



# Full wwPDB X-ray Structure Validation Report ⓘ

Jan 23, 2018 – 08:04 PM EST

PDB ID : 1D2E  
Title : CRYSTAL STRUCTURE OF MITOCHONDRIAL EF-TU IN COMPLEX WITH GDP  
Authors : Andersen, G.R.; Thirup, S.; Spemulli, L.L.; Nyborg, J.  
Deposited on : 1999-09-23  
Resolution : 1.94 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 : 1.7.2 (RC1), CSD as538be (2017)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20030736  
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) : rb-20030736

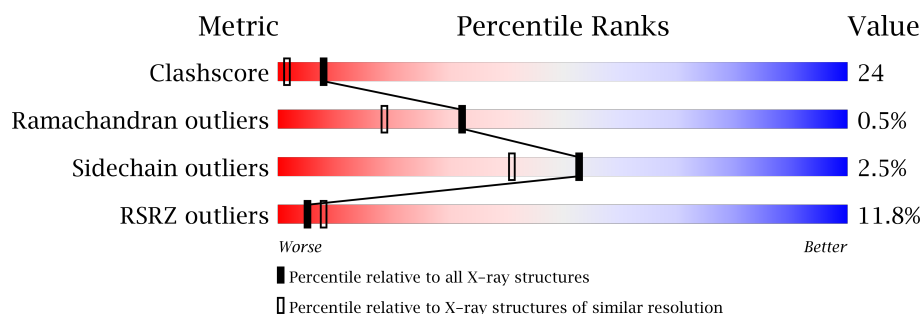
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.94 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	112137	3430 (1.96-1.92)
Ramachandran outliers	110173	3395 (1.96-1.92)
Sidechain outliers	110143	3395 (1.96-1.92)
RSRZ outliers	101464	3250 (1.96-1.92)

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	397	 3% 72% 26% .
1	B	397	 11% 58% 41% .
1	C	397	 8% 64% 35% .
1	D	397	 25% 52% 46% .

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 13597 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.

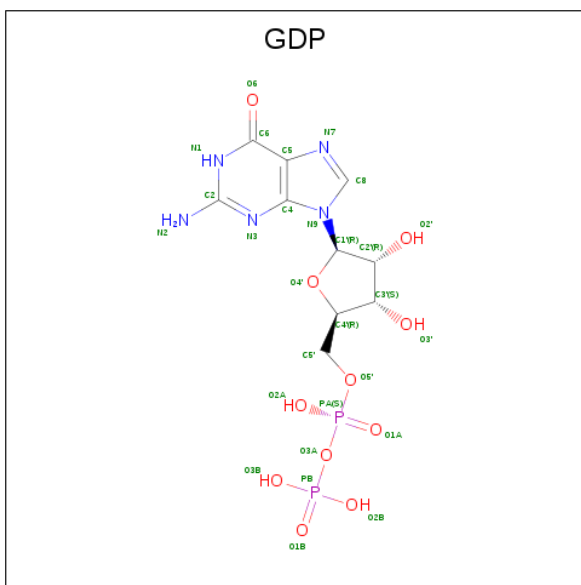
- Molecule 1 is a protein called ELONGATION FACTOR TU (EF-TU).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	397	Total	C	N	O	S	0	0	0
			3070	1938	539	577	16			
1	B	397	Total	C	N	O	S	0	0	0
			3070	1938	539	577	16			
1	C	397	Total	C	N	O	S	0	0	0
			3070	1938	539	577	16			
1	D	397	Total	C	N	O	S	0	0	0
			3070	1938	539	577	16			

- Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	1	Total	Mg	0	0
			1	1		
2	A	1	Total	Mg	0	0
			1	1		
2	D	1	Total	Mg	0	0
			1	1		
2	C	1	Total	Mg	0	0
			1	1		

- Molecule 3 is GUANOSINE-5'-DIPHOSPHATE (three-letter code: GDP) (formula: C<sub>10</sub>H<sub>15</sub>N<sub>5</sub>O<sub>11</sub>P<sub>2</sub>).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total 28	C 10	N 5	O 11	P 2	0	0
3	B	1	Total 28	C 10	N 5	O 11	P 2	0	0
3	C	1	Total 28	C 10	N 5	O 11	P 2	0	0
3	D	1	Total 28	C 10	N 5	O 11	P 2	0	0

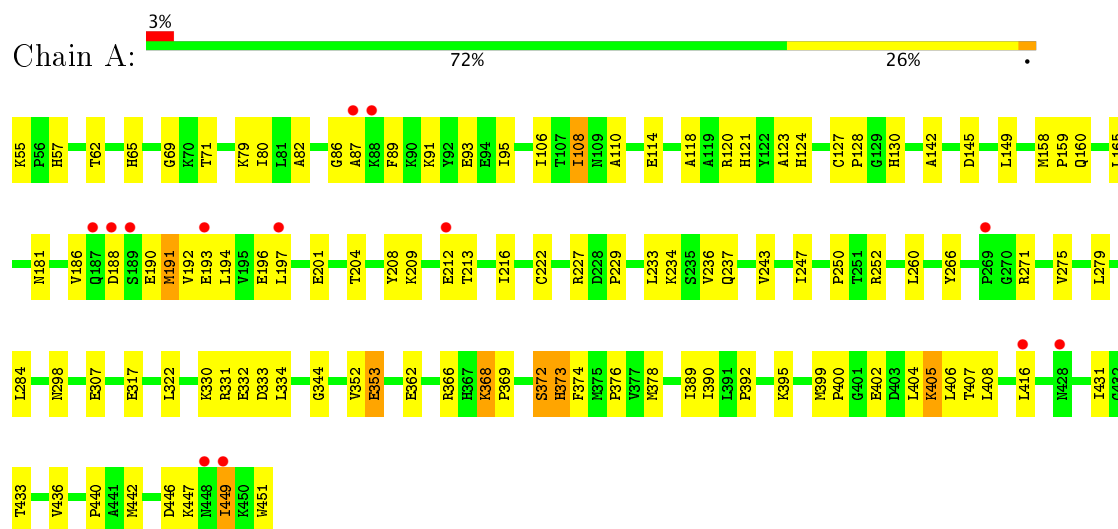
- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	387	Total O 387 387	0	0
4	B	274	Total O 274 274	0	0
4	C	295	Total O 295 295	0	0
4	D	245	Total O 245 245	0	0

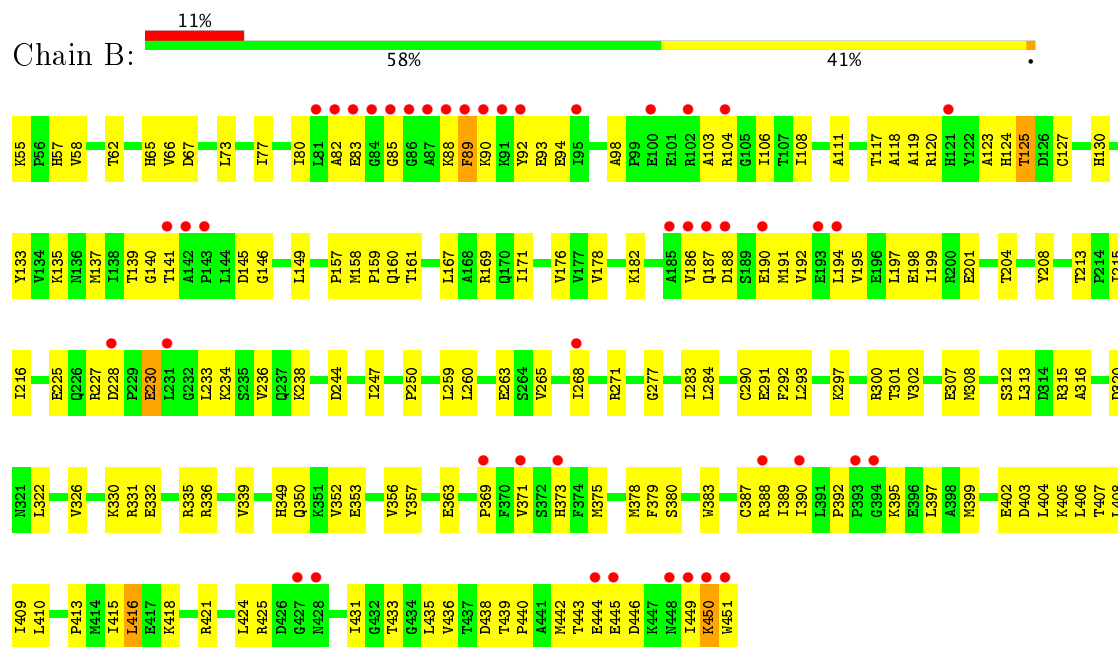
### 3 Residue-property plots

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

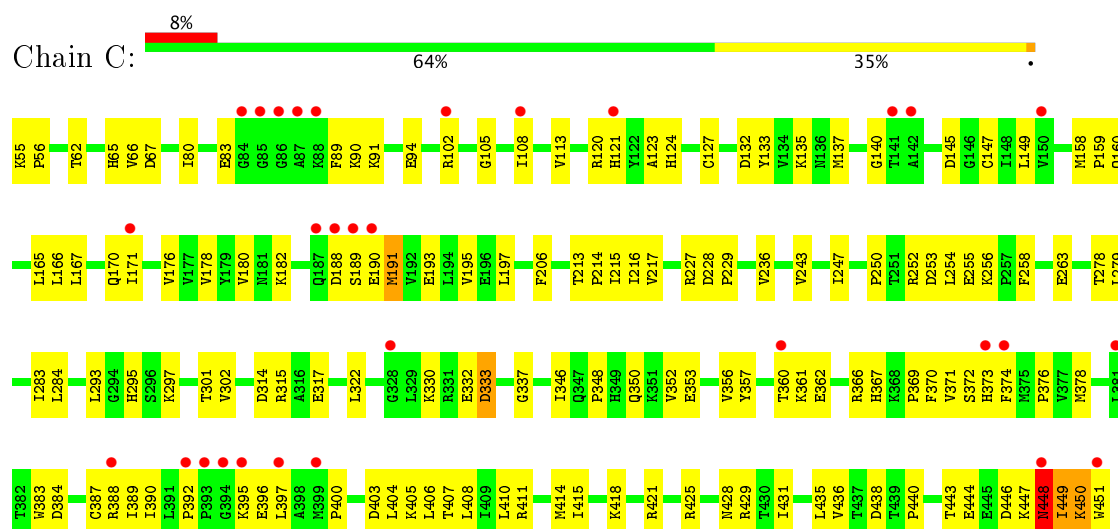
#### • Molecule 1: ELONGATION FACTOR TU (EF-TU)



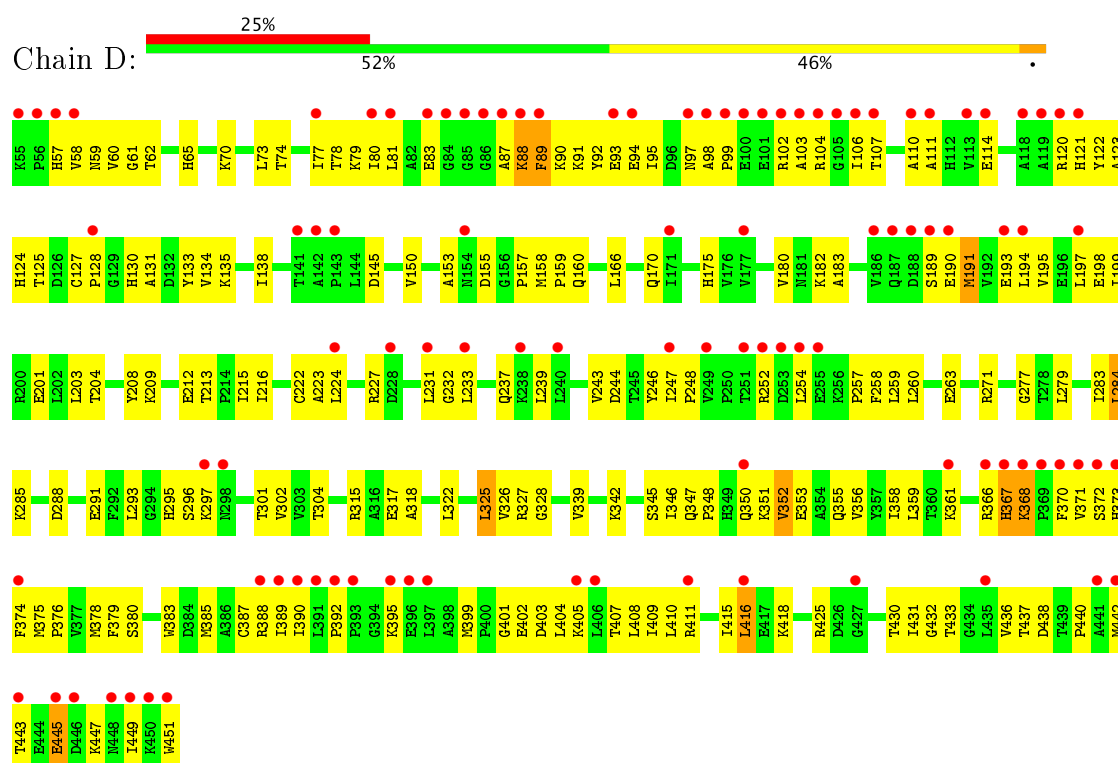
#### • Molecule 1: ELONGATION FACTOR TU (EF-TU)



#### • Molecule 1: ELONGATION FACTOR TU (EF-TU)



• Molecule 1: ELONGATION FACTOR TU (EF-TU)



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	59.09Å 119.78Å 128.89Å 90.00° 96.97° 90.00°	Depositor
Resolution (Å)	34.70 – 1.94 33.87 – 1.94	Depositor EDS
% Data completeness (in resolution range)	98.0 (34.70-1.94) 98.1 (33.87-1.94)	Depositor EDS
$R_{merge}$	0.05	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.26 (at 1.94Å)	Xtriage
Refinement program	CNS 0.3	Depositor
R, $R_{free}$	0.237 , 0.257 0.254 , (Not available)	Depositor DCC
$R_{free}$ test set	No test flags present.	DCC
Wilson B-factor (Å <sup>2</sup> )	36.9	Xtriage
Anisotropy	0.085	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 51.3	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	13597	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	46.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.73% 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, 0.333 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: GDP, MG

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	0.38	0/3127	0.73	1/4232 (0.0%)
1	B	0.32	0/3127	0.66	0/4232
1	C	0.33	0/3127	0.68	1/4232 (0.0%)
1	D	0.32	0/3127	0.67	0/4232
All	All	0.34	0/12508	0.69	2/16928 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	123	ALA	N-CA-C	-5.08	97.27	111.00
1	A	353	GLU	N-CA-C	-5.02	97.44	111.00

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	3070	0	3122	106	0
1	B	3070	0	3122	164	0
1	C	3070	0	3122	132	0
1	D	3070	0	3123	194	0
2	A	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
3	A	28	0	12	0	0
3	B	28	0	12	1	0
3	C	28	0	12	1	0
3	D	28	0	12	1	0
4	A	387	0	0	7	0
4	B	274	0	0	8	0
4	C	295	0	0	12	0
4	D	245	0	0	15	0
All	All	13597	0	12537	592	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 24.

All (592) 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:368:LYS:HD3	1:A:368:LYS:H	1.08	1.08
1:A:352:VAL:HG11	1:A:416:LEU:HD12	1.30	1.06
1:A:352:VAL:HG11	1:A:416:LEU:CD1	1.92	0.99
1:B:388:ARG:HH12	1:B:450:LYS:HE2	1.30	0.97
1:D:405:LYS:NZ	1:D:437:THR:HG21	1.80	0.96
1:A:449:ILE:H	1:A:449:ILE:HD13	1.35	0.91
1:A:368:LYS:HD3	1:A:368:LYS:N	1.86	0.88
1:B:352:VAL:CG2	1:B:436:VAL:HG13	2.02	0.88
1:A:446:ASP:O	1:A:449:ILE:HG23	1.74	0.87
1:D:405:LYS:HZ1	1:D:437:THR:HG21	1.40	0.86
1:D:416:LEU:HD22	1:D:436:VAL:HG21	1.58	0.86
1:D:443:THR:HG22	1:D:445:GLU:H	1.42	0.84
1:A:332:GLU:HB3	1:C:229:PRO:HG3	1.60	0.84
1:D:81:LEU:HB2	4:D:1380:HOH:O	1.78	0.84
1:A:446:ASP:O	1:A:449:ILE:HD12	1.78	0.83
1:D:91:LYS:HD3	1:D:92:TYR:H	1.42	0.82
1:A:449:ILE:HG12	1:A:451:TRP:HE1	1.41	0.82
1:B:352:VAL:HG21	1:B:436:VAL:HG13	1.59	0.82
1:C:108:ILE:HD11	1:C:135:LYS:HB2	1.59	0.82
1:C:392:PRO:HG3	1:C:405:LYS:O	1.78	0.82
1:D:368:LYS:HD3	1:D:368:LYS:N	1.95	0.81
1:A:392:PRO:HG3	1:A:405:LYS:O	1.81	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:416:LEU:HD22	1:B:436:VAL:HG21	1.62	0.80
1:C:189:SER:O	1:C:193:GLU:HG3	1.82	0.80
1:D:78:THR:HB	1:D:89:PHE:HA	1.63	0.79
1:C:145:ASP:CG	1:C:250:PRO:HG3	2.02	0.79
1:C:361:LYS:HE2	1:C:367:HIS:O	1.82	0.79
1:A:108:ILE:HD11	1:A:110:ALA:HB2	1.66	0.78
1:D:73:LEU:O	1:D:77:ILE:HG13	1.83	0.78
1:A:416:LEU:CD1	1:A:436:VAL:HG21	2.13	0.78
1:D:304:THR:OG1	1:D:325:LEU:HD22	1.83	0.78
1:D:368:LYS:HD3	1:D:368:LYS:H	1.48	0.77
1:C:352:VAL:CG2	1:C:436:VAL:HG13	2.13	0.77
1:B:90:LYS:NZ	1:B:94:GLU:HG2	2.01	0.76
1:A:374:PHE:CE2	1:A:376:PRO:HG3	2.20	0.76
1:D:97:ASN:HB3	4:D:1533:HOH:O	1.86	0.76
1:A:193:GLU:O	1:A:197:LEU:HG	1.86	0.76
1:A:449:ILE:CG1	1:A:451:TRP:HE1	1.96	0.75
1:D:90:LYS:HG2	1:D:94:GLU:HG2	1.68	0.75
1:A:449:ILE:HG12	1:A:451:TRP:NE1	2.00	0.75
1:D:98:ALA:HB2	1:D:111:ALA:HB2	1.65	0.75
1:B:145:ASP:CG	1:B:250:PRO:HG3	2.07	0.75
1:B:353:GLU:HG3	1:B:440:PRO:HG2	1.67	0.75
1:B:98:ALA:HB2	1:B:111:ALA:HB2	1.66	0.75
1:D:375:MET:HE2	1:D:388:ARG:HD3	1.68	0.75
1:A:209:LYS:HB3	1:A:212:GLU:OE2	1.87	0.74
1:D:79:LYS:O	1:D:83:GLU:HG2	1.87	0.74
1:D:153:ALA:HB2	1:D:180:VAL:HG12	1.70	0.74
1:A:266:TYR:HA	1:A:331:ARG:HE	1.52	0.73
1:D:418:LYS:HE2	1:D:438:ASP:HA	1.70	0.73
1:B:228:ASP:HB3	1:B:230:GLU:OE2	1.89	0.72
1:B:58:VAL:HG21	1:B:120:ARG:HH21	1.55	0.72
1:C:243:VAL:HG13	1:C:247:ILE:HD12	1.72	0.71
1:D:392:PRO:HD2	1:D:395:LYS:HD2	1.73	0.70
1:D:375:MET:CE	1:D:388:ARG:HD3	2.21	0.70
1:D:405:LYS:NZ	1:D:437:THR:CG2	2.55	0.70
1:B:58:VAL:HG21	1:B:120:ARG:NH2	2.06	0.70
1:D:353:GLU:HG3	1:D:440:PRO:HG2	1.73	0.70
1:C:387:CYS:HB3	1:C:410:LEU:HD23	1.72	0.69
1:A:416:LEU:HD11	1:A:436:VAL:HG21	1.75	0.69
1:B:388:ARG:NH1	1:B:450:LYS:HE2	2.07	0.69
1:C:443:THR:HG22	1:C:446:ASP:OD2	1.93	0.68
1:C:352:VAL:HG21	1:C:436:VAL:HG13	1.73	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:252:ARG:HH21	1:D:254:LEU:HD11	1.57	0.68
1:D:301:THR:OG1	1:D:327:ARG:HG2	1.93	0.68
1:B:389:ILE:HG12	1:B:408:LEU:CD2	2.23	0.68
1:A:352:VAL:CG1	1:A:416:LEU:HD12	2.15	0.67
1:B:66:VAL:HG13	1:B:160:GLN:OE1	1.95	0.67
1:B:387:CYS:HB3	1:B:410:LEU:HD23	1.76	0.67
1:B:450:LYS:HD3	1:B:450:LYS:H	1.59	0.67
1:B:268:ILE:HG23	1:B:271:ARG:HB2	1.75	0.67
1:D:104:ARG:HH11	1:D:104:ARG:HG2	1.60	0.67
1:C:166:LEU:O	1:C:170:GLN:HG3	1.94	0.66
1:D:209:LYS:O	1:D:213:THR:HG23	1.94	0.66
1:A:145:ASP:CG	1:A:250:PRO:HG3	2.16	0.66
1:D:447:LYS:HB3	4:D:1522:HOH:O	1.95	0.66
1:B:291:GLU:OE2	1:B:293:LEU:HD21	1.95	0.66
1:B:332:GLU:H	1:B:332:GLU:CD	1.99	0.66
1:B:451:TRP:HB3	4:B:1451:HOH:O	1.96	0.66
1:D:65:HIS:HD2	1:D:160:GLN:H	1.44	0.66
1:A:368:LYS:H	1:A:368:LYS:CD	1.97	0.66
1:C:371:VAL:HG12	1:C:397:LEU:HD23	1.78	0.66
1:C:145:ASP:OD1	1:C:250:PRO:HG3	1.95	0.65
1:C:371:VAL:HG12	1:C:397:LEU:CD2	2.27	0.65
1:A:416:LEU:HD13	1:A:436:VAL:HG21	1.78	0.65
1:A:372:SER:O	1:A:373:HIS:HB2	1.97	0.65
1:B:331:ARG:HG3	1:B:331:ARG:HH11	1.61	0.65
1:A:93:GLU:H	1:A:93:GLU:CD	2.00	0.65
1:C:102:ARG:HE	1:C:105:GLY:HA2	1.61	0.65
1:A:298:ASN:HB2	4:A:1664:HOH:O	1.97	0.64
1:B:90:LYS:HZ1	1:B:94:GLU:HG2	1.60	0.64
1:A:449:ILE:H	1:A:449:ILE:CD1	2.08	0.64
1:A:416:LEU:HD11	1:A:436:VAL:CG2	2.27	0.64
1:B:352:VAL:HG23	1:B:438:ASP:O	1.98	0.63
1:A:344:GLY:O	1:D:418:LYS:NZ	2.31	0.63
1:C:102:ARG:HB2	4:C:1543:HOH:O	1.99	0.63
1:D:231:LEU:HD23	4:D:1351:HOH:O	1.98	0.63
1:D:252:ARG:NH2	1:D:254:LEU:HD21	2.14	0.63
1:A:229:PRO:O	1:A:234:LYS:HG2	1.98	0.63
1:C:140:GLY:HA3	1:C:421:ARG:NE	2.13	0.63
1:B:390:ILE:HB	1:B:407:THR:HB	1.81	0.62
1:B:268:ILE:HD13	1:B:271:ARG:HD3	1.81	0.62
1:B:65:HIS:HD2	1:B:160:GLN:H	1.46	0.62
1:D:246:TYR:O	1:D:248:PRO:HD3	2.00	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:268:ILE:CG2	1:B:271:ARG:HB2	2.29	0.62
1:B:409:ILE:HG23	1:B:442:MET:HE1	1.83	0.61
1:D:60:VAL:HG12	1:D:61:GLY:N	2.15	0.61
1:D:366:ARG:NH1	1:D:368:LYS:O	2.33	0.61
1:D:239:LEU:O	1:D:243:VAL:HG23	2.01	0.60
1:C:389:ILE:C	1:C:390:ILE:HD12	2.20	0.60
1:D:322:LEU:C	1:D:322:LEU:HD12	2.22	0.60
1:D:80:ILE:HD13	1:D:233:LEU:HD12	1.82	0.60
1:B:216:ILE:HD12	1:B:216:ILE:N	2.16	0.60
1:C:108:ILE:HD12	1:C:132:ASP:HA	1.83	0.60
1:D:431:ILE:HD12	1:D:432:GLY:N	2.16	0.60
1:D:353:GLU:HG3	1:D:440:PRO:CG	2.31	0.60
1:C:443:THR:HG22	1:C:446:ASP:CG	2.22	0.60
1:D:131:ALA:O	1:D:135:LYS:HG3	2.01	0.60
1:D:352:VAL:HG22	1:D:436:VAL:HG13	1.83	0.60
1:B:308:MET:HE2	1:B:313:LEU:HD12	1.84	0.60
1:D:350:GLN:HG3	1:D:410:LEU:O	2.02	0.59
1:C:65:HIS:HE1	4:C:1571:HOH:O	1.85	0.59
1:D:194:LEU:HD23	4:D:1541:HOH:O	2.01	0.59
1:D:405:LYS:HZ2	1:D:437:THR:CB	2.15	0.59
1:C:425:ARG:HD3	4:C:1546:HOH:O	2.01	0.59
1:A:330:LYS:HG2	1:A:333:ASP:OD1	2.03	0.59
1:C:293:LEU:HB3	1:C:348:PRO:HG3	1.83	0.59
1:C:171:ILE:HG22	1:C:435:LEU:HD22	1.83	0.59
1:B:265:VAL:HB	1:B:331:ARG:HH12	1.68	0.59
1:A:368:LYS:N	1:A:368:LYS:CD	2.63	0.59
1:B:192:VAL:O	1:B:195:VAL:HG12	2.02	0.58
1:C:279:LEU:HD23	1:C:317:GLU:C	2.23	0.58
1:D:433:THR:HG22	4:D:1362:HOH:O	2.03	0.58
1:A:65:HIS:HD2	1:A:160:GLN:H	1.51	0.58
1:C:390:ILE:HD12	1:C:390:ILE:N	2.17	0.58
1:C:449:ILE:HD12	1:C:449:ILE:C	2.23	0.58
1:D:374:PHE:CD2	1:D:376:PRO:HG3	2.39	0.58
1:B:373:HIS:HA	1:B:388:ARG:CG	2.33	0.58
1:C:137:MET:CE	1:C:167:LEU:HD23	2.33	0.58
1:D:385:MET:SD	1:D:411:ARG:HG3	2.44	0.58
1:C:360:THR:HG22	1:C:362:GLU:H	1.67	0.58
1:B:352:VAL:HG23	1:B:436:VAL:HG13	1.82	0.58
1:C:137:MET:HE3	1:C:167:LEU:HD23	1.85	0.57
1:B:146:GLY:HA3	1:B:247:ILE:HD12	1.85	0.57
1:C:278:THR:HG23	4:C:1367:HOH:O	2.04	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:361:LYS:HD3	1:D:367:HIS:CD2	2.38	0.57
1:A:307:GLU:HG2	4:A:1352:HOH:O	2.02	0.57
1:D:166:LEU:O	1:D:170:GLN:HG3	2.05	0.57
1:D:315:ARG:HG2	4:D:1394:HOH:O	2.05	0.57
1:D:385:MET:SD	1:D:411:ARG:CG	2.92	0.57
1:D:89:PHE:CD1	1:D:89:PHE:C	2.78	0.57
1:C:428:ASN:HA	4:C:1546:HOH:O	2.04	0.57
1:D:368:LYS:N	1:D:368:LYS:CD	2.66	0.57
1:A:197:LEU:O	1:A:201:GLU:HG3	2.04	0.57
1:C:372:SER:O	1:C:373:HIS:HB2	2.04	0.57
1:A:449:ILE:CG1	1:A:451:TRP:NE1	2.61	0.57
1:C:145:ASP:OD2	1:C:250:PRO:HG3	2.04	0.57
1:B:395:LYS:HE2	1:B:404:LEU:HD13	1.86	0.56
1:A:449:ILE:N	1:A:449:ILE:HD13	2.15	0.56
1:B:135:LYS:HE2	1:B:357:TYR:CZ	2.40	0.56
1:B:395:LYS:HE2	1:B:404:LEU:CD1	2.36	0.56
1:D:366:ARG:HD3	1:D:370:PHE:HD2	1.71	0.56
1:A:120:ARG:NH1	1:A:247:ILE:O	2.37	0.56
1:B:127:CYS:HB2	1:B:133:TYR:CE1	2.40	0.56
1:C:62:THR:HG23	1:C:124:HIS:CE1	2.40	0.56
1:D:197:LEU:O	1:D:201:GLU:HG2	2.05	0.56
1:D:295:HIS:O	1:D:297:LYS:HG3	2.05	0.56
1:D:258:PHE:HB2	1:D:279:LEU:HD11	1.88	0.56
1:B:83:GLU:C	1:B:85:GLY:H	2.09	0.56
1:C:188:ASP:HB2	1:C:190:GLU:OE1	2.06	0.56
1:B:93:GLU:CD	1:B:93:GLU:H	2.08	0.56
1:B:335:ARG:NH2	4:B:1309:HOH:O	2.39	0.55
1:B:57:HIS:HB2	4:B:1431:HOH:O	2.05	0.55
1:C:429:ARG:HB2	1:C:429:ARG:HH11	1.71	0.55
1:B:392:PRO:HG3	1:B:405:LYS:O	2.07	0.55
1:D:222:CYS:HB3	1:D:227:ARG:O	2.07	0.55
1:A:216:ILE:N	1:A:216:ILE:HD12	2.22	0.55
1:B:65:HIS:CD2	1:B:160:GLN:HB2	2.42	0.55
1:D:390:ILE:HB	1:D:407:THR:HB	1.86	0.55
1:B:433:THR:HG22	4:B:1357:HOH:O	2.06	0.55
1:B:330:LYS:HB3	1:B:332:GLU:OE2	2.07	0.55
1:C:121:HIS:HB2	4:C:1471:HOH:O	2.07	0.55
1:C:65:HIS:HD2	1:C:160:GLN:H	1.53	0.55
1:D:57:HIS:CE1	1:D:123:ALA:HB2	2.41	0.55
1:D:431:ILE:HD12	1:D:431:ILE:C	2.27	0.55
1:C:102:ARG:NE	1:C:105:GLY:HA2	2.22	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:79:LYS:HD2	1:D:91:LYS:NZ	2.22	0.55
1:D:191:MET:O	1:D:195:VAL:HG23	2.07	0.54
1:D:58:VAL:HB	1:D:122:TYR:CE1	2.41	0.54
1:D:263:GLU:HG3	4:D:1384:HOH:O	2.06	0.54
1:A:390:ILE:N	1:A:390:ILE:HD12	2.22	0.54
1:B:438:ASP:C	1:B:440:PRO:HD3	2.28	0.54
1:D:351:LYS:HB2	1:D:442:MET:SD	2.47	0.54
1:A:209:LYS:O	1:A:213:THR:HG23	2.08	0.54
1:A:404:LEU:HD23	1:A:404:LEU:N	2.22	0.54
1:B:312:SER:O	1:B:313:LEU:HD23	2.08	0.54
1:B:353:GLU:HG3	1:B:440:PRO:CG	2.37	0.54
1:C:378:MET:CE	1:C:408:LEU:HD22	2.38	0.54
1:A:243:VAL:HG13	1:A:247:ILE:HD12	1.88	0.54
1:D:233:LEU:O	1:D:237:GLN:HG3	2.08	0.54
1:C:135:LYS:HE2	1:C:357:TYR:CZ	2.42	0.54
1:B:416:LEU:HD22	1:B:436:VAL:CG2	2.35	0.53
1:D:60:VAL:CG1	1:D:61:GLY:N	2.71	0.53
1:B:139:THR:O	1:B:139:THR:HG22	2.08	0.53
1:C:322:LEU:C	1:C:322:LEU:HD12	2.28	0.53
1:B:106:ILE:HG23	1:B:363:GLU:OE2	2.08	0.53
1:C:353:GLU:OE2	1:C:440:PRO:HG2	2.08	0.53
1:A:352:VAL:HG11	1:A:416:LEU:HD11	1.87	0.53
1:C:252:ARG:HH21	1:C:254:LEU:HD11	1.73	0.53
1:B:140:GLY:HA3	1:B:421:ARG:NE	2.24	0.53
1:B:62:THR:HG23	1:B:124:HIS:CE1	2.44	0.53
1:D:104:ARG:NH1	1:D:104:ARG:HG2	2.23	0.53
1:C:360:THR:CG2	1:C:362:GLU:HG2	2.38	0.53
1:C:360:THR:HG22	1:C:361:LYS:N	2.23	0.53
1:A:392:PRO:HD2	1:A:395:LYS:CB	2.39	0.53
1:B:450:LYS:HD2	4:B:1457:HOH:O	2.09	0.53
1:C:366:ARG:NH1	1:C:370:PHE:HB3	2.23	0.52
1:B:120:ARG:HH11	1:B:244:ASP:HA	1.73	0.52
1:D:378:MET:CE	1:D:408:LEU:HD13	2.39	0.52
1:D:443:THR:CG2	1:D:445:GLU:HB3	2.38	0.52
1:A:65:HIS:CD2	1:A:160:GLN:HB2	2.44	0.52
1:B:65:HIS:CE1	1:B:66:VAL:HG22	2.45	0.52
1:A:82:ALA:HA	1:A:87:ALA:O	2.09	0.52
1:B:178:VAL:HB	1:B:215:ILE:HG12	1.91	0.52
1:B:119:ALA:C	1:B:120:ARG:HG3	2.30	0.52
1:C:411:ARG:HA	1:C:451:TRP:CZ2	2.45	0.52
1:D:257:PRO:CB	1:D:345:SER:HB2	2.39	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:387:CYS:HB3	1:D:410:LEU:HD23	1.91	0.52
1:A:158:MET:HB3	1:A:159:PRO:CD	2.39	0.52
1:A:89:PHE:CE2	1:A:91:LYS:HG2	2.45	0.52
1:A:260:LEU:HD13	1:A:260:LEU:C	2.30	0.52
1:C:448:ASN:ND2	1:C:448:ASN:O	2.43	0.52
1:D:375:MET:HA	1:D:387:CYS:O	2.09	0.52
1:D:62:THR:O	1:D:133:TYR:CE2	2.63	0.52
1:D:243:VAL:HG13	1:D:247:ILE:HD12	1.90	0.52
1:D:404:LEU:N	1:D:404:LEU:HD23	2.25	0.52
1:B:58:VAL:CG2	1:B:120:ARG:HH21	2.22	0.51
1:B:316:ALA:CB	1:B:322:LEU:HD22	2.41	0.51
1:D:352:VAL:CG2	1:D:436:VAL:HG13	2.40	0.51
1:B:118:ALA:HB3	4:B:1561:HOH:O	2.09	0.51
1:B:187:GLN:HA	4:B:1458:HOH:O	2.11	0.51
1:D:213:THR:HG22	4:D:1500:HOH:O	2.11	0.51
1:D:346:ILE:CD1	1:D:415:ILE:HG23	2.41	0.51
1:B:352:VAL:HG22	1:B:353:GLU:N	2.26	0.51
1:B:389:ILE:HG12	1:B:408:LEU:HD21	1.91	0.51
1:B:409:ILE:HG23	1:B:442:MET:CE	2.40	0.51
1:A:374:PHE:CD2	1:A:376:PRO:HG3	2.45	0.51
1:B:449:ILE:HG12	1:B:450:LYS:N	2.26	0.51
1:B:57:HIS:CE1	1:B:123:ALA:HB2	2.45	0.51
1:A:322:LEU:HD12	1:A:322:LEU:C	2.31	0.51
1:B:188:ASP:HB3	1:B:190:GLU:OE1	2.11	0.51
1:B:349:HIS:ND1	1:B:439:THR:HG21	2.25	0.51
1:D:98:ALA:HB1	1:D:110:ALA:C	2.31	0.51
1:D:271:ARG:HG2	1:D:325:LEU:HD11	1.92	0.51
1:B:350:GLN:HG2	1:B:442:MET:HE2	1.93	0.51
1:B:443:THR:CG2	1:B:445:GLU:HG2	2.40	0.51
1:B:399:MET:O	1:B:402:GLU:HB3	2.11	0.51
1:D:65:HIS:HA	1:D:160:GLN:HB2	1.92	0.51
1:B:350:GLN:HG2	1:B:442:MET:CE	2.41	0.51
1:D:284:LEU:HD23	1:D:285:LYS:N	2.26	0.51
1:C:55:LYS:HB2	1:C:56:PRO:CD	2.40	0.50
1:A:332:GLU:CB	1:C:229:PRO:HG3	2.39	0.50
1:C:147:CYS:O	1:C:176:VAL:HG13	2.11	0.50
1:C:369:PRO:HG3	1:C:400:PRO:CG	2.42	0.50
1:D:106:ILE:HD11	1:D:433:THR:OG1	2.11	0.50
1:D:399:MET:HB2	1:D:402:GLU:CD	2.32	0.50
1:B:167:LEU:O	1:B:171:ILE:HG23	2.11	0.50
1:D:104:ARG:NH2	1:D:430:THR:OG1	2.44	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:234:LYS:O	1:B:238:LYS:HG3	2.11	0.50
1:D:74:THR:HG22	1:D:95:ILE:HD13	1.92	0.50
1:A:252:ARG:HD3	4:A:1418:HOH:O	2.12	0.50
1:B:283:ILE:HD13	1:B:315:ARG:NH2	2.27	0.50
1:C:451:TRP:HB2	4:C:1523:HOH:O	2.12	0.50
1:D:98:ALA:CB	1:D:111:ALA:HB2	2.36	0.50
1:B:378:MET:CE	1:B:408:LEU:HD13	2.42	0.50
1:C:443:THR:HG23	1:C:446:ASP:H	1.77	0.50
1:D:283:ILE:HD12	1:D:315:ARG:NH2	2.27	0.50
1:D:389:ILE:HG12	1:D:408:LEU:CD2	2.42	0.50
1:B:265:VAL:HB	1:B:331:ARG:NH1	2.26	0.50
1:B:58:VAL:HG21	1:B:120:ARG:CZ	2.42	0.50
1:C:91:LYS:HD3	1:C:94:GLU:OE2	2.12	0.50
1:D:259:LEU:HD11	1:D:339:VAL:HG11	1.93	0.50
1:D:285:LYS:N	1:D:288:ASP:OD2	2.44	0.49
1:B:443:THR:HG22	1:B:445:GLU:H	1.76	0.49
1:D:216:ILE:HD12	1:D:216:ILE:N	2.26	0.49
1:A:57:HIS:CE1	1:A:123:ALA:HB2	2.47	0.49
1:B:369:PRO:CG	1:B:399:MET:SD	3.00	0.49
1:B:446:ASP:O	1:B:449:ILE:HG22	2.13	0.49
1:A:86:GLY:O	1:A:87:ALA:HB2	2.12	0.49
1:B:308:MET:CE	1:B:313:LEU:HD12	2.41	0.49
1:B:418:LYS:HA	1:B:436:VAL:HG12	1.95	0.49
1:C:450:LYS:HD3	1:C:450:LYS:N	2.28	0.49
1:D:285:LYS:NZ	1:D:285:LYS:HB2	2.28	0.49
1:D:418:LYS:HA	1:D:436:VAL:HG12	1.95	0.49
1:C:89:PHE:CZ	1:C:91:LYS:HE3	2.48	0.49
1:D:158:MET:HB3	1:D:159:PRO:CD	2.43	0.49
1:D:62:THR:HG23	1:D:124:HIS:NE2	2.28	0.49
1:C:188:ASP:OD2	1:C:191:MET:HB2	2.13	0.49
1:B:186:VAL:HG12	1:B:188:ASP:H	1.78	0.49
1:D:120:ARG:HD2	1:D:122:TYR:OH	2.12	0.49
1:C:127:CYS:HB2	1:C:133:TYR:CE1	2.48	0.49
1:C:216:ILE:N	1:C:216:ILE:HD12	2.28	0.49
1:A:192:VAL:HG12	1:A:196:GLU:OE2	2.12	0.48
1:A:204:THR:HA	1:A:208:TYR:O	2.12	0.48
1:B:149:LEU:HD11	1:B:161:THR:HG23	1.94	0.48
1:B:350:GLN:HB2	1:B:413:PRO:HG3	1.95	0.48
1:C:65:HIS:HA	1:C:160:GLN:HB2	1.95	0.48
1:D:223:ALA:HB2	1:D:232:GLY:C	2.33	0.48
1:D:346:ILE:HD11	1:D:415:ILE:HG23	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:355:GLN:OE1	1:D:405:LYS:HE2	2.14	0.48
1:B:190:GLU:CD	1:B:190:GLU:H	2.17	0.48
1:C:418:LYS:HA	1:C:436:VAL:HG12	1.94	0.48
1:D:366:ARG:C	1:D:368:LYS:H	2.16	0.48
1:B:227:ARG:O	1:B:228:ASP:C	2.51	0.48
1:C:373:HIS:CD2	1:C:388:ARG:NE	2.81	0.48
1:A:369:PRO:CG	1:A:399:MET:SD	3.01	0.48
1:B:380:SER:HB3	1:B:383:TRP:CZ2	2.49	0.48
1:B:443:THR:HB	1:B:446:ASP:OD2	2.12	0.48
1:C:279:LEU:HD23	1:C:317:GLU:CA	2.42	0.48
1:D:371:VAL:HG23	1:D:373:HIS:H	1.78	0.48
1:B:88:LYS:HD3	1:B:89:PHE:N	2.28	0.48
1:B:404:LEU:HD11	1:B:406:LEU:HD21	1.95	0.48
1:C:137:MET:HE3	1:C:167:LEU:HB3	1.96	0.48
1:C:295:HIS:O	1:C:297:LYS:HG3	2.13	0.48
1:A:188:ASP:OD2	1:A:190:GLU:HG2	2.14	0.48
1:B:373:HIS:HA	1:B:388:ARG:HG2	1.94	0.48
1:B:67:ASP:OD1	1:B:67:ASP:O	2.31	0.48
1:A:442:MET:HE3	1:A:446:ASP:HB3	1.96	0.48
1:B:225:GLU:HB2	1:B:227:ARG:HD3	1.96	0.48
1:A:142:ALA:HB2	4:A:1496:HOH:O	2.14	0.48
1:B:204:THR:HA	1:B:208:TYR:O	2.14	0.47
1:B:418:LYS:HE2	1:B:439:THR:H	1.79	0.47
1:C:102:ARG:HE	1:C:105:GLY:CA	2.26	0.47
1:C:350:GLN:HG3	1:C:410:LEU:O	2.14	0.47
1:B:73:LEU:O	1:B:77:ILE:HG13	2.14	0.47
1:D:283:ILE:HD12	1:D:315:ARG:CZ	2.44	0.47
1:D:443:THR:C	1:D:445:GLU:N	2.66	0.47
1:A:279:LEU:HD23	1:A:317:GLU:C	2.35	0.47
1:A:62:THR:HG23	1:A:124:HIS:CE1	2.50	0.47
1:B:145:ASP:OD1	1:B:250:PRO:HG3	2.13	0.47
1:D:342:LYS:HE3	4:D:1451:HOH:O	2.13	0.47
1:D:358:ILE:O	1:D:401:GLY:N	2.38	0.47
1:D:79:LYS:HD3	1:D:224:LEU:HD12	1.96	0.47
1:C:252:ARG:NH2	1:C:317:GLU:OE2	2.48	0.47
1:D:405:LYS:NZ	1:D:437:THR:OG1	2.43	0.47
1:B:190:GLU:O	1:B:194:LEU:HG	2.15	0.47
1:B:89:PHE:C	1:B:89:PHE:CD1	2.88	0.47
1:B:225:GLU:O	1:B:227:ARG:HG3	2.14	0.47
1:C:374:PHE:HE2	1:C:431:ILE:CD1	2.27	0.47
1:B:371:VAL:HG12	1:B:397:LEU:HD23	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:58:VAL:HG21	1:B:120:ARG:NE	2.30	0.47
1:C:451:TRP:N	1:C:451:TRP:CD1	2.83	0.47
1:D:130:HIS:ND1	1:D:160:GLN:HG2	2.30	0.47
1:C:158:MET:HB3	1:C:159:PRO:CD	2.45	0.46
1:C:346:ILE:HD12	1:C:415:ILE:HD12	1.97	0.46
1:A:79:LYS:HB2	1:A:89:PHE:CE1	2.51	0.46
1:A:80:ILE:HD12	1:A:236:VAL:HG11	1.96	0.46
1:C:188:ASP:C	1:C:190:GLU:N	2.69	0.46
1:D:252:ARG:NH2	1:D:317:GLU:OE2	2.35	0.46
1:D:385:MET:SD	1:D:411:ARG:NE	2.80	0.46
1:D:405:LYS:HB3	4:D:1478:HOH:O	2.15	0.46
1:B:260:LEU:HD13	1:B:260:LEU:C	2.36	0.46
1:B:82:ALA:HA	4:B:1330:HOH:O	2.15	0.46
1:C:421:ARG:HG2	1:C:421:ARG:HH11	1.79	0.46
1:A:114:GLU:OE1	1:A:121:HIS:NE2	2.46	0.46
1:B:404:LEU:HD23	1:B:404:LEU:N	2.30	0.46
1:C:90:LYS:HD2	1:C:113:VAL:HG12	1.96	0.46
1:D:366:ARG:HG3	1:D:368:LYS:O	2.16	0.46
1:B:263:GLU:HG2	1:B:277:GLY:HA2	1.97	0.46
1:D:283:ILE:HG22	4:D:1450:HOH:O	2.16	0.46
1:D:57:HIS:HE1	1:D:123:ALA:HB2	1.81	0.46
1:B:331:ARG:HG3	1:B:331:ARG:NH1	2.28	0.46
1:B:443:THR:HG22	1:B:445:GLU:HG2	1.98	0.46
1:C:253:ASP:HB3	1:C:256:LYS:HD2	1.97	0.46
1:D:195:VAL:O	1:D:199:ILE:HG13	2.15	0.46
1:D:252:ARG:NH2	1:D:254:LEU:HD11	2.27	0.46
1:D:260:LEU:HD11	1:D:277:GLY:HA3	1.98	0.46
1:B:225:GLU:OE1	1:B:227:ARG:NH1	2.46	0.46
1:C:376:PRO:HG3	1:C:389:ILE:HD11	1.97	0.46
1:D:190:GLU:O	1:D:194:LEU:HG	2.16	0.46
1:D:366:ARG:HD3	1:D:370:PHE:CD2	2.49	0.46
1:D:373:HIS:HB3	1:D:388:ARG:NH2	2.30	0.46
1:D:79:LYS:HD2	1:D:91:LYS:HZ3	1.81	0.46
1:D:91:LYS:HD3	1:D:92:TYR:N	2.20	0.46
1:D:134:VAL:O	1:D:138:ILE:HG13	2.16	0.46
1:B:442:MET:SD	1:B:446:ASP:HB3	2.56	0.46
1:C:254:LEU:HD22	1:C:317:GLU:HB2	1.98	0.46
1:A:392:PRO:HD2	1:A:395:LYS:HB2	1.98	0.45
1:B:297:LYS:HE2	1:B:297:LYS:HB3	1.77	0.45
1:B:292:PHE:HZ	1:B:326:VAL:HG11	1.81	0.45
1:A:222:CYS:HB3	1:A:227:ARG:O	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:103:ALA:O	1:B:104:ARG:HB2	2.16	0.45
1:B:158:MET:HB3	1:B:159:PRO:CD	2.46	0.45
1:D:366:ARG:O	1:D:368:LYS:N	2.49	0.45
1:D:392:PRO:HG2	1:D:405:LYS:O	2.16	0.45
1:D:409:ILE:O	1:D:451:TRP:HH2	1.99	0.45
1:A:108:ILE:CD1	1:A:110:ALA:HB2	2.40	0.45
1:A:188:ASP:OD2	1:A:190:GLU:HB2	2.17	0.45
1:B:356:VAL:O	1:B:403:ASP:HA	2.17	0.45
1:D:157:PRO:HD2	1:D:198:GLU:OE2	2.16	0.45
1:B:418:LYS:HE2	1:B:438:ASP:HA	1.98	0.45
1:C:182:LYS:HG2	3:C:1303:GDP:C6	2.52	0.45
1:C:366:ARG:HH11	1:C:370:PHE:HB3	1.80	0.45
1:D:60:VAL:O	1:D:124:HIS:HA	2.16	0.45
1:D:120:ARG:NH1	1:D:247:ILE:O	2.44	0.45
1:D:449:ILE:HG22	4:D:1508:HOH:O	2.15	0.45
1:D:65:HIS:CD2	1:D:160:GLN:HB2	2.51	0.45
1:D:93:GLU:CD	1:D:93:GLU:H	2.20	0.45
1:D:90:LYS:HE2	1:D:94:GLU:HG2	1.98	0.45
1:C:252:ARG:NH2	1:C:254:LEU:HD11	2.30	0.45
1:D:271:ARG:NH2	4:D:1448:HOH:O	2.49	0.45
1:D:170:GLN:HE22	1:D:405:LYS:HZ1	1.64	0.45
1:A:404:LEU:HD11	1:A:406:LEU:HD21	1.99	0.45
1:C:404:LEU:HD11	1:C:406:LEU:HD21	1.99	0.45
1:C:383:TRP:CG	1:C:414:MET:HE2	2.51	0.45
1:B:195:VAL:O	1:B:199:ILE:HG13	2.17	0.45
1:D:91:LYS:HG3	1:D:93:GLU:OE1	2.15	0.45
1:A:106:ILE:HD13	1:A:433:THR:HG21	1.98	0.45
1:B:55:LYS:NZ	1:B:117:THR:O	2.48	0.45
1:B:388:ARG:NH2	1:B:449:ILE:HG13	2.32	0.45
1:D:356:VAL:O	1:D:403:ASP:HA	2.17	0.45
1:C:149:LEU:HD22	1:C:165:LEU:HD21	1.98	0.45
1:D:353:GLU:HB2	1:D:438:ASP:HB2	1.98	0.45
1:D:158:MET:HB3	1:D:159:PRO:HD2	1.99	0.45
1:B:108:ILE:HD11	1:B:135:LYS:HB3	1.98	0.44
1:D:62:THR:O	1:D:133:TYR:HE2	1.99	0.44
1:D:366:ARG:H	1:D:431:ILE:HG22	1.82	0.44
1:A:190:GLU:O	1:A:194:LEU:HG	2.17	0.44
1:A:362:GLU:OE1	1:A:362:GLU:N	2.41	0.44
1:A:431:ILE:C	1:A:431:ILE:HD12	2.38	0.44
1:A:449:ILE:HG13	1:A:451:TRP:HE1	1.80	0.44
1:C:283:ILE:HD13	1:C:315:ARG:NH2	2.32	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:367:HIS:HA	4:D:1336:HOH:O	2.16	0.44
1:A:188:ASP:HA	4:A:1477:HOH:O	2.17	0.44
1:B:182:LYS:HG2	3:B:1302:GDP:C6	2.52	0.44
1:D:291:GLU:CD	1:D:293:LEU:HD21	2.37	0.44
1:A:57:HIS:HE1	1:A:123:ALA:HB2	1.83	0.44
1:C:378:MET:O	1:C:384:ASP:HA	2.17	0.44
1:C:102:ARG:HD3	4:C:1508:HOH:O	2.17	0.44
1:C:337:GLY:CA	1:C:383:TRP:HB3	2.48	0.44
1:C:443:THR:CG2	1:C:446:ASP:H	2.30	0.44
1:D:209:LYS:CB	1:D:212:GLU:HG2	2.46	0.44
1:A:212:GLU:N	1:A:212:GLU:OE2	2.49	0.44
1:D:62:THR:HG23	1:D:124:HIS:CE1	2.52	0.44
1:A:390:ILE:HB	1:A:407:THR:HB	2.00	0.44
1:D:405:LYS:NZ	1:D:437:THR:CB	2.81	0.44
1:A:366:ARG:NH2	1:A:368:LYS:HG2	2.33	0.44
1:B:140:GLY:HA3	1:B:421:ARG:CZ	2.48	0.44
1:C:180:VAL:HB	1:C:217:VAL:HG22	2.00	0.44
1:D:102:ARG:NH1	1:D:102:ARG:HG3	2.32	0.44
1:D:103:ALA:O	1:D:104:ARG:HB3	2.18	0.44
1:D:291:GLU:HG2	1:D:293:LEU:HD21	2.00	0.44
1:A:353:GLU:HG3	1:A:440:PRO:HG2	1.99	0.44
1:C:263:GLU:HG3	4:C:1514:HOH:O	2.18	0.44
1:D:380:SER:HB3	1:D:383:TRP:CZ2	2.53	0.44
1:D:98:ALA:HA	1:D:99:PRO:HD3	1.80	0.44
1:D:130:HIS:O	1:D:134:VAL:HG23	2.18	0.43
1:D:252:ARG:CZ	1:D:254:LEU:HD21	2.47	0.43
1:A:378:MET:CE	1:A:408:LEU:HD22	2.48	0.43
1:B:301:THR:OG1	1:B:302:VAL:N	2.48	0.43
1:B:349:HIS:CE1	1:B:439:THR:HG21	2.53	0.43
1:D:87:ALA:O	1:D:88:LYS:C	2.56	0.43
1:B:111:ALA:O	1:B:125:THR:HA	2.18	0.43
1:B:373:HIS:O	1:B:375:MET:HG3	2.19	0.43
1:B:388:ARG:HH12	1:B:450:LYS:CE	2.15	0.43
1:D:153:ALA:HB2	1:D:180:VAL:CG1	2.42	0.43
1:D:203:LEU:HD13	1:D:213:THR:OG1	2.18	0.43
1:D:347:GLN:HA	1:D:348:PRO:HD3	1.82	0.43
1:D:411:ARG:HA	1:D:451:TRP:CZ2	2.54	0.43
1:B:188:ASP:O	1:B:191:MET:HB3	2.19	0.43
1:B:157:PRO:HD2	1:B:198:GLU:OE1	2.18	0.43
1:B:431:ILE:HD12	1:B:431:ILE:C	2.39	0.43
1:C:171:ILE:HA	1:C:435:LEU:HD21	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:170:GLN:NE2	1:D:405:LYS:HZ1	2.17	0.43
1:D:70:LYS:HA	1:D:150:VAL:HG21	2.00	0.43
1:A:233:LEU:O	1:A:237:GLN:HG3	2.19	0.43
1:B:171:ILE:HG22	1:B:435:LEU:HD22	2.00	0.43
1:B:290:CYS:SG	1:B:301:THR:HG23	2.59	0.43
1:C:374:PHE:HE2	1:C:431:ILE:HD11	1.83	0.43
1:C:55:LYS:HB2	1:C:56:PRO:HD2	1.99	0.43
1:A:130:HIS:ND1	1:A:160:GLN:HG2	2.34	0.43
1:C:356:VAL:O	1:C:403:ASP:HA	2.19	0.43
1:D:114:GLU:HB3	1:D:121:HIS:HE1	1.83	0.43
1:A:106:ILE:CD1	1:A:433:THR:HG21	2.49	0.43
1:C:330:LYS:HB3	1:C:333:ASP:OD1	2.18	0.43
1:C:444:GLU:HA	1:C:447:LYS:HD3	2.01	0.43
1:B:216:ILE:CD1	1:B:216:ILE:N	2.81	0.42
1:B:353:GLU:CG	1:B:440:PRO:HG2	2.44	0.42
1:C:373:HIS:HD2	1:C:388:ARG:NE	2.17	0.42
1:C:396:GLU:O	1:C:397:LEU:HD23	2.18	0.42
1:B:395:LYS:HB3	1:B:395:LYS:HE3	1.88	0.42
1:C:360:THR:HG21	1:C:362:GLU:HG2	2.01	0.42
1:D:79:LYS:CD	1:D:224:LEU:HD12	2.49	0.42
1:D:183:ALA:HB3	1:D:231:LEU:HD22	2.01	0.42
1:C:176:VAL:O	1:C:213:THR:HG23	2.19	0.42
1:C:258:PHE:HB2	1:C:279:LEU:HD11	2.02	0.42
1:D:372:SER:O	1:D:389:ILE:O	2.38	0.42
1:A:69:GLY:HA3	1:A:181:ASN:ND2	2.35	0.42
1:B:335:ARG:HG3	1:B:336:ARG:N	2.34	0.42
1:D:107:THR:O	1:D:135:LYS:NZ	2.45	0.42
1:D:189:SER:O	1:D:193:GLU:HG3	2.20	0.42
1:A:266:TYR:HB2	1:A:331:ARG:HH21	1.84	0.42
1:A:399:MET:O	1:A:402:GLU:HB3	2.20	0.42
1:B:58:VAL:HG21	1:B:120:ARG:HE	1.83	0.42
1:B:133:TYR:HB3	1:B:137:MET:HE1	2.01	0.42
1:C:332:GLU:N	1:C:332:GLU:CD	2.72	0.42
1:C:392:PRO:HD2	1:C:395:LYS:HB2	2.02	0.42
1:D:209:LYS:HB2	1:D:212:GLU:HG2	2.00	0.42
1:D:379:PHE:CE1	1:D:425:ARG:HD3	2.54	0.42
1:A:389:ILE:C	1:A:390:ILE:HD12	2.39	0.42
1:B:169:ARG:HD2	1:B:169:ARG:HA	1.91	0.42
1:C:390:ILE:HB	1:C:407:THR:HB	2.01	0.42
1:C:425:ARG:CD	4:C:1546:HOH:O	2.65	0.42
1:D:127:CYS:HB2	1:D:133:TYR:CE1	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:285:LYS:HB2	1:D:288:ASP:OD2	2.20	0.42
1:A:372:SER:O	1:A:373:HIS:CB	2.67	0.42
1:B:379:PHE:CE1	1:B:425:ARG:HD2	2.54	0.42
1:C:197:LEU:HD23	4:C:1405:HOH:O	2.20	0.42
1:B:204:THR:HG23	1:C:255:GLU:HB3	2.01	0.42
1:C:56:PRO:HB2	1:C:120:ARG:HG2	2.02	0.42
1:D:260:LEU:HD13	1:D:260:LEU:C	2.39	0.42
1:A:71:THR:HG23	1:A:95:ILE:HG22	2.02	0.42
1:A:79:LYS:HE3	1:A:89:PHE:CD1	2.55	0.42
1:B:80:ILE:HD13	1:B:233:LEU:HD12	2.02	0.42
1:C:191:MET:O	1:C:195:VAL:HG23	2.20	0.42
1:D:215:ILE:C	1:D:216:ILE:HD12	2.39	0.42
1:D:301:THR:OG1	1:D:302:VAL:N	2.49	0.42
1:D:405:LYS:HD3	1:D:405:LYS:HA	1.85	0.42
1:D:90:LYS:CG	1:D:94:GLU:HG2	2.45	0.42
1:C:404:LEU:HD23	1:C:404:LEU:N	2.35	0.42
1:C:438:ASP:C	1:C:440:PRO:HD3	2.41	0.42
1:C:91:LYS:N	1:C:91:LYS:HD2	2.35	0.42
1:A:400:PRO:HD2	4:A:1631:HOH:O	2.20	0.41
1:A:447:LYS:O	1:A:449:ILE:HD13	2.20	0.41
1:B:190:GLU:N	1:B:190:GLU:CD	2.73	0.41
1:A:127:CYS:HA	1:A:128:PRO:HD3	1.89	0.41
1:A:404:LEU:H	1:A:404:LEU:HD23	1.85	0.41
1:A:55:LYS:HE2	1:A:118:ALA:O	2.19	0.41
1:B:176:VAL:O	1:B:213:THR:HG23	2.21	0.41
1:B:145:ASP:OD2	1:B:250:PRO:HG3	2.21	0.41
1:C:80:ILE:HD12	1:C:236:VAL:HG11	2.02	0.41
1:C:135:LYS:HE2	1:C:357:TYR:CE1	2.55	0.41
1:A:408:LEU:HD12	1:A:408:LEU:N	2.34	0.41
1:B:339:VAL:HB	1:B:415:ILE:HG13	2.02	0.41
1:C:411:ARG:HH11	1:C:411:ARG:HG2	1.85	0.41
1:D:204:THR:HA	1:D:208:TYR:O	2.21	0.41
1:D:252:ARG:NH1	1:D:318:ALA:O	2.53	0.41
1:B:308:MET:SD	1:B:320:ASP:HB3	2.60	0.41
1:A:158:MET:HB3	1:A:159:PRO:HD2	2.02	0.41
1:C:158:MET:HB3	1:C:159:PRO:HD2	2.03	0.41
1:D:352:VAL:HG22	1:D:438:ASP:O	2.20	0.41
1:B:135:LYS:HE2	1:B:357:TYR:OH	2.20	0.41
1:C:166:LEU:HB2	1:C:206:PHE:CE2	2.56	0.41
1:D:325:LEU:HD23	1:D:326:VAL:N	2.35	0.41
1:A:186:VAL:CG1	1:A:191:MET:HB3	2.51	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:93:GLU:N	1:A:93:GLU:CD	2.71	0.41
1:B:215:ILE:C	1:B:216:ILE:HD12	2.41	0.41
1:B:291:GLU:OE1	1:B:300:ARG:HD3	2.21	0.41
1:B:352:VAL:CG2	1:B:353:GLU:N	2.84	0.41
1:C:227:ARG:O	1:C:228:ASP:C	2.58	0.41
1:D:182:LYS:HG2	3:D:1304:GDP:C6	2.55	0.41
1:D:180:VAL:N	1:D:216:ILE:O	2.51	0.41
1:D:122:TYR:OH	1:D:244:ASP:HA	2.20	0.41
1:D:104:ARG:CZ	1:D:430:THR:OG1	2.68	0.41
1:A:275:VAL:CG1	1:A:334:LEU:HD13	2.51	0.41
1:B:124:HIS:CD2	1:B:124:HIS:C	2.94	0.41
1:C:55:LYS:N	4:C:1510:HOH:O	2.54	0.41
1:B:443:THR:HG22	1:B:444:GLU:N	2.35	0.41
1:C:374:PHE:CD2	1:C:376:PRO:HD3	2.56	0.41
1:B:389:ILE:HD11	1:B:424:LEU:HD13	2.03	0.41
1:C:66:VAL:O	1:C:67:ASP:HB2	2.21	0.41
1:D:359:LEU:N	1:D:359:LEU:HD12	2.35	0.41
1:D:361:LYS:HD3	1:D:367:HIS:NE2	2.35	0.41
1:D:416:LEU:HD22	1:D:436:VAL:CG2	2.38	0.41
1:D:74:THR:O	1:D:77:ILE:HB	2.20	0.41
1:A:149:LEU:HD22	1:A:165:LEU:HD21	2.01	0.41
1:B:80:ILE:HD12	1:B:236:VAL:HG11	2.03	0.41
1:C:213:THR:HA	1:C:214:PRO:HD3	1.95	0.41
1:C:421:ARG:NH1	1:C:421:ARG:HG2	2.36	0.41
1:B:268:ILE:O	1:B:268:ILE:HG23	2.21	0.40
1:C:228:ASP:N	1:C:229:PRO:HD3	2.35	0.40
1:A:271:ARG:HD2	4:A:1684:HOH:O	2.21	0.40
1:B:259:LEU:C	1:B:259:LEU:HD23	2.42	0.40
1:C:188:ASP:O	1:C:191:MET:HB3	2.20	0.40
1:C:178:VAL:HB	1:C:215:ILE:HG12	2.02	0.40
1:C:301:THR:OG1	1:C:302:VAL:N	2.51	0.40
1:D:175:HIS:CD2	1:D:248:PRO:HD2	2.56	0.40
1:B:130:HIS:HB2	1:B:160:GLN:OE1	2.21	0.40
1:B:197:LEU:O	1:B:201:GLU:HG3	2.22	0.40
1:D:59:ASN:N	1:D:145:ASP:OD2	2.41	0.40
1:D:89:PHE:CE1	1:D:91:LYS:HE2	2.57	0.40
1:D:293:LEU:CD1	1:D:346:ILE:HG23	2.51	0.40

There are no symmetry-related clashes.

## 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	395/397 (100%)	381 (96%)	14 (4%)	0	100	100
1	B	395/397 (100%)	376 (95%)	18 (5%)	1 (0%)	44	33
1	C	395/397 (100%)	381 (96%)	12 (3%)	2 (0%)	32	19
1	D	395/397 (100%)	361 (91%)	29 (7%)	5 (1%)	14	4
All	All	1580/1588 (100%)	1499 (95%)	73 (5%)	8 (0%)	32	19

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	83	GLU
1	D	88	LYS
1	D	367	HIS
1	C	448	ASN
1	D	128	PRO
1	D	328	GLY
1	B	92	TYR
1	D	296	SER

### 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	332/332 (100%)	324 (98%)	8 (2%)	54	43
1	B	332/332 (100%)	324 (98%)	8 (2%)	54	43

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	C	332/332 (100%)	325 (98%)	7 (2%)	59	49
1	D	332/332 (100%)	322 (97%)	10 (3%)	46	32
All	All	1328/1328 (100%)	1295 (98%)	33 (2%)	53	41

All (33) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	108	ILE
1	A	191	MET
1	A	284	LEU
1	A	368	LYS
1	A	372	SER
1	A	373	HIS
1	A	405	LYS
1	A	449	ILE
1	B	89	PHE
1	B	125	THR
1	B	141	THR
1	B	230	GLU
1	B	284	LEU
1	B	307	GLU
1	B	416	LEU
1	B	450	LYS
1	C	191	MET
1	C	284	LEU
1	C	314	ASP
1	C	333	ASP
1	C	448	ASN
1	C	449	ILE
1	C	450	LYS
1	D	89	PHE
1	D	125	THR
1	D	155	ASP
1	D	191	MET
1	D	284	LEU
1	D	325	LEU
1	D	352	VAL
1	D	368	LYS
1	D	416	LEU
1	D	445	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (21) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	65	HIS
1	A	175	HIS
1	A	347	GLN
1	A	367	HIS
1	A	448	ASN
1	B	65	HIS
1	B	97	ASN
1	B	170	GLN
1	B	355	GLN
1	C	65	HIS
1	C	347	GLN
1	C	349	HIS
1	C	373	HIS
1	C	428	ASN
1	C	448	ASN
1	D	65	HIS
1	D	170	GLN
1	D	175	HIS
1	D	367	HIS
1	D	412	GLN
1	D	448	ASN

### 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 8 ligands modelled in this entry, 4 are monoatomic - leaving 4 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z  > 2$	Counts	RMSZ	# $ Z  > 2$
3	GDP	A	1301	2	25,30,30	1.31	2 (8%)	26,47,47	2.26	5 (19%)
3	GDP	B	1302	2	25,30,30	1.22	4 (16%)	26,47,47	2.28	5 (19%)
3	GDP	C	1303	2	25,30,30	1.21	3 (12%)	26,47,47	2.29	5 (19%)
3	GDP	D	1304	2	25,30,30	1.25	2 (8%)	26,47,47	2.27	5 (19%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	GDP	A	1301	2	-	0/12/32/32	0/3/3/3
3	GDP	B	1302	2	-	0/12/32/32	0/3/3/3
3	GDP	C	1303	2	-	0/12/32/32	0/3/3/3
3	GDP	D	1304	2	-	0/12/32/32	0/3/3/3

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	1303	GDP	PB-O2B	-2.14	1.46	1.54
3	B	1302	GDP	PB-O2B	-2.09	1.46	1.54
3	B	1302	GDP	C2-N1	2.13	1.39	1.35
3	B	1302	GDP	O4'-C1'	2.15	1.44	1.41
3	D	1304	GDP	C2-N1	2.29	1.39	1.35
3	A	1301	GDP	C2-N1	2.39	1.39	1.35
3	C	1303	GDP	C2-N1	2.49	1.39	1.35
3	C	1303	GDP	C6-N1	3.20	1.38	1.33
3	B	1302	GDP	C6-N1	3.29	1.39	1.33
3	D	1304	GDP	C6-N1	3.76	1.39	1.33
3	A	1301	GDP	C6-N1	4.03	1.40	1.33

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	1303	GDP	C5-C6-N1	-7.08	113.41	123.48
3	A	1301	GDP	C5-C6-N1	-7.04	113.45	123.48
3	B	1302	GDP	C5-C6-N1	-6.98	113.55	123.48
3	D	1304	GDP	C5-C6-N1	-6.97	113.56	123.48
3	D	1304	GDP	C6-C5-C4	-3.60	117.26	120.84
3	C	1303	GDP	C6-C5-C4	-3.60	117.26	120.84
3	B	1302	GDP	C6-C5-C4	-3.57	117.30	120.84
3	A	1301	GDP	C6-C5-C4	-3.31	117.56	120.84
3	B	1302	GDP	N3-C2-N1	-3.30	122.63	127.46
3	A	1301	GDP	N3-C2-N1	-3.30	122.65	127.46
3	C	1303	GDP	N3-C2-N1	-3.29	122.66	127.46
3	D	1304	GDP	N3-C2-N1	-3.24	122.73	127.46
3	C	1303	GDP	O3'-C3'-C4'	-2.35	104.22	111.09
3	D	1304	GDP	O3'-C3'-C4'	-2.30	104.36	111.09
3	B	1302	GDP	O3'-C3'-C4'	-2.26	104.48	111.09
3	A	1301	GDP	O3'-C3'-C4'	-2.21	104.64	111.09
3	D	1304	GDP	C6-N1-C2	6.11	124.86	116.06
3	A	1301	GDP	C6-N1-C2	6.20	124.98	116.06
3	B	1302	GDP	C6-N1-C2	6.30	125.13	116.06
3	C	1303	GDP	C6-N1-C2	6.34	125.19	116.06

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	1302	GDP	1	0
3	C	1303	GDP	1	0
3	D	1304	GDP	1	0

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 6 Fit of model and data

### 6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	A	397/397 (100%)	0.45	13 (3%) 47 56	19, 35, 58, 69	0
1	B	397/397 (100%)	0.80	45 (11%) 6 8	33, 47, 66, 71	0
1	C	397/397 (100%)	0.65	30 (7%) 15 21	28, 44, 63, 71	0
1	D	397/397 (100%)	1.41	100 (25%) 1 0	27, 53, 67, 71	0
All	All	1588/1588 (100%)	0.83	188 (11%) 5 8	19, 45, 65, 71	0

All (188) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	85	GLY	11.1
1	B	87	ALA	8.8
1	B	141	THR	8.7
1	D	373	HIS	8.3
1	C	86	GLY	8.0
1	B	142	ALA	6.4
1	D	99	PRO	6.4
1	B	86	GLY	6.4
1	B	89	PHE	6.4
1	D	397	LEU	6.2
1	D	86	GLY	6.1
1	D	389	ILE	6.1
1	B	188	ASP	6.0
1	C	393	PRO	5.9
1	A	187	GLN	5.8
1	D	81	LEU	5.8
1	D	374	PHE	5.5
1	B	88	LYS	5.4
1	B	451	TRP	5.4
1	D	367	HIS	5.2
1	D	371	VAL	5.2

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Mol	Chain	Res	Type	RSRZ
1	B	84	GLY	5.1
1	D	370	PHE	5.1
1	D	393	PRO	5.0
1	D	89	PHE	4.8
1	D	451	TRP	4.8
1	D	392	PRO	4.8
1	B	394	GLY	4.6
1	D	233	LEU	4.5
1	D	94	GLU	4.5
1	D	98	ALA	4.5
1	D	97	ASN	4.5
1	D	187	GLN	4.4
1	D	450	LYS	4.4
1	D	118	ALA	4.3
1	D	448	ASN	4.3
1	D	119	ALA	4.3
1	D	87	ALA	4.3
1	D	186	VAL	4.2
1	B	85	GLY	4.2
1	C	84	GLY	4.1
1	C	448	ASN	4.0
1	D	88	LYS	4.0
1	B	393	PRO	4.0
1	B	187	GLN	4.0
1	D	188	ASP	3.9
1	D	249	VAL	3.9
1	B	450	LYS	3.8
1	D	441	ALA	3.8
1	C	451	TRP	3.7
1	D	391	LEU	3.7
1	D	194	LEU	3.7
1	D	372	SER	3.6
1	B	449	ILE	3.6
1	D	190	GLU	3.6
1	D	103	ALA	3.6
1	A	188	ASP	3.6
1	B	427	GLY	3.6
1	D	85	GLY	3.6
1	B	102	ARG	3.5
1	D	55	LYS	3.5
1	C	87	ALA	3.5
1	D	369	PRO	3.4

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Mol	Chain	Res	Type	RSRZ
1	B	185	ALA	3.4
1	D	111	ALA	3.3
1	C	328	GLY	3.3
1	B	92	TYR	3.3
1	D	57	HIS	3.3
1	D	406	LEU	3.3
1	D	252	ARG	3.3
1	C	88	LYS	3.3
1	D	84	GLY	3.2
1	D	110	ALA	3.2
1	A	448	ASN	3.2
1	D	93	GLU	3.2
1	D	251	THR	3.2
1	D	449	ILE	3.2
1	A	449	ILE	3.1
1	C	397	LEU	3.1
1	D	390	ILE	3.1
1	C	141	THR	3.1
1	D	120	ARG	3.1
1	B	95	ILE	3.1
1	D	128	PRO	3.1
1	C	187	GLN	3.0
1	D	101	GLU	3.0
1	D	113	VAL	3.0
1	D	396	GLU	3.0
1	D	58	VAL	3.0
1	D	253	ASP	3.0
1	B	83	GLU	3.0
1	D	121	HIS	3.0
1	B	371	VAL	3.0
1	B	428	ASN	2.9
1	A	189	SER	2.9
1	B	121	HIS	2.9
1	D	141	THR	2.9
1	D	77	ILE	2.8
1	D	189	SER	2.8
1	B	104	ARG	2.8
1	D	368	LYS	2.8
1	D	443	THR	2.8
1	B	194	LEU	2.8
1	D	388	ARG	2.8
1	D	154	ASN	2.8

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Mol	Chain	Res	Type	RSRZ
1	D	100	GLU	2.8
1	C	102	ARG	2.7
1	B	90	LYS	2.7
1	C	108	ILE	2.7
1	B	91	LYS	2.6
1	C	399	MET	2.6
1	C	388	ARG	2.6
1	D	405	LYS	2.6
1	A	197	LEU	2.6
1	D	224	LEU	2.6
1	C	373	HIS	2.6
1	C	188	ASP	2.6
1	D	56	PRO	2.5
1	C	395	LYS	2.5
1	D	102	ARG	2.5
1	D	193	GLU	2.5
1	D	228	ASP	2.5
1	B	388	ARG	2.5
1	D	416	LEU	2.5
1	B	373	HIS	2.5
1	D	297	LYS	2.5
1	D	83	GLU	2.5
1	C	142	ALA	2.4
1	B	268	ILE	2.4
1	D	446	ASP	2.4
1	A	428	ASN	2.4
1	C	190	GLU	2.4
1	D	114	GLU	2.4
1	D	238	LYS	2.4
1	B	100	GLU	2.4
1	D	231	LEU	2.4
1	D	105	GLY	2.4
1	B	186	VAL	2.4
1	B	448	ASN	2.4
1	D	427	GLY	2.4
1	B	444	GLU	2.4
1	D	142	ALA	2.4
1	B	228	ASP	2.3
1	B	390	ILE	2.3
1	D	255	GLU	2.3
1	D	240	LEU	2.3
1	C	394	GLY	2.3

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Mol	Chain	Res	Type	RSRZ
1	D	366	ARG	2.3
1	A	212	GLU	2.3
1	D	106	ILE	2.3
1	C	392	PRO	2.3
1	D	254	LEU	2.3
1	D	298	ASN	2.3
1	B	82	ALA	2.2
1	C	150	VAL	2.2
1	B	369	PRO	2.2
1	D	435	LEU	2.2
1	C	121	HIS	2.2
1	D	411	ARG	2.2
1	A	193	GLU	2.2
1	B	193	GLU	2.2
1	D	171	ILE	2.2
1	B	81	LEU	2.2
1	C	381	LEU	2.2
1	D	197	LEU	2.2
1	C	360	THR	2.1
1	D	350	GLN	2.1
1	C	374	PHE	2.1
1	B	445	GLU	2.1
1	D	104	ARG	2.1
1	D	361	LYS	2.1
1	D	445	GLU	2.1
1	D	442	MET	2.1
1	A	87	ALA	2.1
1	D	143	PRO	2.1
1	D	177	VAL	2.1
1	C	171	ILE	2.1
1	D	80	ILE	2.1
1	B	231	LEU	2.1
1	B	143	PRO	2.1
1	A	88	LYS	2.1
1	D	107	THR	2.0
1	A	269	PRO	2.0
1	D	247	ILE	2.0
1	B	190	GLU	2.0
1	C	189	SER	2.0
1	D	395	LYS	2.0
1	A	416	LEU	2.0

## 6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

## 6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
3	GDP	A	1301	28/28	0.97	0.13	0.75	18,29,31,32	0
2	MG	B	502	1/1	0.93	0.11	-0.14	49,49,49,49	0
3	GDP	C	1303	28/28	0.97	0.11	-0.26	31,34,37,39	0
3	GDP	B	1302	28/28	0.96	0.09	-0.88	44,51,53,55	0
2	MG	D	504	1/1	0.86	0.13	-0.97	52,52,52,52	0
3	GDP	D	1304	28/28	0.90	0.12	-1.07	50,54,58,58	0
2	MG	A	501	1/1	0.97	0.07	-1.37	26,26,26,26	0
2	MG	C	503	1/1	0.99	0.08	-2.24	35,35,35,35	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.