



Full wwPDB X-ray Structure Validation Report

Feb 27, 2014 – 02:46 PM GMT

PDB ID : 1OIY
Title : STRUCTURE OF HUMAN THR160-PHOSPHO CDK2/CYCLIN A COM-
PLEXED WITH A 6-CYCLOHEXYLMETHYLOXY-2-ANILINO-PURIN
EINHIBITOR
Authors : Pratt, D.J.; Endicott, J.A.; Noble, M.E.M.
Deposited on : 2003-06-26
Resolution : 2.40 Å(reported)

This is a full wwPDB validation report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

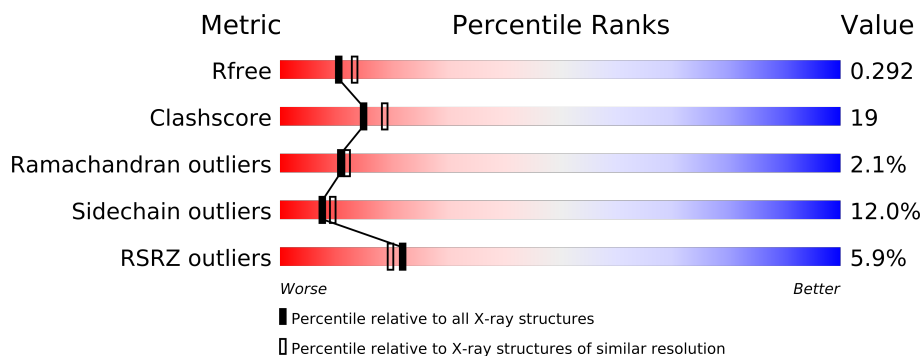
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : stable22639
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

The reported resolution of this entry is 2.40 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}	66092	2207 (2.40-2.40)
Clashscore	79885	2789 (2.40-2.40)
Ramachandran outliers	78287	2736 (2.40-2.40)
Sidechain outliers	78261	2737 (2.40-2.40)
RSRZ outliers	66119	2210 (2.40-2.40)

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 ≥ 3 , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	302	
1	C	302	
2	B	260	
2	D	260	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
3	N41	C	1298	-	X

2 Entry composition i

There are 6 unique types of molecules in this entry. The entry contains 9273 atoms, of which 0 are hydrogen and 0 are deuterium.

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.

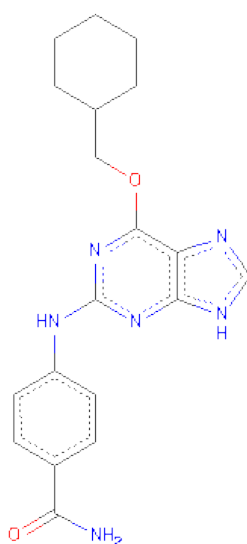
- Molecule 1 is a protein called CELL DIVISION PROTEIN KINASE 2.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	294	Total	C	N	O	P	S	0	1	0
			2366	1538	401	418	1	8			
1	C	297	Total	C	N	O	P	S	0	1	0
			2391	1552	404	426	1	8			

- Molecule 2 is a protein called CYCLIN A2.

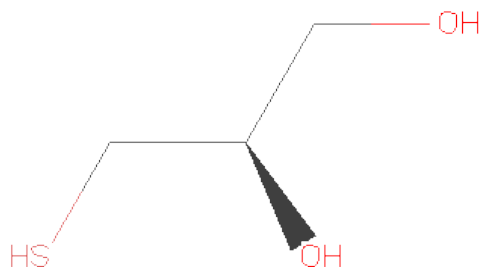
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	258	Total	C	N	O	S	0	1	0
			2088	1354	340	383	11			
2	D	258	Total	C	N	O	S	0	0	0
			2083	1350	339	383	11			

- Molecule 3 is 4-(6-CYCLOHEXYLMETHOXY-9H-PURIN-2-YLAMINO)--BENZAMIDE (three-letter code: N41) (formula: C₁₉H₂₂N₆O₂).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			27	19	6	2		
3	C	1	Total	C	N	O	0	0
			27	19	6	2		

- Molecule 4 is MONOTHIOGLYCEROL (three-letter code: SGM) (formula: $C_3H_8O_2S$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	B	1	Total	C	O	S	0	0
			6	3	2	1		
4	D	1	Total	C	O	S	0	0
			6	3	2	1		

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	1	Total	Mg	0	0
			1	1		

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	119	Total	O	0	0
			119	119		
6	B	107	Total	O	0	0
			107	107		

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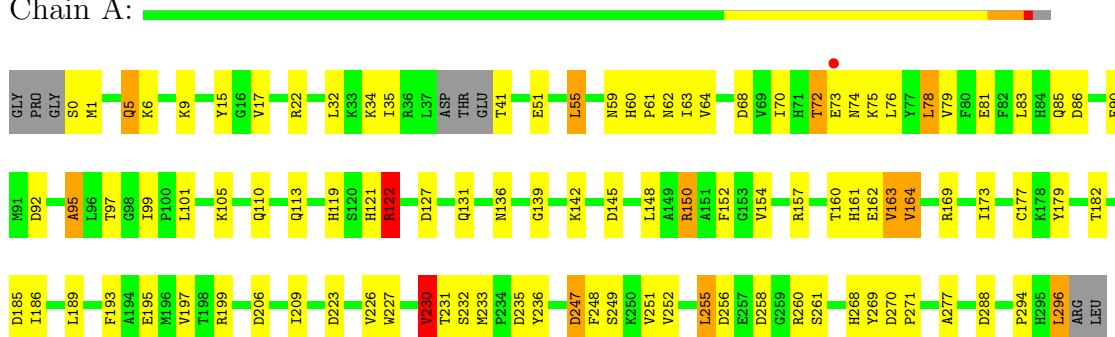
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	C	35	Total 35	O 35	0	0
6	D	17	Total 17	O 17	0	0

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 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.

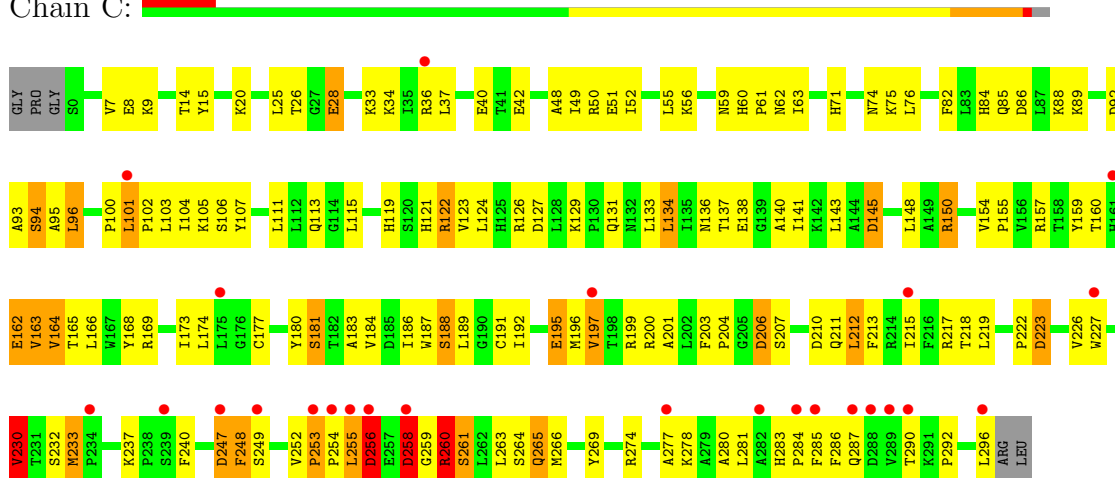
• Molecule 1: CELL DIVISION PROTEIN KINASE 2

Chain A:



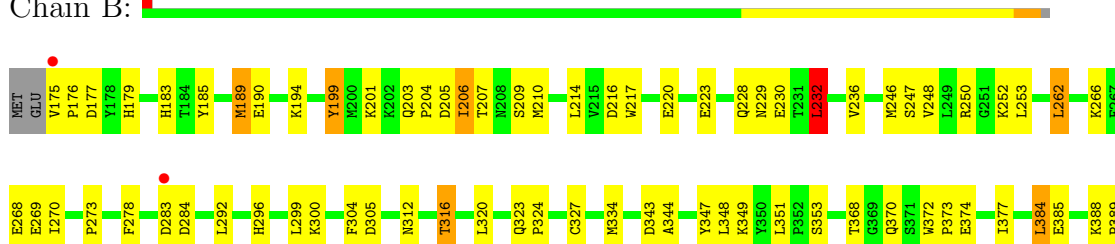
• Molecule 1: CELL DIVISION PROTEIN KINASE 2

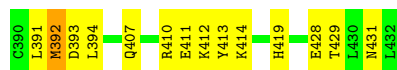
Chain C:



• Molecule 2: CYCLIN A2

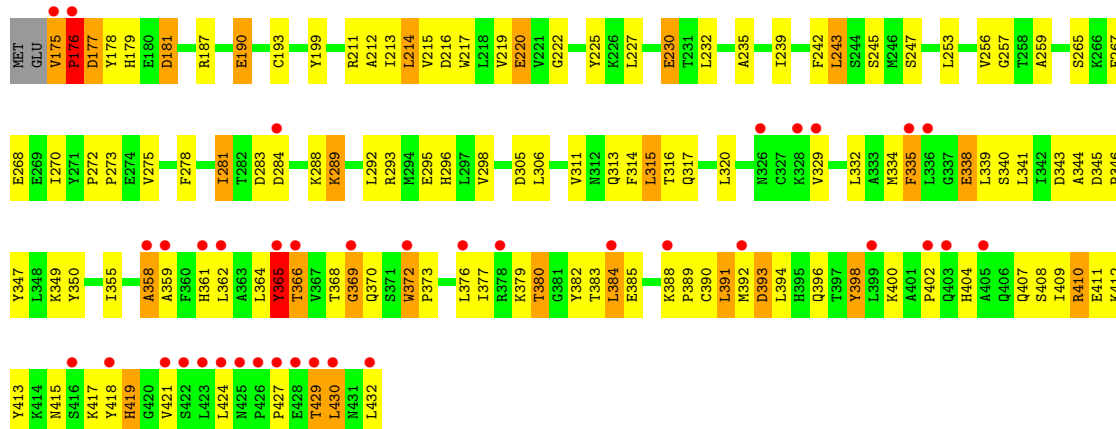
Chain B:





• Molecule 2: CYCLIN A2

Chain D:



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	74.00Å 134.87Å 147.87Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	100.00 – 2.40 41.02 – 2.40	Depositor EDS
% Data completeness (in resolution range)	91.6 (100.00-2.40) 91.6 (41.02-2.40)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.81 (at 2.39Å)	Xtriage
Refinement program	REFMAC 5.1.24	Depositor
R, R_{free}	0.244 , 0.309 0.232 , 0.292	Depositor DCC
R_{free} test set	2717 reflections (5.33%)	DCC
Wilson B-factor (Å ²)	33.3	Xtriage
Anisotropy	0.454	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 32.0	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.27$	Xtriage
Outliers	0 of 53707 reflections	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	9273	wwPDB-VP
Average B, all atoms (Å ²)	37.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.03% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: TPO, N41, MG, SGM

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	0.86	0/2419	0.98	14/3280 (0.4%)
1	C	0.66	0/2445	0.90	9/3318 (0.3%)
2	B	0.81	0/2142	0.94	9/2908 (0.3%)
2	D	0.64	0/2133	0.87	5/2897 (0.2%)
All	All	0.75	0/9139	0.93	37/12403 (0.3%)

There are no bond length outliers.

All (37) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	216	ASP	CB-CG-OD2	8.37	125.83	118.30
2	B	393	ASP	CB-CG-OD2	7.88	125.39	118.30
1	A	68	ASP	CB-CG-OD2	7.33	124.89	118.30
1	C	145	ASP	CB-CG-OD2	6.93	124.54	118.30
1	C	256	ASP	CB-CG-OD2	6.86	124.47	118.30
2	D	283	ASP	CB-CG-OD2	6.60	124.24	118.30
1	A	256	ASP	CB-CG-OD2	6.26	123.94	118.30
2	D	393	ASP	CB-CG-OD2	6.24	123.92	118.30
2	B	205	ASP	CB-CG-OD2	6.21	123.89	118.30
1	A	157	ARG	NE-CZ-NH2	-6.18	117.21	120.30
1	C	247	ASP	CB-CG-OD2	6.12	123.81	118.30
2	B	343	ASP	CB-CG-OD2	6.12	123.81	118.30
2	D	181	ASP	CB-CG-OD2	6.11	123.80	118.30
1	A	145	ASP	CB-CG-OD2	6.08	123.77	118.30
1	C	206	ASP	CB-CG-OD2	5.87	123.58	118.30
1	A	235	ASP	CB-CG-OD2	5.85	123.57	118.30
1	A	296	LEU	CA-CB-CG	5.78	128.59	115.30
2	D	305	ASP	CB-CG-OD2	5.78	123.50	118.30
1	C	210	ASP	CB-CG-OD2	5.77	123.49	118.30
1	A	247	ASP	CB-CG-OD2	5.73	123.46	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	230	VAL	CB-CA-C	-5.66	100.65	111.40
2	B	252	LYS	CD-CE-NZ	-5.64	98.74	111.70
1	C	223	ASP	CB-CG-OD2	5.53	123.28	118.30
1	A	86	ASP	CB-CG-OD2	5.51	123.26	118.30
1	A	288	ASP	CB-CG-OD2	5.40	123.16	118.30
1	C	258	ASP	CB-CG-OD2	5.40	123.16	118.30
1	C	86	ASP	CB-CG-OD2	5.36	123.12	118.30
2	B	305	ASP	CB-CG-OD2	5.30	123.07	118.30
1	A	127	ASP	CB-CG-OD2	5.23	123.01	118.30
2	D	243	LEU	CB-CG-CD1	-5.21	102.13	111.00
1	A	270	ASP	CB-CG-OD2	5.19	122.97	118.30
2	B	189	MET	CG-SD-CE	-5.13	92.00	100.20
1	A	76	LEU	CA-CB-CG	5.11	127.05	115.30
2	B	284	ASP	CB-CG-OD2	5.10	122.89	118.30
1	A	122	ARG	NE-CZ-NH2	-5.04	117.78	120.30
2	B	232	LEU	CA-CB-CG	5.04	126.88	115.30
1	C	212	LEU	CA-CB-CG	5.02	126.84	115.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Close contacts ⓘ

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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2366	0	2413	75	0
1	C	2391	0	2433	126	0
2	B	2088	0	2115	61	0
2	D	2083	0	2107	102	0
3	A	27	0	22	4	0
3	C	27	0	22	2	0
4	B	6	0	7	0	0
4	D	6	0	8	1	0
5	B	1	0	0	0	0
6	A	119	0	0	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	B	107	0	0	7	0
6	C	35	0	0	9	0
6	D	17	0	0	2	0
All	All	9273	0	9127	347	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 19.

All (347) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:C:60:HIS:HD2	1:C:62:ASN:H	1.09	0.99
1:C:162:GLU:OE1	1:C:162:GLU:HA	1.65	0.93
1:A:15:TYR:HE2	1:A:35:ILE:CD1	1.82	0.92
1:A:197:VAL:HG11	1:A:252:VAL:CG1	2.00	0.91
1:A:15:TYR:HE2	1:A:35:ILE:HD11	1.40	0.86
2:D:332:LEU:HD11	2:D:398:TYR:OH	1.76	0.86
2:D:412:LYS:HE2	2:D:418:TYR:HE2	1.39	0.85
1:A:163:VAL:HG13	1:A:164:VAL:HG23	1.58	0.83
1:C:203:PHE:CE1	1:C:215:ILE:HA	2.15	0.81
1:C:60:HIS:CD2	1:C:62:ASN:H	1.98	0.80
1:C:259:GLY:O	1:C:261:SER:N	2.13	0.80
1:A:177:CYS:HB2	1:A:233:MET:CE	2.11	0.80
1:C:183:ALA:HB1	1:C:274:ARG:NH1	1.97	0.80
1:C:201:ALA:HB3	1:C:204:PRO:HG3	1.64	0.78
2:B:229:ASN:HD22	2:B:334:MET:CE	1.96	0.78
1:C:154:VAL:HG12	2:D:317:GLN:HG2	1.63	0.78
1:A:60:HIS:CD2	1:A:62:ASN:H	2.02	0.77
1:C:115:LEU:HD11	1:C:119:HIS:CE1	2.18	0.77
2:D:362:LEU:HB2	2:D:391:LEU:HD11	1.66	0.77
2:B:374:GLU:HA	2:B:377:ILE:HD12	1.66	0.76
1:A:154:VAL:O	2:B:316:THR:CG2	2.33	0.76
2:B:229:ASN:HD22	2:B:334:MET:HE3	1.51	0.74
1:A:227:TRP:O	1:A:230:VAL:HG22	1.87	0.74
1:C:223:ASP:O	1:C:226:VAL:HG12	1.87	0.74
2:B:388:LYS:HB3	2:B:389:PRO:HD3	1.70	0.74
2:D:214:LEU:HD21	2:D:239:ILE:HD13	1.68	0.74
2:D:230:GLU:HB3	2:D:268:GLU:HG2	1.69	0.74
1:C:163:VAL:CG1	1:C:164:VAL:HG23	2.19	0.73
1:C:136:ASN:HD21	1:C:140:ALA:HB3	1.54	0.73
1:A:197:VAL:HG11	1:A:252:VAL:HG12	1.72	0.71
1:A:161:HIS:O	6:A:2063:HOH:O	2.08	0.71
1:C:258:ASP:HB3	1:C:285:PHE:HD1	1.55	0.71

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:B:175:VAL:N	2:B:179:HIS:CE1	2.59	0.71
1:A:154:VAL:O	2:B:316:THR:HG23	1.90	0.70
1:A:15:TYR:CE2	1:A:35:ILE:HD11	2.25	0.70
1:C:115:LEU:HD22	1:C:189:LEU:HD12	1.74	0.70
2:D:372:TRP:HZ2	2:D:382:TYR:HB2	1.55	0.70
2:D:222:GLY:HA2	2:D:227:LEU:HD12	1.73	0.70
2:B:392:MET:CE	2:B:392:MET:HA	2.22	0.69
1:C:258:ASP:HB3	1:C:285:PHE:CD1	2.27	0.69
1:A:197:VAL:CG1	1:A:252:VAL:CG1	2.70	0.69
1:C:136:ASN:ND2	1:C:140:ALA:HB3	2.08	0.69
2:B:177:ASP:HB3	6:B:2015:HOH:O	1.91	0.69
2:D:372:TRP:NE1	2:D:382:TYR:O	2.26	0.69
2:B:175:VAL:N	2:B:179:HIS:HE1	1.92	0.68
2:D:361:HIS:HD2	2:D:391:LEU:HD21	1.58	0.68
1:A:227:TRP:O	1:A:230:VAL:CG2	2.41	0.68
2:D:215:VAL:O	2:D:219:VAL:HG23	1.94	0.67
2:B:407:GLN:OE1	2:B:410:ARG:HD3	1.95	0.67
1:A:60:HIS:HD2	1:A:62:ASN:H	1.38	0.67
1:C:183:ALA:HB1	1:C:274:ARG:HH11	1.57	0.67
1:A:92:ASP:O	1:A:95:ALA:HB2	1.94	0.67
1:A:177:CYS:SG	1:A:179:TYR:O	2.52	0.67
1:C:60:HIS:HD2	1:C:62:ASN:N	1.90	0.67
1:A:197:VAL:HG11	1:A:252:VAL:HG11	1.75	0.67
1:A:195:GLU:O	1:A:199:ARG:HA	1.94	0.67
1:C:155:PRO:HD2	2:D:316:THR:HG22	1.77	0.66
1:C:71:HIS:CD2	1:C:76:LEU:HD13	2.31	0.66
1:C:154:VAL:CG1	2:D:317:GLN:HG2	2.25	0.66
2:D:346:PRO:O	2:D:349:LYS:HG2	1.96	0.65
2:B:347:TYR:OH	2:B:394:LEU:HA	1.96	0.65
1:C:163:VAL:HG12	1:C:164:VAL:HG23	1.79	0.65
1:C:71:HIS:NE2	2:D:296:HIS:NE2	2.44	0.65
2:B:223:GLU:CD	2:B:412:LYS:HG3	2.17	0.65
1:C:255:LEU:HG	1:C:259:GLY:HA3	1.78	0.65
2:D:335:PHE:CZ	2:D:339:LEU:HD11	2.32	0.65
1:A:177:CYS:HB2	1:A:233:MET:HE1	1.79	0.64
1:C:133:LEU:C	1:C:134:LEU:HD23	2.17	0.64
1:A:15:TYR:CE2	1:A:35:ILE:CD1	2.74	0.64
1:A:60:HIS:CG	1:A:61:PRO:HD2	2.32	0.64
1:C:188:SER:O	1:C:192:ILE:HG13	1.98	0.64
2:B:229:ASN:ND2	2:B:334:MET:CE	2.61	0.64
2:B:207:THR:OG1	2:B:210:MET:HG3	1.98	0.64
2:D:214:LEU:HD22	2:D:253:LEU:HD11	1.79	0.64

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:C:258:ASP:O	1:C:261:SER:OG	2.16	0.63
2:D:396:GLN:HB3	2:D:400:LYS:NZ	2.12	0.63
1:C:195:GLU:HG3	1:C:201:ALA:HA	1.80	0.63
1:A:9:LYS:HE3	1:A:17:VAL:HG13	1.79	0.62
2:D:412:LYS:HE2	2:D:418:TYR:CE2	2.29	0.62
1:C:212:LEU:O	1:C:215:ILE:HB	1.99	0.62
1:C:115:LEU:CD2	1:C:189:LEU:HD12	2.30	0.62
1:A:15:TYR:HE2	1:A:35:ILE:HD13	1.65	0.62
2:D:407:GLN:O	2:D:411:GLU:HG2	1.99	0.62
1:C:261:SER:O	1:C:265:GLN:HG3	2.01	0.61
1:C:71:HIS:CE1	2:D:296:HIS:CD2	2.88	0.61
2:B:262:LEU:HD11	2:B:266:LYS:HE3	1.82	0.61
1:C:82:PHE:CE1	3:C:1298:N41:H18	2.36	0.61
1:C:107:TYR:O	1:C:111:LEU:HD12	2.02	0.60
1:C:129:LYS:HB3	6:C:2028:HOH:O	2.01	0.60
2:D:346:PRO:HD2	2:D:347:TYR:CE2	2.36	0.60
1:C:196:MET:O	6:C:2034:HOH:O	2.15	0.60
2:D:329:VAL:HG21	2:D:364:LEU:HD12	1.83	0.60
1:A:90:PHE:CE2	1:A:99:ILE:HD13	2.37	0.60
1:C:50:ARG:NE	2:D:267:PHE:O	2.34	0.59
1:C:237:LYS:HB2	1:C:240:PHE:CE1	2.37	0.59
2:B:392:MET:HE3	2:B:392:MET:HA	1.83	0.59
1:A:131:GLN:HG2	3:A:1298:N41:H141	1.83	0.59
2:B:232:LEU:O	2:B:236:VAL:HG23	2.01	0.59
1:C:71:HIS:CD2	2:D:296:HIS:NE2	2.71	0.59
1:A:160:TPO:HG23	1:A:162:GLU:H	1.67	0.59
2:D:368:THR:O	2:D:370:GLN:N	2.35	0.58
1:C:60:HIS:HB3	1:C:63:ILE:HG13	1.85	0.58
1:C:280:ALA:O	1:C:286:PHE:HE2	1.86	0.58
1:C:163:VAL:HG13	1:C:164:VAL:HG23	1.84	0.58
2:B:175:VAL:O	2:B:177:ASP:N	2.37	0.58
1:C:169:ARG:HD2	1:C:174:LEU:HD23	1.86	0.58
1:C:100:PRO:O	1:C:104:ILE:HG13	2.04	0.57
3:A:1298:N41:H22	3:A:1298:N41:N1	2.19	0.57
2:B:411:GLU:HA	2:B:414:LYS:HD2	1.87	0.57
1:A:90:PHE:HE2	1:A:99:ILE:HD13	1.69	0.57
1:C:223:ASP:H	1:C:226:VAL:HG12	1.69	0.57
2:D:372:TRP:HE1	2:D:383:THR:HA	1.70	0.57
1:A:249:SER:HA	1:A:260:ARG:HD3	1.87	0.57
2:D:230:GLU:HA	2:D:230:GLU:OE1	2.05	0.57
2:D:366:THR:OG1	2:D:427:PRO:HD3	2.05	0.56
1:C:40:GLU:O	2:D:288:LYS:HE3	2.05	0.56

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:60:HIS:HB3	1:A:63:ILE:HG13	1.87	0.56
2:D:335:PHE:HB2	2:D:413:TYR:CD2	2.40	0.56
2:B:210:MET:HE2	2:B:250:ARG:HB2	1.87	0.56
1:C:168:TYR:OH	1:C:195:GLU:OE1	2.16	0.56
1:A:51:GLU:O	1:A:55:LEU:HB2	2.05	0.56
2:D:187:ARG:HD2	2:D:190:GLU:OE2	2.06	0.56
2:D:346:PRO:HB2	2:D:349:LYS:HE2	1.87	0.56
2:D:404:HIS:CE1	6:D:2015:HOH:O	2.59	0.55
1:A:62:ASN:HA	1:A:142:LYS:HG2	1.88	0.55
1:A:154:VAL:O	2:B:316:THR:HG22	2.05	0.55
2:D:213:ILE:O	2:D:216:ASP:HB3	2.07	0.55
2:D:273:PRO:HG2	2:D:278:PHE:CZ	2.42	0.55
1:C:256:ASP:OD2	1:C:256:ASP:N	2.38	0.55
2:B:190:GLU:HG3	2:B:351:LEU:HD22	1.88	0.54
1:A:72:THR:HB	1:A:75:LYS:O	2.07	0.54
1:C:197:VAL:HG11	1:C:255:LEU:HD13	1.88	0.54
1:A:95:ALA:HA	6:A:2081:HOH:O	2.06	0.54
2:B:210:MET:CE	2:B:250:ARG:HB2	2.37	0.54
1:C:111:LEU:HD11	1:C:141:ILE:HD13	1.88	0.54
1:C:253:PRO:HB2	1:C:254:PRO:HD3	1.88	0.54
1:C:263:LEU:O	1:C:266:MET:N	2.41	0.54
1:C:111:LEU:HD23	1:C:143:LEU:HD23	1.90	0.54
2:D:239:ILE:HG22	2:D:243:LEU:CD1	2.38	0.54
2:D:383:THR:O	2:D:385:GLU:N	2.41	0.54
2:B:428:GLU:HG2	6:B:2105:HOH:O	2.07	0.53
2:D:211:ARG:O	2:D:215:VAL:HG23	2.08	0.53
1:A:85:GLN:HE21	1:A:90:PHE:HB2	1.73	0.53
1:C:278:LYS:HA	1:C:281:LEU:HD12	1.90	0.53
2:B:299:LEU:HD13	2:B:304:PHE:CE1	2.43	0.53
2:B:273:PRO:HB2	2:B:278:PHE:CE2	2.44	0.53
1:A:72:THR:HG22	1:A:75:LYS:H	1.74	0.53
1:C:71:HIS:CE1	2:D:296:HIS:NE2	2.77	0.53
3:A:1298:N41:C22	3:A:1298:N41:N1	2.71	0.53
1:C:183:ALA:O	1:C:186:ILE:HB	2.10	0.52
2:D:346:PRO:HD2	2:D:347:TYR:CD2	2.44	0.52
1:C:187:TRP:NE1	1:C:191:CYS:SG	2.82	0.52
1:A:121:HIS:HD2	2:B:185:TYR:CE1	2.27	0.52
1:C:292:PRO:HD2	6:C:2026:HOH:O	2.08	0.52
1:C:165:THR:HB	6:C:2028:HOH:O	2.08	0.52
1:A:51:GLU:HG3	1:A:55:LEU:HD22	1.91	0.52
1:C:95:ALA:O	1:C:96:LEU:O	2.28	0.52
1:C:173:ILE:HD11	1:C:184:VAL:HG11	1.92	0.52

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:B:412:LYS:HD3	2:B:413:TYR:CE1	2.46	0.51
2:D:388:LYS:HG2	2:D:392:MET:HG2	1.92	0.51
1:A:177:CYS:HB2	1:A:233:MET:HE3	1.91	0.51
2:D:421:VAL:HA	2:D:424:LEU:HG	1.92	0.51
2:D:239:ILE:HG22	2:D:243:LEU:HD11	1.93	0.51
1:A:223:ASP:OD1	1:A:226:VAL:HG12	2.11	0.51
1:A:64:VAL:HG13	1:A:64:VAL:O	2.10	0.51
2:D:313:GLN:O	2:D:317:GLN:HG3	2.10	0.51
1:C:160:TPO:OG1	2:D:270:ILE:HG23	2.11	0.51
1:C:255:LEU:CG	1:C:259:GLY:HA3	2.41	0.50
2:D:175:VAL:O	2:D:177:ASP:N	2.45	0.50
1:C:219:LEU:HB3	1:C:269:TYR:HE2	1.75	0.50
1:C:283:HIS:CG	1:C:284:PRO:HD2	2.47	0.50
1:C:183:ALA:CB	1:C:274:ARG:NH1	2.71	0.50
2:D:372:TRP:CZ2	2:D:382:TYR:HB2	2.42	0.50
2:D:216:ASP:O	2:D:219:VAL:N	2.45	0.50
2:B:296:HIS:C	2:B:296:HIS:CD2	2.86	0.50
2:D:176:PRO:HA	2:D:179:HIS:CG	2.47	0.49
1:A:251:VAL:HG12	1:A:252:VAL:HG23	1.93	0.49
1:A:64:VAL:CG1	1:A:64:VAL:O	2.60	0.49
2:D:235:ALA:O	2:D:239:ILE:HG13	2.10	0.49
2:B:270:ILE:HG13	6:B:2048:HOH:O	2.12	0.49
2:D:358:ALA:O	2:D:359:ALA:C	2.50	0.49
2:B:388:LYS:HB3	2:B:389:PRO:CD	2.42	0.49
2:D:350:TYR:CE1	2:D:390:CYS:HB2	2.48	0.49
1:C:92:ASP:O	1:C:94:SER:N	2.46	0.49
1:A:5:GLN:HA	1:A:5:GLN:HE21	1.78	0.49
2:D:376:LEU:O	2:D:380:THR:HG23	2.13	0.49
2:D:365:TYR:O	2:D:369:GLY:N	2.46	0.49
2:B:190:GLU:OE2	2:B:353:SER:HB3	2.12	0.49
1:C:84:HIS:CD2	1:C:85:GLN:HG2	2.49	0.48
2:D:344:ALA:O	2:D:347:TYR:N	2.47	0.48
1:C:223:ASP:N	1:C:226:VAL:HG12	2.29	0.48
2:D:259:ALA:HB1	2:D:295:GLU:HA	1.95	0.48
1:C:124:LEU:HB3	1:C:126:ARG:HG3	1.94	0.48
2:D:365:TYR:O	2:D:366:THR:C	2.51	0.48
1:A:169:ARG:HD3	1:A:173:ILE:CG2	2.43	0.48
2:D:419:HIS:N	2:D:419:HIS:ND1	2.62	0.47
1:C:20:LYS:HD2	1:C:82:PHE:CE1	2.49	0.47
1:C:222:PRO:HA	1:C:226:VAL:HG11	1.96	0.47
2:D:193:CYS:SG	4:D:1193:SGM:S1	2.40	0.47
2:D:362:LEU:HD13	2:D:430:LEU:HD22	1.96	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:D:338:GLU:HB3	2:D:409:ILE:HG21	1.96	0.47
1:A:162:GLU:HA	6:A:2063:HOH:O	2.15	0.47
2:B:407:GLN:O	2:B:411:GLU:HG2	2.15	0.47
1:A:78:LEU:HD23	1:A:78:LEU:N	2.28	0.47
2:B:327:CYS:HB3	2:B:419:HIS:CE1	2.49	0.47
1:C:51:GLU:O	1:C:55:LEU:HB2	2.15	0.47
1:A:231:THR:HA	1:A:236:TYR:CD1	2.50	0.47
2:D:338:GLU:O	2:D:340:SER:N	2.47	0.47
1:A:136:ASN:OD1	1:A:136:ASN:C	2.54	0.47
1:C:71:HIS:HD2	1:C:76:LEU:HD13	1.76	0.47
1:C:7:VAL:HB	1:C:20:LYS:HB3	1.97	0.46
2:D:343:ASP:HA	6:D:2014:HOH:O	2.15	0.46
1:A:269:TYR:O	1:A:271:PRO:HD3	2.15	0.46
1:A:186:ILE:HD11	1:A:277:ALA:N	2.29	0.46
1:C:49:ILE:HG23	2:D:306:LEU:CD1	2.46	0.46
2:B:214:LEU:HD22	2:B:253:LEU:HG	1.97	0.46
1:C:121:HIS:O	1:C:123:VAL:HG23	2.15	0.46
1:C:134:LEU:HD23	1:C:134:LEU:N	2.30	0.46
2:D:314:PHE:O	2:D:315:LEU:C	2.53	0.46
2:B:183:HIS:HE1	6:B:2064:HOH:O	1.98	0.46
1:A:161:HIS:O	1:A:161:HIS:CD2	2.68	0.46
1:A:150:ARG:NH1	2:B:268:GLU:O	2.47	0.45
1:C:201:ALA:CB	1:C:204:PRO:HG3	2.41	0.45
2:D:253:LEU:HD12	2:D:253:LEU:O	2.16	0.45
2:D:329:VAL:HG11	2:D:364:LEU:CD1	2.46	0.45
2:D:365:TYR:HB3	2:D:366:THR:H	1.66	0.45
2:D:427:PRO:HB2	2:D:429:THR:O	2.15	0.45
1:C:253:PRO:CB	1:C:254:PRO:HD3	2.47	0.45
1:A:32:LEU:CD2	1:A:79:VAL:HG22	2.46	0.45
1:C:55:LEU:HA	1:C:55:LEU:HD12	1.59	0.45
2:D:242:PHE:CD1	2:D:298:VAL:HG22	2.50	0.45
1:A:1:MET:SD	1:A:70:ILE:HD13	2.57	0.45
2:D:212:ALA:O	2:D:216:ASP:HB2	2.16	0.45
2:D:345:ASP:HA	2:D:346:PRO:HA	1.63	0.45
2:D:176:PRO:HA	2:D:179:HIS:ND1	2.32	0.45
1:C:59:ASN:ND2	6:C:2017:HOH:O	2.49	0.45
2:D:361:HIS:CD2	2:D:391:LEU:HD21	2.46	0.45
2:B:175:VAL:C	2:B:177:ASP:H	2.18	0.45
3:C:1298:N41:H141	6:C:2029:HOH:O	2.17	0.45
1:A:119:HIS:HD2	6:B:2016:HOH:O	2.00	0.45
1:C:52:ILE:O	1:C:56:LYS:HG3	2.16	0.45
1:C:115:LEU:HD11	1:C:119:HIS:NE2	2.32	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:D:372:TRP:NE1	2:D:383:THR:HA	2.32	0.45
2:B:223:GLU:OE2	2:B:412:LYS:HE3	2.16	0.44
2:B:372:TRP:HA	2:B:373:PRO:HD2	1.88	0.44
1:C:154:VAL:HA	1:C:155:PRO:HA	1.66	0.44
2:D:225:TYR:HE1	2:D:281:ILE:HG21	1.82	0.44
1:C:121:HIS:O	1:C:122:ARG:HG3	2.17	0.44
1:C:37:LEU:HB2	1:C:74:ASN:O	2.17	0.44
2:D:281:ILE:HG13	2:D:281:ILE:H	1.49	0.44
2:D:390:CYS:O	2:D:394:LEU:N	2.42	0.44
1:C:261:SER:O	1:C:265:GLN:CG	2.65	0.44
2:D:317:GLN:O	2:D:320:LEU:HD12	2.18	0.44
2:D:430:LEU:HG	2:D:430:LEU:H	1.54	0.44
2:D:373:PRO:HD2	2:D:376:LEU:HD12	1.98	0.44
2:D:329:VAL:HG11	2:D:364:LEU:HD13	1.98	0.44
1:C:89:LYS:NZ	6:C:2025:HOH:O	2.50	0.44
1:C:15:TYR:CZ	1:C:33:LYS:HE2	2.53	0.43
1:C:207:SER:O	1:C:211:GLN:N	2.41	0.43
2:D:362:LEU:CD1	2:D:430:LEU:HD22	2.48	0.43
2:B:206:ILE:HD12	2:B:253:LEU:HD13	1.99	0.43
1:A:110:GLN:O	1:A:113:GLN:HB2	2.17	0.43
2:D:217:TRP:HA	2:D:220:GLU:HG3	2.00	0.43
1:C:25:LEU:HD23	1:C:25:LEU:HA	1.90	0.43
2:B:247:SER:OG	1:C:28:GLU:HG3	2.18	0.43
2:D:338:GLU:O	2:D:341:LEU:N	2.52	0.43
2:B:344:ALA:HB1	2:B:348:LEU:HD22	1.99	0.43
2:B:316:THR:HG21	6:B:2009:HOH:O	2.19	0.43
2:B:392:MET:HE2	2:B:392:MET:HA	2.00	0.43
2:D:396:GLN:HB3	2:D:400:LYS:CE	2.48	0.43
1:A:55:LEU:HD12	1:A:55:LEU:HA	1.76	0.43
1:C:249:SER:HA	1:C:260:ARG:HD3	1.99	0.43
1:C:159:TYR:HB2	1:C:180:TYR:CZ	2.53	0.43
2:D:214:LEU:HD22	2:D:253:LEU:CD1	2.49	0.43
1:C:113:GLN:HG2	1:C:281:LEU:HD21	2.01	0.43
1:A:169:ARG:HD3	1:A:173:ILE:HG22	2.01	0.43
1:C:177:CYS:HB2	1:C:233:MET:CE	2.48	0.43
2:B:199:TYR:CE2	2:B:348:LEU:HD21	2.54	0.43
2:B:194:LYS:NZ	6:B:2024:HOH:O	2.51	0.43
1:A:15:TYR:CE2	1:A:35:ILE:HD13	2.50	0.43
2:D:273:PRO:HG2	2:D:278:PHE:CE2	2.54	0.43
1:C:255:LEU:HD12	1:C:255:LEU:HA	1.86	0.42
1:C:213:PHE:O	1:C:217:ARG:N	2.51	0.42
2:B:248:VAL:HG22	1:C:26:THR:HB	1.99	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:C:248:PHE:CZ	1:C:263:LEU:HD23	2.54	0.42
2:D:402:PRO:HD3	2:D:410:ARG:HH11	1.83	0.42
1:A:122:ARG:HA	1:A:152:PHE:CE1	2.55	0.42
1:A:139:GLY:HA2	1:A:294:PRO:HD3	2.01	0.42
2:B:384:LEU:HA	2:B:384:LEU:HD12	1.82	0.42
2:B:203:GLN:HA	2:B:204:PRO:HD2	1.85	0.42
1:C:227:TRP:O	1:C:230:VAL:HG22	2.20	0.42
2:D:265:SER:HB3	2:D:272:PRO:HB3	2.02	0.42
2:D:362:LEU:HB2	2:D:391:LEU:CD1	2.41	0.42
1:C:136:ASN:HD21	1:C:140:ALA:CB	2.26	0.42
1:C:104:ILE:HD13	1:C:196:MET:HB3	2.01	0.42
1:C:126:ARG:CZ	1:C:150:ARG:HB3	2.49	0.42
2:B:217:TRP:O	2:B:220:GLU:HB2	2.19	0.42
1:A:268:HIS:CD2	6:A:2091:HOH:O	2.72	0.42
1:C:227:TRP:O	1:C:230:VAL:CG2	2.68	0.42
1:C:105:LYS:O	1:C:106:SER:C	2.58	0.42
1:C:277:ALA:HB3	2:D:178:TYR:OH	2.20	0.42
2:B:320:LEU:HD23	2:B:320:LEU:HA	1.81	0.42
2:D:407:GLN:OE1	2:D:410:ARG:HD3	2.19	0.41
1:A:197:VAL:CG1	1:A:252:VAL:HG11	2.45	0.41
1:C:280:ALA:O	1:C:286:PHE:CE2	2.70	0.41
2:B:228:GLN:N	2:B:269:GLU:OE2	2.48	0.41
1:C:101:LEU:N	1:C:102:PRO:CD	2.83	0.41
2:B:230:GLU:OE1	2:B:312:ASN:HB3	2.20	0.41
2:B:323:GLN:HA	2:B:324:PRO:HA	1.84	0.41
2:B:175:VAL:C	2:B:177:ASP:N	2.73	0.41
1:A:83:LEU:O	3:A:1298:N41:N2	2.46	0.41
2:D:388:LYS:O	2:D:389:PRO:C	2.58	0.41
1:C:255:LEU:CD2	1:C:259:GLY:HA3	2.50	0.41
1:C:92:ASP:C	1:C:94:SER:N	2.73	0.41
1:C:88:LYS:HB2	1:C:131:GLN:HE21	1.86	0.41
2:B:246:MET:HE3	6:C:2004:HOH:O	2.19	0.41
1:C:253:PRO:HD2	1:C:254:PRO:HD3	2.03	0.41
1:C:121:HIS:C	1:C:122:ARG:HG3	2.40	0.41
1:C:60:HIS:CG	1:C:61:PRO:HD2	2.56	0.41
2:B:368:THR:CB	2:B:370:GLN:HE21	2.34	0.41
1:A:258:ASP:O	1:A:261:SER:HB3	2.20	0.41
2:D:409:ILE:O	2:D:413:TYR:HD1	2.03	0.41
2:D:396:GLN:HB3	2:D:400:LYS:HZ2	1.85	0.41
2:D:278:PHE:HA	2:D:281:ILE:HD11	2.01	0.41
2:D:175:VAL:C	2:D:179:HIS:CE1	2.94	0.41
2:D:289:LYS:HG3	2:D:293:ARG:HD2	2.01	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:C:101:LEU:HD22	1:C:101:LEU:HA	1.91	0.41
1:C:263:LEU:O	1:C:265:GLN:N	2.54	0.41
1:A:199:ARG:HD2	6:A:2081:HOH:O	2.21	0.41
1:A:195:GLU:O	1:A:199:ARG:CA	2.66	0.41
1:C:219:LEU:HB3	1:C:269:TYR:CE2	2.53	0.41
1:A:119:HIS:CD2	1:A:182:THR:HB	2.56	0.41
2:D:256:VAL:O	2:D:257:GLY:C	2.57	0.41
1:C:137:THR:O	1:C:138:GLU:HG3	2.20	0.41
1:A:9:LYS:HE3	1:A:17:VAL:CG1	2.48	0.41
1:A:119:HIS:HE1	1:A:185:ASP:OD2	2.04	0.41
1:A:209:ILE:HA	1:A:209:ILE:HD12	1.94	0.41
1:C:42:GLU:HA	2:D:275:VAL:CG2	2.51	0.40
1:A:105:LYS:HE3	1:A:105:LYS:HB2	1.72	0.40
2:B:388:LYS:O	2:B:392:MET:HG2	2.21	0.40
1:C:103:LEU:HD11	1:C:107:TYR:CZ	2.56	0.40
1:C:169:ARG:HD2	1:C:174:LEU:CD2	2.49	0.40
1:A:255:LEU:O	1:A:260:ARG:NH1	2.54	0.40
1:C:15:TYR:OH	1:C:48:ALA:HA	2.22	0.40
1:C:181:SER:N	6:C:2033:HOH:O	2.52	0.40
1:C:105:LYS:HE3	1:C:105:LYS:HB2	1.73	0.40
2:B:429:THR:OG1	2:B:431:ASN:ND2	2.54	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	290/302 (96%)	272 (94%)	16 (6%)	2 (1%)	30	43
1	C	295/302 (98%)	250 (85%)	33 (11%)	12 (4%)	4	3
2	B	257/260 (99%)	248 (96%)	8 (3%)	1 (0%)	43	61
2	D	256/260 (98%)	217 (85%)	31 (12%)	8 (3%)	7	5
All	All	1098/1124 (98%)	987 (90%)	88 (8%)	23 (2%)	11	12

All (23) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	96	LEU
1	C	260	ARG
2	D	176	PRO
2	D	365	TYR
2	D	369	GLY
1	A	95	ALA
1	A	164	VAL
1	C	93	ALA
1	C	166	LEU
1	C	264	SER
2	D	311	VAL
2	B	176	PRO
1	C	127	ASP
1	C	145	ASP
1	C	164	VAL
1	C	261	SER
2	D	384	LEU
1	C	258	ASP
2	D	315	LEU
2	D	358	ALA
2	D	372	TRP
1	C	253	PRO
1	C	230	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	259/264 (98%)	231 (89%)	28 (11%)	9	13
1	C	262/264 (99%)	225 (86%)	37 (14%)	5	6
2	B	233/234 (100%)	217 (93%)	16 (7%)	22	33
2	D	232/234 (99%)	195 (84%)	37 (16%)	4	4
All	All	986/996 (99%)	868 (88%)	118 (12%)	7	9

All (118) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	0	SER
1	A	5	GLN
1	A	6	LYS
1	A	22	ARG
1	A	34	LYS
1	A	41	THR
1	A	55	LEU
1	A	59	ASN
1	A	72	THR
1	A	73	GLU
1	A	74	ASN
1	A	78	LEU
1	A	81	GLU
1	A	97	THR
1	A	101	LEU
1	A	122	ARG
1	A	148	LEU
1	A	150	ARG
1	A	163	VAL
1	A	189	LEU
1	A	193	PHE
1	A	206	ASP
1	A	230	VAL
1	A	232	SER
1	A	247	ASP
1	A	248	PHE
1	A	255	LEU
1	A	296	LEU
2	B	189	MET
2	B	199	TYR
2	B	201	LYS
2	B	206	ILE
2	B	209	SER
2	B	232	LEU
2	B	262	LEU
2	B	283	ASP
2	B	292	LEU
2	B	300	LYS
2	B	316	THR
2	B	349	LYS
2	B	384	LEU
2	B	385	GLU
2	B	391	LEU

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Mol	Chain	Res	Type
2	B	392	MET
1	C	8	GLU
1	C	9	LYS
1	C	14	THR
1	C	28	GLU
1	C	34	LYS
1	C	36	ARG
1	C	75	LYS
1	C	94	SER
1	C	101	LEU
1	C	122	ARG
1	C	134	LEU
1	C	148	LEU
1	C	150	ARG
1	C	157	ARG
1	C	162	GLU
1	C	163	VAL
1	C	181	SER
1	C	188	SER
1	C	195	GLU
1	C	197	VAL
1	C	199	ARG
1	C	200	ARG
1	C	206	ASP
1	C	218	THR
1	C	230	VAL
1	C	232	SER
1	C	233	MET
1	C	247	ASP
1	C	248	PHE
1	C	252	VAL
1	C	255	LEU
1	C	256	ASP
1	C	260	ARG
1	C	265	GLN
1	C	287	GLN
1	C	290	THR
1	C	296	LEU
2	D	175	VAL
2	D	176	PRO
2	D	177	ASP
2	D	181	ASP

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Mol	Chain	Res	Type
2	D	190	GLU
2	D	199	TYR
2	D	214	LEU
2	D	220	GLU
2	D	230	GLU
2	D	232	LEU
2	D	245	SER
2	D	247	SER
2	D	281	ILE
2	D	284	ASP
2	D	289	LYS
2	D	292	LEU
2	D	334	MET
2	D	335	PHE
2	D	338	GLU
2	D	355	ILE
2	D	365	TYR
2	D	366	THR
2	D	377	ILE
2	D	379	LYS
2	D	380	THR
2	D	384	LEU
2	D	391	LEU
2	D	393	ASP
2	D	398	TYR
2	D	408	SER
2	D	410	ARG
2	D	415	ASN
2	D	417	LYS
2	D	419	HIS
2	D	429	THR
2	D	430	LEU
2	D	432	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (23) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	5	GLN
1	A	60	HIS
1	A	85	GLN
1	A	119	HIS
1	A	161	HIS

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Mol	Chain	Res	Type
1	A	265	GLN
2	B	179	HIS
2	B	183	HIS
2	B	254	GLN
2	B	296	HIS
2	B	312	ASN
2	B	370	GLN
2	B	425	ASN
2	B	431	ASN
1	C	60	HIS
1	C	71	HIS
1	C	74	ASN
1	C	265	GLN
1	C	295	HIS
2	D	254	GLN
2	D	313	GLN
2	D	322	GLN
2	D	395	HIS

5.3.3 RNA ⓘ

There are no RNA chains in this entry.

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

2 non-standard protein/DNA/RNA residues 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	$\# Z > 2$
1	TPO	A	160	1	10,10,11	5.53	2 (20%)	12,14,16	1.68	2 (16%)
1	TPO	C	160	1	10,10,11	4.79	2 (20%)	12,14,16	1.14	1 (8%)

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
1	TPO	A	160	1	-	0/9/11/13	0/0/0/0
1	TPO	C	160	1	-	0/9/11/13	0/0/0/0

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	160	TPO	O-C	16.92	1.23	1.11
1	C	160	TPO	O-C	14.68	1.21	1.11
1	A	160	TPO	P-O1P	2.84	1.60	1.51
1	C	160	TPO	P-O1P	2.18	1.58	1.51

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	160	TPO	OG1-CB-CG2	-3.58	104.15	110.13
1	C	160	TPO	CB-CA-N	2.35	112.88	109.60
1	A	160	TPO	O2P-P-O1P	-2.24	103.12	110.44

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5.5 Carbohydrates

There are no carbohydrates in this entry.

5.6 Ligand geometry

Of 5 ligands modelled in this entry, 1 is 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	N41	A	1298	-	30,30,30	1.32	5 (16%)	41,41,41	2.17	11 (26%)
4	SGM	B	1193	2	5,5,5	0.59	0	5,5,5	1.10	1 (20%)
3	N41	C	1298	-	30,30,30	0.92	2 (6%)	41,41,41	2.08	11 (26%)
4	SGM	D	1193	-	5,5,5	0.38	0	5,5,5	1.14	1 (20%)

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	N41	A	1298	-	-	0/13/21/21	0/2/4/4
4	SGM	B	1193	2	-	0/4/4/4	0/0/0/0
3	N41	C	1298	-	-	0/13/21/21	0/2/4/4
4	SGM	D	1193	-	-	0/4/4/4	0/0/0/0

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1298	N41	C8-N9	3.22	1.39	1.34
3	A	1298	N41	C8-N7	2.70	1.40	1.34
3	A	1298	N41	C6-N1	2.64	1.36	1.32
3	C	1298	N41	C8-N9	2.47	1.38	1.34
3	A	1298	N41	C6-C5	2.33	1.47	1.43
3	C	1298	N41	C6-C5	2.12	1.47	1.43
3	A	1298	N41	O6-C6	2.04	1.38	1.34

All (24) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1298	N41	C5-C4-N9	5.52	111.46	106.07
3	C	1298	N41	N9-C4-N3	5.38	128.84	124.37
3	A	1298	N41	C8-N9-C4	-5.17	101.23	107.69
3	A	1298	N41	C5-C6-N1	-4.66	117.44	123.75
3	C	1298	N41	C10-O6-C6	4.38	121.73	117.52
3	A	1298	N41	C2-N3-C4	4.03	120.20	115.15
3	C	1298	N41	C2-N1-C6	3.95	122.88	115.09
3	C	1298	N41	C2-N3-C4	3.95	120.10	115.15
3	A	1298	N41	C2-N1-C6	3.76	122.51	115.09
3	C	1298	N41	N3-C2-N1	-3.64	120.58	126.19
3	A	1298	N41	N9-C4-N3	3.46	127.25	124.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1298	N41	O6-C6-C5	3.45	121.52	115.93
3	C	1298	N41	C8-N9-C4	-3.40	103.44	107.69
3	C	1298	N41	C5-C6-N1	-3.39	119.16	123.75
3	A	1298	N41	C5-C4-N3	-3.22	121.28	125.94
3	C	1298	N41	C17-N2-C2	-3.14	119.87	128.77
3	A	1298	N41	N3-C2-N1	-3.11	121.40	126.19
3	C	1298	N41	C5-C4-N9	2.98	108.98	106.07
3	C	1298	N41	C5-C4-N3	-2.60	122.17	125.94
3	C	1298	N41	O6-C6-C5	2.44	119.88	115.93
3	A	1298	N41	C16-C11-C12	2.41	114.80	109.19
3	A	1298	N41	C4-C5-N7	-2.40	107.60	109.93
4	D	1193	SGM	C2-C1-S1	-2.32	111.00	114.66
4	B	1193	SGM	C2-C1-S1	-2.13	111.31	114.66

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

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, 95th 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 ²)	Q<0.9
1	A	294/302 (97%)	-0.22	1 (0%) 91 92	11, 22, 45, 55	0
1	C	297/302 (98%)	0.44	25 (8%) 11 10	24, 47, 70, 80	0
2	B	258/260 (99%)	-0.22	2 (0%) 83 82	11, 25, 44, 55	0
2	D	258/260 (99%)	0.59	38 (14%) 3 2	20, 48, 73, 78	0
All	All	1107/1124 (98%)	0.15	66 (5%) 22 19	11, 35, 69, 80	0

All (66) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	399	LEU	5.7
2	D	336	LEU	4.9
2	D	432	LEU	4.8
1	C	101	LEU	4.5
2	D	326	ASN	4.5
2	B	175	VAL	4.3
2	D	428	GLU	4.3
1	C	234	PRO	4.2
2	D	372	TRP	4.2
2	D	416	SER	4.1
2	D	359	ALA	4.0
1	C	285	PHE	4.0
2	D	378	ARG	3.9
2	D	425	ASN	3.5
1	C	287	GLN	3.5
1	C	258	ASP	3.3
1	C	288	ASP	3.2
1	C	215	ILE	3.2
2	D	418	TYR	3.2
2	D	423	LEU	3.2
2	D	366	THR	3.2

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Mol	Chain	Res	Type	RSRZ
1	C	255	LEU	3.1
2	D	392	MET	3.1
1	C	282	ALA	3.1
2	D	427	PRO	3.1
2	D	422	SER	3.0
2	D	365	TYR	2.9
1	C	289	VAL	2.8
1	A	73	GLU	2.8
1	C	296	LEU	2.8
2	D	430	LEU	2.8
2	D	328	LYS	2.8
1	C	290	THR	2.8
1	C	161	HIS	2.7
2	D	403	GLN	2.7
2	D	384	LEU	2.7
2	D	362	LEU	2.6
2	D	176	PRO	2.6
2	D	388	LYS	2.6
2	D	284	ASP	2.6
1	C	175	LEU	2.6
2	D	329	VAL	2.6
2	D	335	PHE	2.6
1	C	249	SER	2.5
2	D	361	HIS	2.5
2	D	376	LEU	2.5
2	D	175	VAL	2.4
2	D	369	GLY	2.4
1	C	277	ALA	2.3
1	C	227	TRP	2.3
2	D	424	LEU	2.3
1	C	197	VAL	2.3
2	B	283	ASP	2.3
2	D	421	VAL	2.3
2	D	358	ALA	2.2
1	C	247	ASP	2.2
1	C	256	ASP	2.2
1	C	254	PRO	2.2
1	C	284	PRO	2.2
1	C	36	ARG	2.1
2	D	402	PRO	2.1
1	C	253	PRO	2.1
1	C	239	SER	2.0

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Mol	Chain	Res	Type	RSRZ
2	D	429	THR	2.0
2	D	405	ALA	2.0
2	D	426	PRO	2.0

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

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, 95th 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	RSR	LLDF	B-factors(Å ²)	Q<0.9
1	TPO	A	160	11/12	0.12	-0.53	12,16,17,18	0
1	TPO	C	160	11/12	0.14	-0.61	38,46,48,49	0

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

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, 95th 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	RSR	LLDF	B-factors(Å ²)	Q<0.9
3	N41	C	1298	27/27	0.22	2.41	42,45,59,61	0
4	SGM	B	1193	6/6	0.18	1.44	35,37,39,43	0
4	SGM	D	1193	6/6	0.14	0.20	62,63,64,66	0
3	N41	A	1298	27/27	0.11	-0.63	25,30,34,35	0
5	MG	B	1433	1/1	0.12	-0.85	19,19,19,19	0

6.5 Other polymers ⓘ

There are no such residues in this entry.