11	136.96	121.70
2	B	98	GLY	N-CA-C	5.85	127.72	113.10
2	D	249	ASN	C-N-CA	5.62	135.76	121.70

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	3363	0	3274	57	0
1	C	3351	0	3258	50	0
2	B	3342	0	3198	64	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	D	3369	0	3237	62	0
3	E	1008	0	1022	13	0
4	A	32	0	12	1	0
4	C	32	0	12	0	0
5	A	1	0	0	0	0
5	C	1	0	0	0	0
6	B	28	0	12	1	0
6	D	28	0	12	1	0
7	B	29	0	25	0	0
7	D	29	0	25	0	0
8	B	51	0	61	2	0
8	D	51	0	61	4	0
All	All	14715	0	14209	240	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 8.

All (240) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:252:LEU:HD23	1:C:253:THR:H	1.23	1.00
2:D:133:GLN:HE21	2:D:252:LEU:H	1.18	0.88
1:C:308:ARG:NE	1:C:340:THR:HG21	1.89	0.87
2:B:306:ASP:HB3	2:B:309:HIS:HD2	1.42	0.83
1:C:71:GLU:HB3	1:C:98:ASP:HB3	1.64	0.80
2:D:69:ASP:HA	2:D:145:THR:HG21	1.64	0.79
2:B:385:GLN:HB2	2:B:429:VAL:HG13	1.67	0.77
2:D:12:CYS:HB3	2:D:140:SER:HB3	1.66	0.76
1:A:301:GLN:HE22	1:A:307:PRO:HG3	1.52	0.74
2:B:48:ARG:HH12	2:B:249:ASN:H	1.35	0.74
1:A:171:ILE:HG23	1:A:206:ASN:HD21	1.54	0.72
2:B:253:ARG:O	2:B:257:VAL:HG23	1.90	0.71
1:C:338:LYS:HD3	1:C:340:THR:HB	1.74	0.69
1:C:308:ARG:CD	1:C:340:THR:HG21	2.22	0.68
1:A:259:LEU:O	1:A:261:PRO:HD3	1.93	0.68
2:D:106:GLY:O	2:D:111:GLY:HA3	1.92	0.68
1:A:276:ILE:HG23	1:A:369:ALA:HB3	1.75	0.68
2:D:249:ASN:H	2:D:250:ALA:HB2	1.58	0.67
8:D:503:3WV:C25	8:D:503:3WV:H5	2.24	0.67
1:C:252:LEU:HD23	1:C:253:THR:N	2.04	0.66
1:C:4[A]:CYS:SG	1:C:136:LEU:HG	2.36	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:19:LYS:O	2:D:23:VAL:HG23	1.95	0.66
2:B:137:LEU:HB3	2:B:168:THR:HG22	1.78	0.66
2:B:324:SER:HB3	2:B:327:GLU:HB2	1.78	0.66
1:C:287:SER:HA	1:C:373:ARG:HH21	1.61	0.66
1:A:387:ALA:HA	1:A:390:ARG:HE	1.61	0.66
1:C:319:TYR:HB3	1:C:323:VAL:HG21	1.78	0.65
1:C:308:ARG:CZ	1:C:340:THR:HG21	2.26	0.65
2:B:269:MET:HG3	2:B:303:ALA:HB3	1.78	0.65
1:C:172:TYR:HB3	1:C:205:ASP:HA	1.77	0.65
2:B:213:CYS:HA	2:B:217:LEU:HD12	1.79	0.65
1:A:11:GLN:HG3	1:A:74:VAL:HG21	1.78	0.65
2:D:249:ASN:N	2:D:250:ALA:HB2	2.12	0.64
1:C:241:SER:HA	1:C:250:VAL:HB	1.79	0.64
2:D:23:VAL:HG21	2:D:232:SER:HB2	1.78	0.64
2:D:195:VAL:HG22	2:D:264:ARG:HG2	1.80	0.64
2:B:431:GLU:HA	2:B:434:GLN:HE21	1.63	0.63
2:D:192:HIS:O	2:D:195:VAL:HG12	1.99	0.63
8:D:503:3WV:H51	8:D:503:3WV:H5	1.80	0.62
3:E:11:LEU:HB2	3:E:20:TRP:HA	1.82	0.62
3:E:11:LEU:HD23	3:E:21:GLU:HB2	1.80	0.62
1:C:308:ARG:HD2	1:C:340:THR:HG21	1.82	0.61
2:B:331:GLN:O	2:B:335:VAL:HG23	2.01	0.61
2:B:206:ASN:HD21	6:B:501:GDP:HN22	1.48	0.61
3:E:129:HIS:O	3:E:132:GLU:HG3	2.02	0.60
1:A:246:GLY:HA2	3:E:17:GLY:HA3	1.83	0.59
2:B:271:GLY:HA3	2:B:377:PHE:HB3	1.84	0.59
2:D:11:GLN:HG3	2:D:74:THR:HG21	1.83	0.59
1:C:308:ARG:HD2	1:C:340:THR:CG2	2.33	0.59
1:C:141:PHE:CE1	1:C:170:SER:HB2	2.37	0.59
1:A:159:VAL:HG11	3:E:47:LEU:HB2	1.84	0.59
2:B:44:LEU:HD23	2:B:49:ILE:HD13	1.84	0.58
1:C:385:ALA:HA	1:C:388:TRP:HD1	1.68	0.58
1:A:8:HIS:HE1	1:A:21:TRP:HE1	1.51	0.58
2:B:50:ASN:O	2:B:64:ARG:NH2	2.36	0.58
2:D:253:ARG:O	2:D:257:VAL:HG23	2.01	0.58
1:C:302:MET:HA	1:C:302:MET:CE	2.34	0.57
2:D:295:MET:HG2	2:D:377:PHE:HB2	1.85	0.57
2:B:382:THR:HA	2:B:432:TYR:HD2	1.68	0.57
2:B:102:ASN:HB3	2:B:105:LYS:HB2	1.86	0.57
1:C:385:ALA:HA	1:C:388:TRP:CD1	2.40	0.57
1:C:346:TRP:HZ2	1:C:435:VAL:HG22	1.70	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:206:ASN:HD21	6:D:501:GDP:HN22	1.53	0.57
2:D:385:GLN:HB2	2:D:429:VAL:HG13	1.87	0.56
1:A:70:LEU:HD22	1:A:110:ILE:HG22	1.87	0.56
2:D:249:ASN:HA	2:D:250:ALA:CB	2.36	0.56
2:D:44:LEU:HA	2:D:49:ILE:HB	1.88	0.56
2:B:83:PHE:O	2:B:86:ILE:HG22	2.06	0.55
1:A:69:ASP:HB3	1:A:75:ILE:HD12	1.87	0.55
1:A:177:VAL:HG21	1:A:206:ASN:HB3	1.87	0.55
1:A:5:ILE:HG12	1:A:132:LEU:HD11	1.88	0.55
1:A:3:GLU:HG3	1:A:129:CYS:HB3	1.89	0.55
2:B:142:GLY:O	2:B:186:ASN:ND2	2.41	0.54
1:C:21:TRP:CZ3	1:C:63:PRO:HB3	2.43	0.54
2:D:136:GLN:HA	2:D:167:ASN:O	2.07	0.54
2:D:70:LEU:HD12	2:D:99:ALA:HB2	1.90	0.54
1:C:286:LEU:HD23	1:C:290:GLU:HB3	1.88	0.54
2:D:133:GLN:HE21	2:D:252:LEU:N	1.97	0.54
1:C:237:SER:HA	1:C:320:ARG:HH11	1.72	0.54
2:D:137:LEU:HB3	2:D:168:THR:HG22	1.90	0.53
2:B:79:ARG:HH22	2:B:94:PHE:HE2	1.57	0.53
2:B:407:TRP:CZ2	1:C:257:THR:HA	2.43	0.53
1:A:172:TYR:HB3	1:A:205:ASP:HA	1.90	0.53
2:D:205:ASP:HB3	2:D:303:ALA:HA	1.90	0.53
2:D:116:ASP:HA	2:D:119:LEU:HD12	1.90	0.53
1:A:154:MET:HG3	1:A:194:THR:HG23	1.90	0.53
1:C:70:LEU:HG	1:C:145:THR:HG23	1.91	0.53
1:A:139:HIS:CD2	1:A:150:THR:HG21	2.44	0.53
1:A:15:GLN:HA	1:A:18:ASN:HD22	1.73	0.52
1:C:209:ILE:HG23	1:C:230:LEU:HD23	1.90	0.52
2:D:71:GLU:HG2	2:D:98:GLY:HA2	1.91	0.52
2:B:287:THR:HG23	2:B:289:PRO:HD2	1.91	0.52
2:D:133:GLN:NE2	2:D:252:LEU:H	1.98	0.52
1:A:286:LEU:HD23	1:A:290:GLU:HB3	1.92	0.52
1:C:319:TYR:HB2	1:C:355:ILE:HG12	1.91	0.52
2:D:382:THR:OG1	2:D:436:GLN:HG3	2.10	0.51
1:A:23:LEU:HA	1:A:26:LEU:HD12	1.92	0.51
2:B:200:GLU:HB3	2:B:268:PHE:HE1	1.76	0.51
2:D:415:GLU:H	2:D:415:GLU:CD	2.14	0.51
2:B:217:LEU:HD11	2:B:230:LEU:HD21	1.92	0.50
2:D:151:THR:HA	2:D:154:ILE:HD12	1.93	0.50
1:A:21:TRP:CZ2	1:A:65:ALA:HB2	2.46	0.50
1:A:70:LEU:HD21	1:A:114:ILE:HG21	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:328:VAL:HG21	1:A:355:ILE:HD11	1.92	0.50
1:C:269:LEU:HB2	1:C:384:ILE:HD13	1.93	0.50
2:D:166:MET:HG3	2:D:198:THR:HG22	1.93	0.50
1:C:174:ALA:HB1	1:C:176:GLN:HE22	1.76	0.50
2:D:103:TRP:HD1	2:D:147:SER:HB2	1.77	0.50
2:D:83:PHE:O	2:D:85:GLN:N	2.45	0.50
2:D:249:ASN:HA	2:D:250:ALA:HB3	1.93	0.49
2:D:89:PRO:HA	2:D:92:PHE:CD1	2.48	0.49
2:D:68:VAL:HG22	2:D:93:VAL:HB	1.95	0.49
2:B:164:ARG:NH1	2:B:253:ARG:HH22	2.11	0.49
2:B:137:LEU:HD22	2:B:154:ILE:HD11	1.94	0.49
1:A:191:THR:O	1:A:195:LEU:HB2	2.12	0.49
1:A:11:GLN:HG2	1:A:15:GLN:HE21	1.78	0.49
2:D:325:MET:HA	2:D:328:VAL:HB	1.94	0.49
1:A:346:TRP:HE3	3:E:32:VAL:HG13	1.77	0.49
2:D:263:PRO:O	2:D:266:HIS:HD2	1.96	0.48
2:B:34:GLY:O	2:B:60:LYS:HA	2.13	0.48
1:C:176:GLN:NE2	1:C:176:GLN:H	2.11	0.48
2:D:171:VAL:HA	2:D:204:ILE:O	2.13	0.48
1:C:252:LEU:CD2	1:C:253:THR:H	2.11	0.48
1:A:21:TRP:CZ3	1:A:63:PRO:HB3	2.48	0.48
1:A:175:PRO:HA	1:A:179:THR:HG21	1.95	0.48
2:D:312:TYR:CE2	2:D:377:PHE:HZ	2.30	0.48
2:B:200:GLU:HB3	2:B:268:PHE:CE1	2.48	0.48
1:A:329:ASN:ND2	3:E:22:VAL:HG11	2.28	0.48
1:A:96:LYS:HG2	2:B:131:CYS:HB2	1.95	0.48
1:C:141:PHE:HB2	1:C:173:PRO:HD3	1.94	0.48
1:A:407:TRP:CE2	2:B:257:VAL:HA	2.48	0.48
2:D:134:GLY:HA2	2:D:164:ARG:HB3	1.96	0.48
1:C:34:GLY:HA3	1:C:60:LYS:HG2	1.95	0.48
2:D:177:VAL:HA	8:D:503:3WV:H43	1.95	0.48
2:B:295:MET:HG2	2:B:377:PHE:HB2	1.96	0.48
1:C:317:LEU:HD13	1:C:332:ILE:HD11	1.96	0.48
2:B:382:THR:HA	2:B:432:TYR:CD2	2.48	0.47
2:D:213:CYS:HA	2:D:217:LEU:HD12	1.95	0.47
1:A:88:HIS:HB2	1:A:91:GLN:HE21	1.79	0.47
2:D:251:ASP:HB3	2:D:254:LYS:HB2	1.96	0.47
2:D:119:LEU:HA	2:D:122:VAL:HG22	1.95	0.47
1:A:212:ILE:HG23	1:A:275:VAL:HG11	1.95	0.47
2:B:6:HIS:CE1	2:B:8:GLN:HE21	2.33	0.47
2:B:425:MET:O	2:B:429:VAL:HG23	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:260:VAL:HG12	2:B:262:PHE:O	2.15	0.47
2:B:28:HIS:HB3	2:B:49:ILE:HD11	1.96	0.47
1:A:261:PRO:HG2	1:A:313:MET:HG3	1.97	0.47
1:A:5:ILE:HD12	1:A:125:LEU:HD22	1.97	0.46
1:C:271:THR:HG21	1:C:295:CYS:O	2.14	0.46
2:D:249:ASN:CA	2:D:250:ALA:CB	2.93	0.46
4:A:600:GTP:O2A	4:A:600:GTP:H8	1.98	0.46
2:B:78:VAL:O	2:B:84:GLY:HA3	2.15	0.46
1:A:329:ASN:HD21	3:E:22:VAL:HG11	1.79	0.46
1:A:16:ILE:HG12	1:A:231:ILE:HG21	1.97	0.46
1:C:12:ALA:HB3	1:C:140:SER:HB3	1.98	0.46
2:B:371:LEU:HD23	2:B:371:LEU:H	1.81	0.46
1:A:287:SER:HA	1:A:373:ARG:HH11	1.81	0.46
2:B:350:ASN:HD22	2:B:350:ASN:H	1.63	0.46
2:B:166:MET:HB3	2:B:198:THR:HA	1.97	0.46
1:A:8:HIS:CE1	1:A:21:TRP:HE1	2.33	0.46
1:A:123:ARG:HH22	1:A:160:ASP:HB3	1.80	0.46
1:A:248:LEU:HB2	3:E:19:SER:HB3	1.98	0.46
3:E:125:GLU:HA	3:E:128:LYS:HE3	1.98	0.46
1:A:133:GLN:HE22	1:A:251:ASP:HA	1.81	0.45
2:B:385:GLN:HE22	2:B:433:GLN:NE2	2.15	0.45
1:A:75:ILE:HB	1:A:94:THR:HG23	1.99	0.45
1:A:90:GLU:O	1:A:121:ARG:HG2	2.16	0.45
1:C:249:ASN:CB	1:C:355:ILE:H	2.29	0.45
1:A:21:TRP:CE3	1:A:63:PRO:HB3	2.52	0.45
2:D:339:ASN:HB3	2:D:342:TYR:HD2	1.82	0.45
8:B:503:3WV:H24	8:B:503:3WV:H38	1.99	0.45
1:A:141:PHE:HD1	1:A:172:TYR:HA	1.81	0.45
2:D:2:ARG:HB3	2:D:131:CYS:HB3	1.99	0.45
1:A:258:ASN:HA	1:A:352:LYS:HZ3	1.82	0.45
2:B:204:ILE:HG22	2:B:209:LEU:HD11	1.99	0.44
8:B:503:3WV:H46	8:B:503:3WV:H31	1.99	0.44
1:C:249:ASN:HB2	1:C:355:ILE:H	1.81	0.44
2:B:316:ALA:HB3	2:B:378:ILE:HB	1.99	0.44
2:B:165:ILE:HG22	2:B:252:LEU:HD23	2.00	0.44
2:B:28:HIS:HD1	2:B:49:ILE:HD12	1.82	0.44
2:B:280:SER:HA	2:B:281:GLN:HA	1.73	0.43
2:B:114:LEU:O	2:B:118:VAL:HG23	2.17	0.43
2:B:54:ASN:HD21	2:B:64:ARG:HD3	1.83	0.43
2:B:6:HIS:HE1	2:B:8:GLN:HE21	1.64	0.43
1:C:346:TRP:CZ2	1:C:435:VAL:HG22	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:230:LEU:O	1:C:234:ILE:HD12	2.17	0.43
1:C:207:GLU:O	1:C:210:TYR:HB3	2.17	0.43
2:B:172:MET:O	2:B:206:ASN:HB2	2.19	0.43
1:A:75:ILE:HB	1:A:94:THR:CG2	2.48	0.43
2:B:347:ILE:HG22	2:B:350:ASN:HB3	2.00	0.43
3:E:132:GLU:HA	3:E:135:LYS:HB3	1.99	0.43
2:D:68:VAL:HG21	2:D:118:VAL:HG13	2.01	0.43
2:B:104:ALA:HB2	2:B:413:MET:SD	2.58	0.43
8:D:503:3WV:H5	8:D:503:3WV:H50	1.99	0.43
1:C:52:PHE:CD1	1:C:243:ARG:HG2	2.54	0.43
2:D:6:HIS:HD2	2:D:136:GLN:OE1	2.01	0.43
1:C:158:SER:OG	1:C:166:LYS:HE3	2.18	0.43
1:C:425:MET:HB3	1:C:425:MET:HE3	1.91	0.43
1:A:350:GLY:HA2	3:E:24:LEU:HD12	2.01	0.43
2:D:30:ILE:HD11	2:D:49:ILE:HD11	2.00	0.43
1:C:100:ALA:HA	2:D:254:LYS:HG3	2.01	0.42
1:A:316:CYS:HB2	1:A:378:LEU:HB2	2.02	0.42
1:A:175:PRO:HA	1:A:179:THR:CG2	2.49	0.42
2:B:387:LEU:O	2:B:391:ILE:HG12	2.19	0.42
2:D:185:TYR:O	2:D:189:LEU:HG	2.19	0.42
2:B:306:ASP:HB3	2:B:309:HIS:CD2	2.34	0.42
1:C:174:ALA:HB1	1:C:176:GLN:NE2	2.33	0.42
2:B:54:ASN:HB2	2:B:62:VAL:HG13	2.01	0.42
2:B:138:THR:HG22	2:B:169:PHE:HB2	2.01	0.42
1:C:328:VAL:HG11	1:C:353:VAL:HG11	2.01	0.42
2:D:198:THR:OG1	2:D:266:HIS:CE1	2.73	0.42
1:A:317:LEU:HD12	1:A:353:VAL:HG22	2.00	0.42
2:D:112:ALA:O	2:D:115:VAL:HG12	2.19	0.42
1:C:176:GLN:CD	1:C:176:GLN:H	2.22	0.42
2:D:213:CYS:HB3	2:D:219:LEU:HD12	2.02	0.42
1:A:133:GLN:OE1	1:A:251:ASP:HB2	2.19	0.41
1:A:119:LEU:HA	1:A:122:ILE:HD12	2.02	0.41
1:A:112:LYS:HE3	3:E:54:LEU:HB3	2.02	0.41
2:B:154:ILE:HG23	2:B:166:MET:HG3	2.01	0.41
2:D:79:ARG:HH21	2:D:89:PRO:HB3	1.85	0.41
2:D:347:ILE:HG22	2:D:350:ASN:HB3	2.03	0.41
2:B:22:GLU:HB2	2:B:83:PHE:CD2	2.56	0.41
2:D:12:CYS:CB	2:D:140:SER:HB3	2.45	0.41
2:D:249:ASN:CA	2:D:250:ALA:HB2	2.51	0.41
2:D:47:GLU:HB3	2:D:245:PRO:HG3	2.03	0.41
2:D:6:HIS:CE1	2:D:8:GLN:HE21	2.39	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:70:LEU:HD12	1:C:99:ALA:HB2	2.02	0.41
2:B:305:CYS:SG	2:B:384:ILE:HA	2.61	0.41
2:D:91:ASN:HA	2:D:121:VAL:HG11	2.03	0.41
2:B:12:CYS:CB	2:B:140:SER:HB3	2.51	0.41
1:C:154:MET:HG3	1:C:194:THR:HG23	2.02	0.41
2:D:21:TRP:CZ3	2:D:63:PRO:HB3	2.56	0.41
1:A:21:TRP:CE2	1:A:65:ALA:HB2	2.56	0.40
1:C:274:PRO:HG2	1:C:371:VAL:HG11	2.03	0.40
2:B:21:TRP:CZ3	2:B:63:PRO:HB3	2.57	0.40
2:B:98:GLY:C	2:B:100:GLY:H	2.24	0.40
1:A:271:THR:HG23	1:A:301:GLN:HA	2.02	0.40
2:B:74:THR:O	2:B:77:SER:HB3	2.21	0.40
2:B:69:ASP:HA	2:B:145:THR:HG21	2.04	0.40
2:B:205:ASP:O	2:B:209:LEU:HG	2.22	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	425/451 (94%)	378 (89%)	40 (9%)	7 (2%)	12	54
1	C	428/451 (95%)	377 (88%)	41 (10%)	10 (2%)	8	44
2	B	426/445 (96%)	384 (90%)	31 (7%)	11 (3%)	7	40
2	D	429/445 (96%)	396 (92%)	25 (6%)	8 (2%)	10	50
3	E	119/142 (84%)	112 (94%)	4 (3%)	3 (2%)	7	41
All	All	1827/1934 (94%)	1647 (90%)	141 (8%)	39 (2%)	9	46

All (39) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	60	LYS
2	B	98	GLY
1	C	249	ASN
1	C	283	HIS
2	D	84	GLY
2	D	250	ALA
3	E	32	VAL
1	A	178	SER
2	B	109	THR
2	B	282	GLN
2	B	283	TYR
2	B	373	MET
1	C	73	THR
2	D	73	GLY
2	D	109	THR
3	E	31	GLY
2	B	100	GLY
1	C	109	THR
2	D	180	THR
2	D	404	PHE
3	E	15	THR
2	B	284	ARG
1	C	108	TYR
1	C	250	VAL
2	D	82	PRO
1	A	261	PRO
1	A	413	MET
2	B	73	GLY
1	C	241	SER
1	C	336	LYS
1	A	47	ASP
1	A	349	THR
2	B	82	PRO
2	B	178	SER
1	A	341	ILE
1	C	131	GLY
1	A	37	PRO
1	C	115	ILE
2	D	195	VAL

### 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	362/378 (96%)	317 (88%)	45 (12%)	6	27
1	C	359/378 (95%)	312 (87%)	47 (13%)	5	24
2	B	364/383 (95%)	322 (88%)	42 (12%)	7	30
2	D	369/383 (96%)	337 (91%)	32 (9%)	13	45
3	E	107/125 (86%)	89 (83%)	18 (17%)	2	13
All	All	1561/1647 (95%)	1377 (88%)	184 (12%)	6	29

All (184) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	ARG
1	A	3	GLU
1	A	16	ILE
1	A	27	GLU
1	A	33	ASP
1	A	35	GLN
1	A	47	ASP
1	A	71	GLU
1	A	74	VAL
1	A	86	LEU
1	A	94	THR
1	A	105	ARG
1	A	109	THR
1	A	124	LYS
1	A	125	LEU
1	A	141	PHE
1	A	164	LYS
1	A	166	LYS
1	A	170	SER
1	A	171	ILE
1	A	181	VAL
1	A	187	SER
1	A	194	THR

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Mol	Chain	Res	Type
1	A	221	ARG
1	A	230	LEU
1	A	242	LEU
1	A	245	ASP
1	A	253	THR
1	A	271	THR
1	A	285	GLN
1	A	295	CYS
1	A	301	GLN
1	A	302	MET
1	A	315	CYS
1	A	320	ARG
1	A	323	VAL
1	A	336	LYS
1	A	343	PHE
1	A	371	VAL
1	A	379	SER
1	A	384	ILE
1	A	401	LYS
1	A	402	ARG
1	A	414	GLU
1	A	417	GLU
2	B	25	SER
2	B	42	LEU
2	B	49	ILE
2	B	62	VAL
2	B	64	ARG
2	B	67	LEU
2	B	71	GLU
2	B	75	MET
2	B	90	ASP
2	B	105	LYS
2	B	110	GLU
2	B	116	ASP
2	B	117	SER
2	B	132	LEU
2	B	137	LEU
2	B	158	ARG
2	B	163	ASP
2	B	165	ILE
2	B	166	MET
2	B	171	VAL

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Mol	Chain	Res	Type
2	B	177	VAL
2	B	180	THR
2	B	200	GLU
2	B	206	ASN
2	B	216	THR
2	B	223	THR
2	B	227	LEU
2	B	247	GLN
2	B	277	SER
2	B	291	LEU
2	B	296	PHE
2	B	298	SER
2	B	329	ASP
2	B	350	ASN
2	B	356	CYS
2	B	358	ILE
2	B	371	LEU
2	B	373	MET
2	B	387	LEU
2	B	405	LEU
2	B	422	GLU
2	B	431	GLU
1	C	2	ARG
1	C	16	ILE
1	C	48	SER
1	C	49	PHE
1	C	71	GLU
1	C	74	VAL
1	C	77	GLU
1	C	109	THR
1	C	116	ASP
1	C	117	LEU
1	C	120	ASP
1	C	121	ARG
1	C	123	ARG
1	C	128	GLN
1	C	160	ASP
1	C	170	SER
1	C	176	GLN
1	C	178	SER
1	C	179	THR
1	C	181	VAL

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Mol	Chain	Res	Type
1	C	187	SER
1	C	188	ILE
1	C	193	THR
1	C	198	SER
1	C	224	TYR
1	C	233	GLN
1	C	236	SER
1	C	245	ASP
1	C	248	LEU
1	C	251	ASP
1	C	253	THR
1	C	256	GLN
1	C	271	THR
1	C	276	ILE
1	C	290	GLU
1	C	297	GLU
1	C	302	MET
1	C	327	ASP
1	C	332	ILE
1	C	338	LYS
1	C	339	ARG
1	C	349	THR
1	C	352	LYS
1	C	371	VAL
1	C	401	LYS
1	C	402	ARG
1	C	435	VAL
2	D	8	GLN
2	D	26	ASP
2	D	55	GLU
2	D	77	SER
2	D	115	VAL
2	D	117	SER
2	D	136	GLN
2	D	145	THR
2	D	147	SER
2	D	163	ASP
2	D	171	VAL
2	D	177	VAL
2	D	195	VAL
2	D	200	GLU
2	D	219	LEU

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Mol	Chain	Res	Type
2	D	245	PRO
2	D	247	GLN
2	D	249	ASN
2	D	254	LYS
2	D	276	THR
2	D	293	GLN
2	D	323	MET
2	D	325	MET
2	D	326	LYS
2	D	352	LYS
2	D	374	SER
2	D	387	LEU
2	D	402	LYS
2	D	405	LEU
2	D	415	GLU
2	D	416	MET
2	D	430	SER
3	E	11	LEU
3	E	12	ASN
3	E	18	GLN
3	E	22	VAL
3	E	30	ASP
3	E	49	GLU
3	E	64	GLN
3	E	65	GLU
3	E	69	LEU
3	E	72	LEU
3	E	82	VAL
3	E	95	LYS
3	E	103	GLN
3	E	122	ARG
3	E	124	GLN
3	E	132	GLU
3	E	134	ARG
3	E	135	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (40) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	8	HIS
1	A	15	GLN
1	A	28	HIS

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Mol	Chain	Res	Type
1	A	91	GLN
1	A	139	HIS
1	A	206	ASN
1	A	258	ASN
1	A	301	GLN
1	A	329	ASN
2	B	8	GLN
2	B	11	GLN
2	B	14	ASN
2	B	139	HIS
2	B	206	ASN
2	B	229	HIS
2	B	266	HIS
2	B	309	HIS
2	B	350	ASN
2	B	385	GLN
2	B	424	ASN
2	B	426	ASN
2	B	434	GLN
2	B	436	GLN
1	C	8	HIS
1	C	176	GLN
2	D	6	HIS
2	D	14	ASN
2	D	133	GLN
2	D	136	GLN
2	D	139	HIS
2	D	206	ASN
2	D	249	ASN
2	D	266	HIS
2	D	293	GLN
2	D	331	GLN
2	D	339	ASN
2	D	385	GLN
2	D	433	GLN
3	E	111	ASN
3	E	129	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 ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

Of 10 ligands modelled in this entry, 2 are monoatomic - leaving 8 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$
4	GTP	A	600	5	25,34,34	1.13	2 (8%)	34,54,54	2.14	5 (14%)
6	GDP	B	501	-	23,30,30	1.10	2 (8%)	30,47,47	2.28	5 (16%)
7	LOC	B	502	-	29,31,31	1.03	2 (6%)	27,44,44	0.46	0
8	3WV	B	503	-	48,52,52	1.08	4 (8%)	56,73,73	1.41	6 (10%)
4	GTP	C	600	5	25,34,34	1.08	2 (8%)	34,54,54	2.07	4 (11%)
6	GDP	D	501	-	23,30,30	0.97	1 (4%)	30,47,47	2.16	4 (13%)
7	LOC	D	502	-	29,31,31	0.87	2 (6%)	27,44,44	0.63	0
8	3WV	D	503	-	48,52,52	1.06	4 (8%)	56,73,73	1.70	12 (21%)

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
4	GTP	A	600	5	-	0/18/38/38	0/3/3/3
6	GDP	B	501	-	-	0/12/32/32	0/3/3/3
7	LOC	B	502	-	-	0/10/25/25	0/3/3/3
8	3WV	B	503	-	-	0/68/85/85	0/2/2/2
4	GTP	C	600	5	-	0/18/38/38	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	GDP	D	501	-	-	0/12/32/32	0/3/3/3
7	LOC	D	502	-	-	0/10/25/25	0/3/3/3
8	3WV	D	503	-	-	0/68/85/85	0/2/2/2

All (19) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	D	503	3WV	C21-C19	2.01	1.59	1.55
8	B	503	3WV	C6-C8	2.13	1.56	1.52
7	D	502	LOC	C14-C11	2.17	1.56	1.52
7	D	502	LOC	C15-C16	2.39	1.44	1.39
8	D	503	3WV	C6-C8	2.47	1.57	1.52
8	B	503	3WV	C21-C19	2.53	1.60	1.55
7	B	502	LOC	C15-C16	2.59	1.44	1.39
4	C	600	GTP	C6-C5	2.80	1.46	1.41
6	B	501	GDP	C6-C5	2.80	1.46	1.41
4	C	600	GTP	C6-N1	3.05	1.38	1.33
4	A	600	GTP	C6-N1	3.14	1.38	1.33
6	B	501	GDP	C6-N1	3.17	1.39	1.33
6	D	501	GDP	C6-N1	3.21	1.39	1.33
4	A	600	GTP	C6-C5	3.22	1.47	1.41
8	D	503	3WV	C20-C19	3.39	1.58	1.52
7	B	502	LOC	C14-C11	3.53	1.58	1.52
8	B	503	3WV	C20-C19	4.48	1.60	1.52
8	B	503	3WV	C19-N3	4.60	1.57	1.47
8	D	503	3WV	C19-N3	5.16	1.58	1.47

All (36) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	600	GTP	C5-C6-N1	-8.60	111.84	123.59
6	B	501	GDP	C5-C6-N1	-8.48	112.00	123.59
6	D	501	GDP	C5-C6-N1	-8.25	112.32	123.59
4	C	600	GTP	C5-C6-N1	-8.19	112.39	123.59
8	D	503	3WV	O7-C29-C30	-3.64	112.97	120.12
4	C	600	GTP	C6-C5-C4	-2.83	117.52	120.90
8	D	503	3WV	C35-C34-N5	-2.81	105.78	110.51
6	B	501	GDP	C6-C5-C4	-2.76	117.60	120.90
4	A	600	GTP	C6-C5-C4	-2.65	117.73	120.90
4	C	600	GTP	N3-C2-N1	-2.57	123.53	127.44
6	D	501	GDP	C6-C5-C4	-2.57	117.83	120.90
8	B	503	3WV	C35-C34-N5	-2.55	106.22	110.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	D	501	GDP	N3-C2-N1	-2.55	123.57	127.44
6	B	501	GDP	N3-C2-N1	-2.54	123.58	127.44
4	A	600	GTP	N3-C2-N1	-2.43	123.75	127.44
8	D	503	3WV	C7-C6-C8	-2.30	104.51	108.38
8	D	503	3WV	O6-C27-N1	-2.04	117.50	121.51
8	B	503	3WV	C25-N3-C29	-2.04	115.58	122.29
8	D	503	3WV	C26-C27-N1	2.21	121.87	118.44
4	A	600	GTP	O3A-PA-O5'	2.42	109.37	102.94
6	B	501	GDP	PA-O3A-PB	2.64	141.52	132.67
8	B	503	3WV	O1-C5-C6	2.77	112.90	106.02
8	D	503	3WV	C3-C2-C5	2.95	118.15	113.82
8	D	503	3WV	C31-C30-N4	3.09	119.51	111.36
8	D	503	3WV	C25-N3-C29	3.41	133.51	122.29
8	B	503	3WV	C26-C20-C19	3.72	121.09	113.16
8	D	503	3WV	O1-C5-C6	3.81	115.48	106.02
8	D	503	3WV	C30-C29-N3	4.01	127.36	118.45
8	D	503	3WV	C26-C20-C19	4.19	122.10	113.16
8	D	503	3WV	C31-C30-C29	4.26	119.43	110.75
8	B	503	3WV	C3-C2-C5	4.71	120.71	113.82
8	B	503	3WV	C22-C21-C19	5.10	123.78	109.92
4	A	600	GTP	C6-N1-C2	6.71	125.25	115.94
4	C	600	GTP	C6-N1-C2	6.79	125.36	115.94
6	D	501	GDP	C6-N1-C2	6.84	125.44	115.94
6	B	501	GDP	C6-N1-C2	6.90	125.52	115.94

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	600	GTP	1	0
6	B	501	GDP	1	0
8	B	503	3WV	2	0
6	D	501	GDP	1	0
8	D	503	3WV	4	0

## 5.7 Other polymers

There are no such residues in this entry.

## 5.8 Polymer linkage issues ⓘ

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	429/451 (95%)	0.04	22 (5%) 32 18	99, 146, 192, 212	0
1	C	430/451 (95%)	-0.27	4 (0%) 85 78	86, 113, 156, 178	0
2	B	428/445 (96%)	-0.24	5 (1%) 81 69	91, 124, 171, 188	2 (0%)
2	D	430/445 (96%)	-0.26	9 (2%) 67 52	80, 105, 143, 176	2 (0%)
3	E	123/142 (86%)	0.20	11 (8%) 12 6	115, 147, 193, 217	0
All	All	1840/1934 (95%)	-0.16	51 (2%) 56 42	80, 124, 179, 217	4 (0%)

All (51) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	439	THR	4.7
1	A	338	LYS	4.3
1	A	346	TRP	4.3
1	A	373	ARG	4.2
2	B	438	ALA	4.1
2	D	140	SER	4.0
1	A	313	MET	3.9
1	A	134	GLY	3.9
2	B	373	MET	3.7
1	A	322	ASP	3.6
1	A	146	GLY	3.5
1	A	283	HIS	3.5
3	E	16	SER	3.5
3	E	14	ALA	3.4
3	E	26	PRO	3.3
1	A	170	SER	3.3
1	A	150	THR	3.2
1	A	337	THR	3.2
1	A	371	VAL	3.1
3	E	24	LEU	3.1

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Mol	Chain	Res	Type	RSRZ
2	D	441	ASP	3.0
1	A	139	HIS	2.9
3	E	22	VAL	2.9
1	A	286	LEU	2.9
2	D	147	SER	2.9
2	D	170	SER	2.9
3	E	34	GLU	2.8
2	D	168	THR	2.7
1	A	201	ALA	2.7
1	A	372	GLN	2.6
1	A	237	SER	2.5
2	D	146	GLY	2.4
3	E	30	ASP	2.4
3	E	15	THR	2.4
3	E	46	SER	2.4
2	B	440	ALA	2.4
2	D	13	GLY	2.3
1	C	144	GLY	2.3
1	A	282	TYR	2.3
2	D	139	HIS	2.2
1	A	140	SER	2.2
2	D	17	GLY	2.2
1	A	168	GLU	2.1
1	C	140	SER	2.1
3	E	32	VAL	2.1
3	E	13	LYS	2.1
1	A	284	GLU	2.1
2	B	135	PHE	2.0
1	A	147	SER	2.0
1	C	146	GLY	2.0
1	C	143	GLY	2.0

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

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

## 6.3 Carbohydrates ⓘ

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
5	MG	C	601	1/1	0.99	0.42	1.41	60,60,60,60	0
8	3WV	D	503	51/51	0.93	0.30	1.22	88,114,122,128	0
4	GTP	A	600	32/32	0.93	0.27	0.29	120,133,146,146	0
8	3WV	B	503	51/51	0.90	0.21	0.16	105,119,132,137	0
4	GTP	C	600	32/32	0.93	0.25	0.15	99,104,108,110	0
7	LOC	D	502	29/29	0.93	0.22	0.12	88,99,102,103	0
5	MG	A	601	1/1	0.98	0.30	0.09	81,81,81,81	0
6	GDP	B	501	28/28	0.97	0.20	-0.18	106,117,120,123	0
6	GDP	D	501	28/28	0.94	0.21	-0.34	88,94,101,105	0
7	LOC	B	502	29/29	0.96	0.16	-1.32	114,119,124,128	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.