



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 09:20 PM GMT

PDB ID : 1OIY
Title : STRUCTURE OF HUMAN THR160-PHOSPHO CDK2/CYCLIN A COM-
PLEXED WITH A 6-CYCLOHEXYLMETHYLOXY-2-ANILINO-PURINE
INHIBITOR
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 X-ray Structure 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/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (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

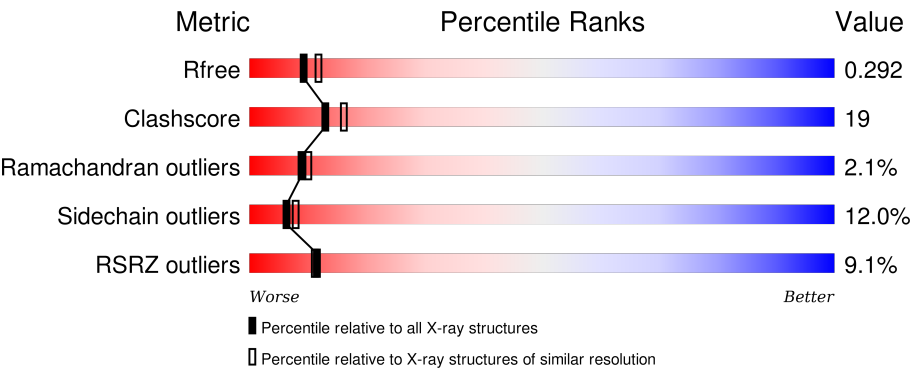
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

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}	91344	2919 (2.40-2.40)
Clashscore	102246	3407 (2.40-2.40)
Ramachandran outliers	100387	3351 (2.40-2.40)
Sidechain outliers	100360	3352 (2.40-2.40)
RSRZ outliers	91569	2928 (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. 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	302	<div><div>2%</div><div>64%</div><div>29%</div><div>• • •</div></div>
1	C	302	<div><div>13%</div><div>47%</div><div>42%</div><div>8%</div><div>• •</div></div>
2	B	260	<div><div>2%</div><div>66%</div><div>30%</div><div>• •</div></div>
2	D	260	<div><div>20%</div><div>51%</div><div>38%</div><div>10%</div><div>• •</div></div>

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 crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	N41	C	1298	-	-	-	X
4	SGM	B	1193	-	-	-	X

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 9273 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.

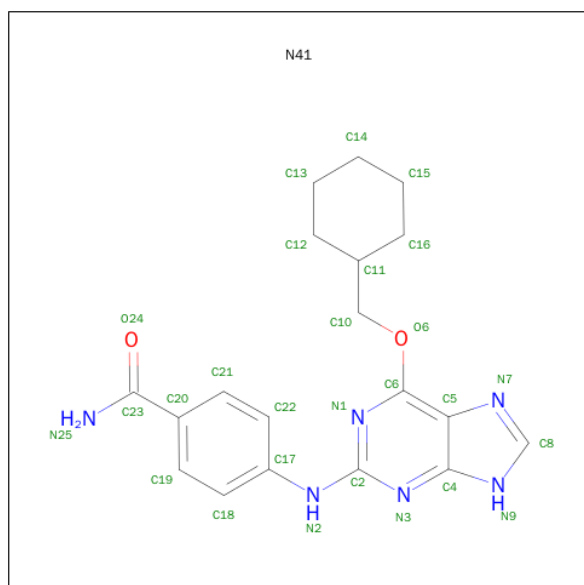
- Molecule 1 is a protein called CELL DIVISION PROTEIN KINASE 2.

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.

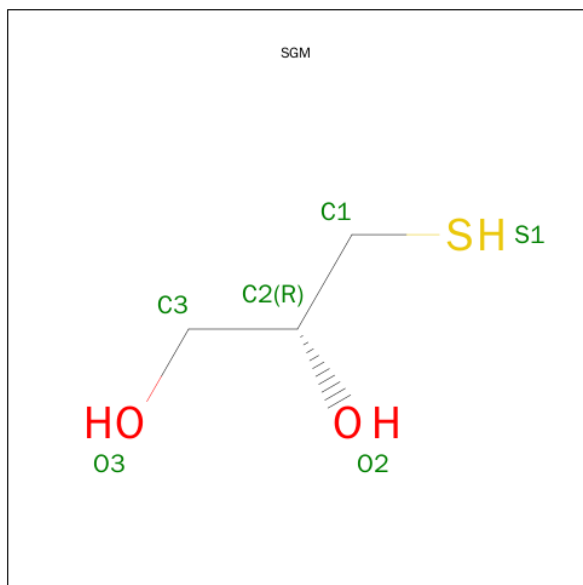
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	258	Total	C	N	O	S	0	1	0
			2088	1354	340	383	11			
2	D	258	Total	C	N	O	S	0	0	0
			2083	1350	339	383	11			

- 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		

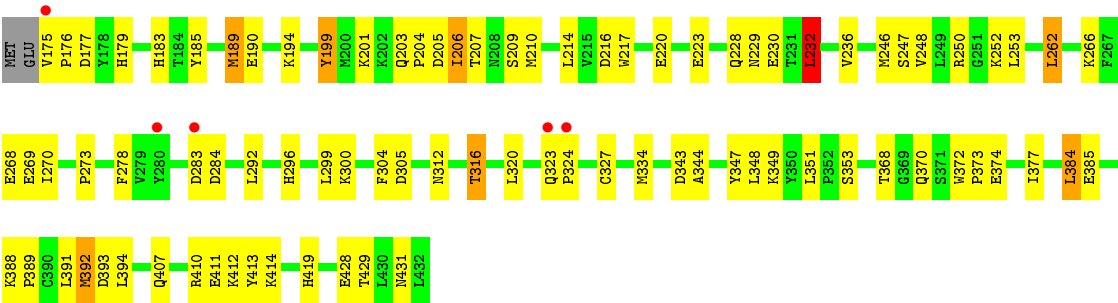
- Molecule 6 is water.

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

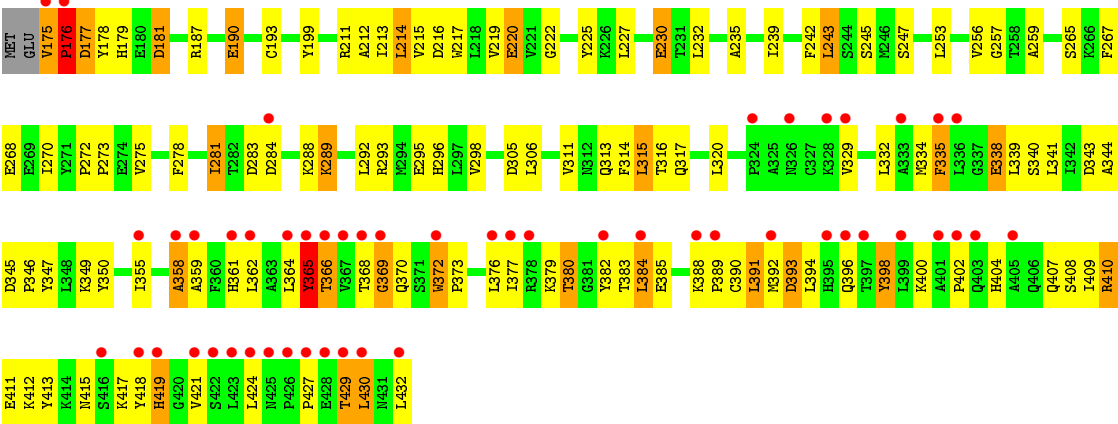
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	C	35	Total	O	0	0
			35	35		
6	D	17	Total	O	0	0
			17	17		



● Molecule 2: CYCLIN A2



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)	0.34 , 54.8	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.27$	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.

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

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 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 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	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
6	B	107	0	0	7	0
6	C	35	0	0	9	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	D	17	0	0	2	0
All	All	9273	0	9127	347	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 19.

All (347) 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: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	Interatomic distance (Å)	Clash overlap (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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:214:LEU:HD22	2:D:253:LEU:HD11	1.79	0.64
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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 [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	290/302 (96%)	272 (94%)	16 (6%)	2 (1%)	26	38
1	C	295/302 (98%)	250 (85%)	33 (11%)	12 (4%)	3	3
2	B	257/260 (99%)	248 (96%)	8 (3%)	1 (0%)	39	56
2	D	256/260 (98%)	217 (85%)	31 (12%)	8 (3%)	5	4
All	All	1098/1124 (98%)	987 (90%)	88 (8%)	23 (2%)	9	10

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%)	8	11
1	C	262/264 (99%)	225 (86%)	37 (14%)	4	5
2	B	233/234 (100%)	217 (93%)	16 (7%)	19	30
2	D	232/234 (99%)	195 (84%)	37 (16%)	3	3
All	All	986/996 (99%)	868 (88%)	118 (12%)	6	8

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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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 molecules 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	8,10,11	1.49	1 (12%)	7,14,16	1.37	1 (14%)
1	TPO	C	160	1	8,10,11	1.22	1 (12%)	7,14,16	1.17	0

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	-	0/8/11/13	0/0/0/0
1	TPO	C	160	1	-	0/8/11/13	0/0/0/0

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	160	TPO	P-O1P	2.24	1.58	1.51
1	A	160	TPO	P-O1P	2.91	1.60	1.51

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	160	TPO	O2P-P-O1P	-2.32	103.12	110.58

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	160	TPO	1	0
1	C	160	TPO	1	0

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	-	27,30,30	1.35	3 (11%)	32,41,41	1.93	8 (25%)
4	SGM	B	1193	2	5,5,5	0.55	0	5,5,5	0.93	0
3	N41	C	1298	-	27,30,30	0.77	0	32,41,41	2.03	7 (21%)
4	SGM	D	1193	-	5,5,5	0.33	0	5,5,5	0.90	0

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

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1298	N41	C4-N9	2.15	1.39	1.34
3	A	1298	N41	C6-N1	2.58	1.36	1.31
3	A	1298	N41	O6-C6	4.37	1.38	1.35

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	1298	N41	N3-C2-N1	-3.68	120.58	126.22
3	A	1298	N41	C5-C6-N1	-3.61	117.44	123.81
3	C	1298	N41	C17-N2-C2	-3.52	119.87	129.19
3	A	1298	N41	N3-C2-N1	-3.14	121.40	126.22

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	1298	N41	C5-C6-N1	-2.63	119.16	123.81
3	A	1298	N41	C17-N2-C2	-2.22	123.32	129.19
3	A	1298	N41	C4-C5-N7	-2.05	107.60	109.48
3	A	1298	N41	C16-C11-C12	2.20	114.80	109.26
3	C	1298	N41	O6-C6-C5	3.07	119.88	115.07
3	A	1298	N41	O6-C6-C5	4.12	121.52	115.07
3	C	1298	N41	C2-N3-C4	4.16	120.10	115.09
3	A	1298	N41	C2-N3-C4	4.25	120.20	115.09
3	C	1298	N41	C10-O6-C6	4.31	121.73	117.23
3	A	1298	N41	C2-N1-C6	5.04	122.51	115.32
3	C	1298	N41	C2-N1-C6	5.30	122.88	115.32

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1298	N41	4	0
3	C	1298	N41	2	0
4	D	1193	SGM	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, 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	293/302 (97%)	0.01	5 (1%) 73 72	11, 22, 45, 55	0
1	C	296/302 (98%)	0.69	39 (13%) 4 4	24, 47, 70, 80	0
2	B	258/260 (99%)	0.01	5 (1%) 70 69	11, 25, 44, 55	0
2	D	258/260 (99%)	0.91	52 (20%) 1 1	20, 48, 73, 78	0
All	All	1105/1124 (98%)	0.40	101 (9%) 11 11	11, 35, 69, 80	0

All (101) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	175	VAL	6.1
2	D	432	LEU	5.7
1	C	234	PRO	5.7
2	D	399	LEU	5.5
2	D	326	ASN	5.2
2	D	416	SER	5.2
2	D	361	HIS	5.1
2	D	336	LEU	5.0
2	D	359	ALA	4.9
1	C	101	LEU	4.9
2	D	176	PRO	4.5
1	C	258	ASP	4.5
2	D	372	TRP	4.5
2	D	428	GLU	4.5
1	C	215	ILE	4.3
2	D	388	LYS	4.1
2	D	422	SER	4.1
2	D	427	PRO	4.1
1	C	296	LEU	4.1
1	C	249	SER	4.0
1	C	285	PHE	4.0

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Mol	Chain	Res	Type	RSRZ
1	A	73	GLU	3.9
2	D	425	ASN	3.9
1	C	288	ASP	3.9
2	D	175	VAL	3.9
1	C	282	ALA	3.8
2	D	329	VAL	3.7
2	D	418	TYR	3.6
1	C	287	GLN	3.6
1	C	254	PRO	3.6
2	D	378	ARG	3.6
1	C	239	SER	3.5
2	D	423	LEU	3.5
1	C	227	TRP	3.5
2	D	328	LYS	3.5
2	D	365	TYR	3.4
1	C	290	THR	3.4
2	D	367	VAL	3.4
1	C	289	VAL	3.3
1	C	238	PRO	3.3
2	D	429	THR	3.3
2	D	366	THR	3.2
1	C	255	LEU	3.2
1	A	295	HIS	3.2
1	C	161	HIS	3.2
2	D	421	VAL	3.1
2	D	392	MET	3.1
2	D	324	PRO	3.1
2	D	402	PRO	3.1
2	D	284	ASP	3.1
2	D	376	LEU	3.1
2	D	426	PRO	3.1
2	D	377	ILE	3.1
2	D	403	GLN	3.1
2	D	362	LEU	3.0
1	C	247	ASP	3.0
2	B	323	GLN	2.9
1	C	36	ARG	2.9
2	D	401	ALA	2.9
2	D	389	PRO	2.9
1	C	175	LEU	2.8
1	C	233	MET	2.8
2	D	358	ALA	2.8

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Mol	Chain	Res	Type	RSRZ
1	C	209	ILE	2.8
1	C	225	VAL	2.8
2	D	405	ALA	2.8
2	D	335	PHE	2.8
1	C	98	GLY	2.7
2	D	355	ILE	2.7
2	D	424	LEU	2.7
2	D	395	HIS	2.6
1	C	173	ILE	2.6
1	C	251	VAL	2.6
2	B	283	ASP	2.5
2	D	364	LEU	2.5
2	D	430	LEU	2.5
1	C	284	PRO	2.5
2	D	369	GLY	2.5
2	D	368	THR	2.5
1	C	277	ALA	2.5
1	C	99	ILE	2.5
1	A	72	THR	2.4
1	C	213	PHE	2.4
1	A	96	LEU	2.4
2	D	384	LEU	2.4
1	C	295	HIS	2.4
2	D	396	GLN	2.3
1	C	235	ASP	2.3
2	D	397	THR	2.2
1	A	2	GLU	2.2
2	B	324	PRO	2.2
1	C	267	LEU	2.2
2	B	280	TYR	2.2
2	D	419	HIS	2.1
1	C	236	TYR	2.1
2	D	333	ALA	2.1
1	C	245	ARG	2.1
1	C	231	THR	2.1
1	C	273	LYS	2.1
2	D	382	TYR	2.0
1	C	286	PHE	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [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, 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	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
1	TPO	C	160	11/12	0.92	0.15	-	38,46,48,49	0
1	TPO	A	160	11/12	0.98	0.13	-	12,16,17,18	0

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, 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	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
4	SGM	B	1193	6/6	0.93	0.21	2.25	35,37,39,43	0
3	N41	C	1298	27/27	0.91	0.23	2.07	42,45,59,61	0
4	SGM	D	1193	6/6	0.91	0.15	0.28	62,63,64,66	0
5	MG	B	1433	1/1	0.95	0.15	-0.21	19,19,19,19	0
3	N41	A	1298	27/27	0.94	0.12	-0.89	25,30,34,35	0

6.5 Other polymers [i](#)

There are no such residues in this entry.