



# Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 07:46 PM GMT

PDB ID : 1H28  
Title : CDK2/CYCLIN A IN COMPLEX WITH AN 11-RESIDUE RECRUITMENT PEPTIDE FROM P107  
Authors : Tews, I.; Cheng, K.Y.; Lowe, E.D.; Noble, M.E.M.; Brown, N.R.; Gul, S.; Gamblin, S.; Johnson, L.N.  
Deposited on : 2002-07-31  
Resolution : 2.80 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.  
We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)  
A user guide is available at  
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467  
Mogul : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

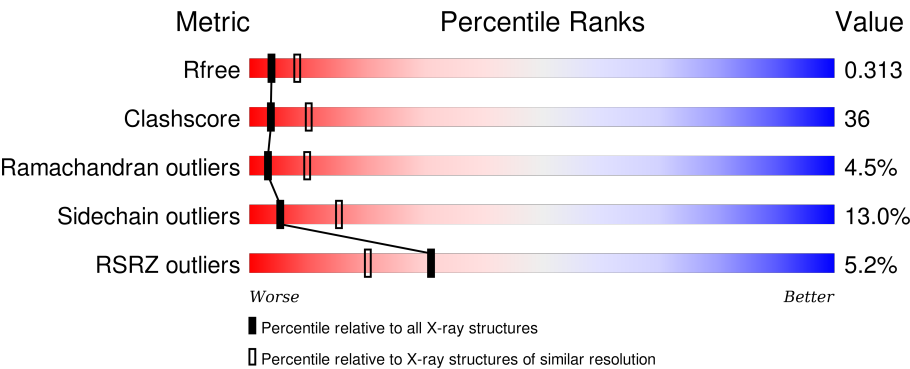
# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.80 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.



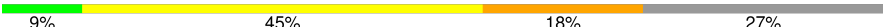
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R <sub>free</sub>	91344	2393 (2.80-2.80)
Clashscore	102246	2827 (2.80-2.80)
Ramachandran outliers	100387	2782 (2.80-2.80)
Sidechain outliers	100360	2784 (2.80-2.80)
RSRZ outliers	91569	2404 (2.80-2.80)

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	303	
1	C	303	
2	B	259	
2	D	259	
3	E	11	

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Mol	Chain	Length	Quality of chain
3	F	11	 A horizontal bar chart showing the quality of chain F. The bar is divided into four segments: green (9%), yellow (45%), orange (18%), and grey (27%).

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
1	TPO	C	160	-	-	X	-

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 9125 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	297	Total	C	N	O	P	S	0	0	0
			2388	1550	404	425	1	8			
1	C	297	Total	C	N	O	P	S	0	0	0
			2388	1550	404	425	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	0	0
			2083	1350	339	383	11			
2	D	258	Total	C	N	O	S	0	0	0
			2083	1350	339	383	11			

- Molecule 3 is a protein called RETINOBLASTOMA-LIKE PROTEIN 1.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	E	10	Total	C	N	O	0	0	0
			78	48	17	13			
3	F	8	Total	C	N	O	0	0	0
			68	43	15	10			

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	12	Total	O	0	0
			12	12		
4	B	11	Total	O	0	0
			11	11		
4	C	10	Total	O	0	0
			10	10		
4	D	3	Total	O	0	0
			3	3		

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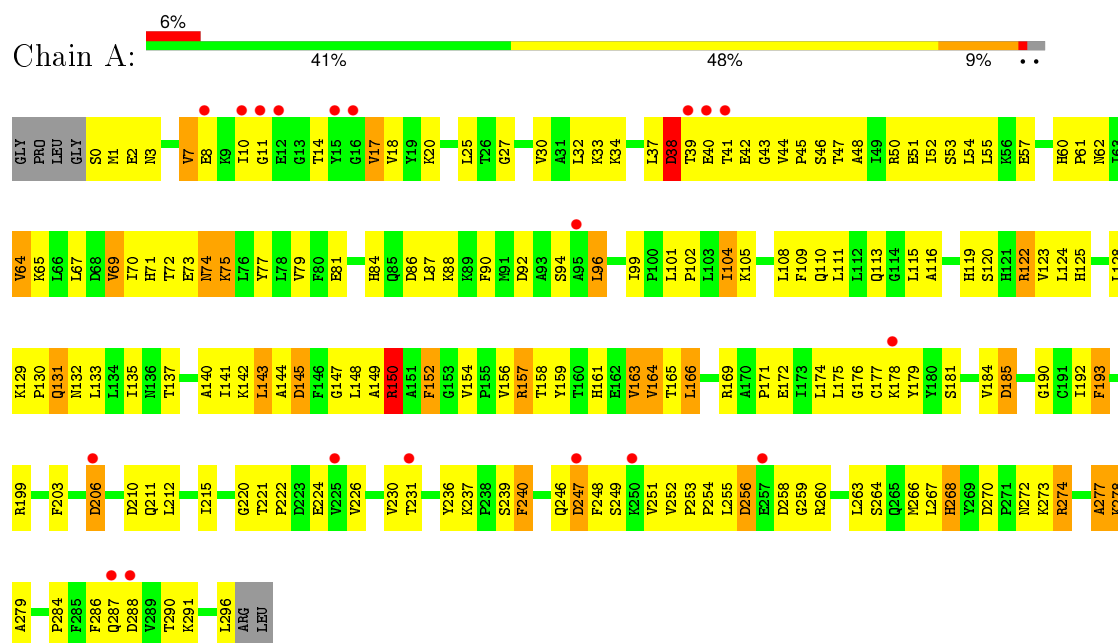
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	F	1	Total	O	0	0
			1	1		

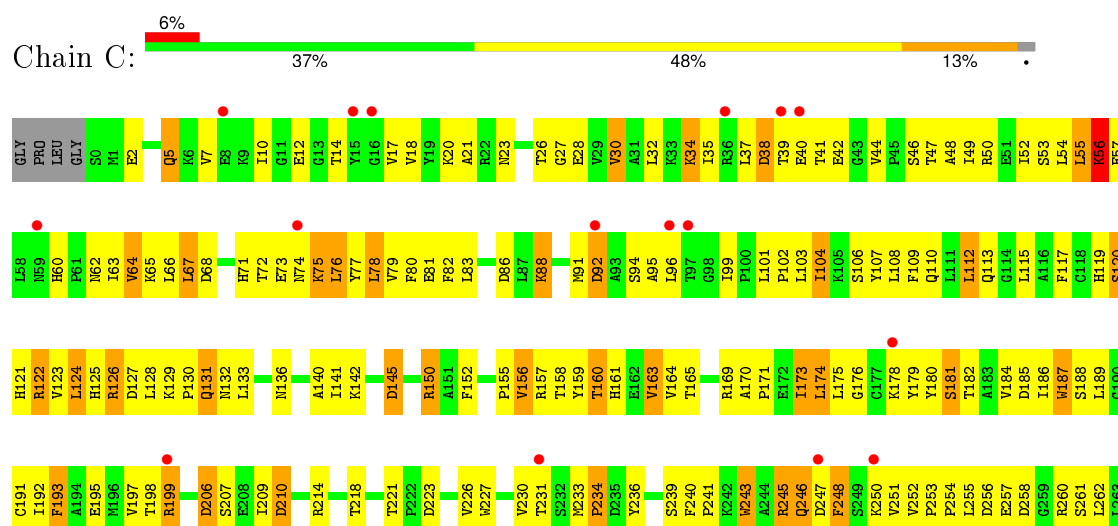
### 3 Residue-property plots

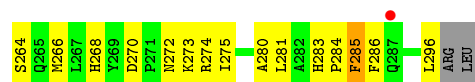
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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

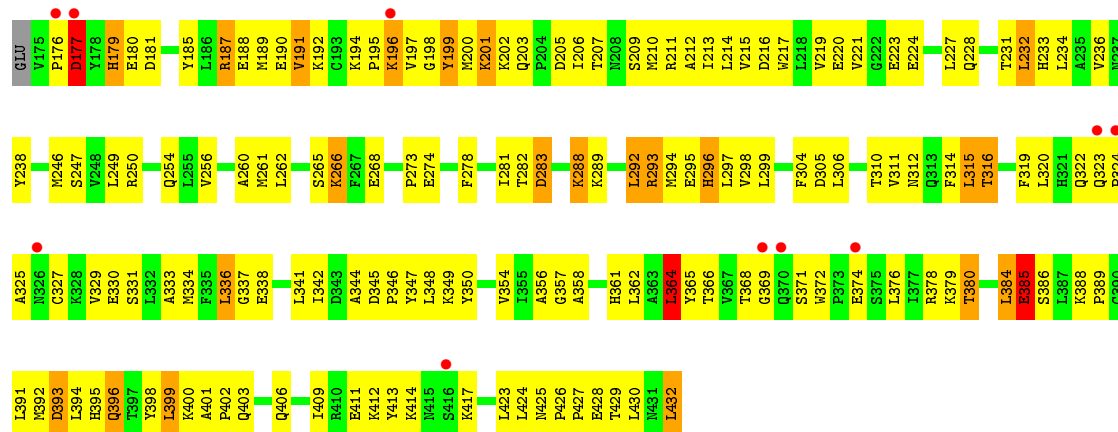


#### • Molecule 1: CELL DIVISION PROTEIN KINASE 2

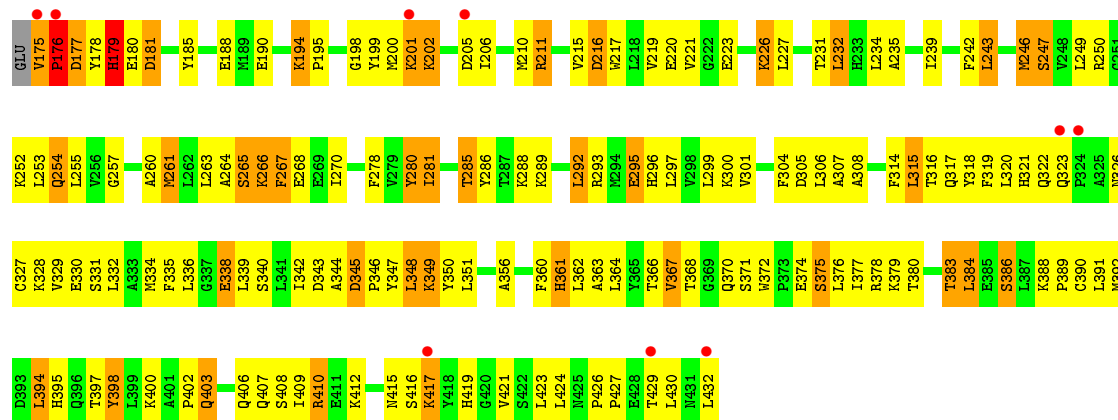




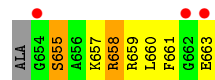
• Molecule 2: CYCLIN A2



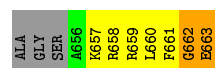
• Molecule 2: CYCLIN A2



• Molecule 3: RETINOBLASTOMA-LIKE PROTEIN 1



• Molecule 3: RETINOBLASTOMA-LIKE PROTEIN 1



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	149.50 Å   162.51 Å   71.38 Å 90.00°   90.00°   90.00°	Depositor
Resolution (Å)	29.62 – 2.80 29.23 – 2.80	Depositor EDS
% Data completeness (in resolution range)	95.1 (29.62-2.80) 95.1 (29.23-2.80)	Depositor EDS
$R_{merge}$	0.17	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.44 (at 2.80 Å)	Xtriage
Refinement program	REFMAC	Depositor
R, $R_{free}$	0.243   ,   0.323 0.241   ,   0.313	Depositor DCC
$R_{free}$ test set	2095 reflections (5.32%)	DCC
Wilson B-factor (Å <sup>2</sup> )	42.2	Xtriage
Anisotropy	0.208	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.40 , 57.4	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	1 of 41503 reflections (0.002%)	Xtriage
$F_o, F_c$ correlation	0.91	EDS
Total number of atoms	9125	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	31.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 40.90 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 2.5558e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.375 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

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	0.92	2/2438 (0.1%)	1.03	10/3308 (0.3%)
1	C	0.95	1/2438 (0.0%)	1.06	12/3308 (0.4%)
2	B	1.03	0/2133	1.05	7/2897 (0.2%)
2	D	1.03	3/2133 (0.1%)	1.02	6/2897 (0.2%)
3	E	0.93	0/78	0.97	0/100
3	F	0.83	0/68	1.09	0/87
All	All	0.98	6/9288 (0.1%)	1.04	35/12597 (0.3%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	C	0	1
All	All	0	2

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	267	PHE	CD2-CE2	-7.79	1.23	1.39
2	D	261	MET	CG-SD	6.12	1.97	1.81
1	C	187	TRP	CE3-CZ3	-5.53	1.29	1.38
1	A	64	VAL	CA-CB	-5.52	1.43	1.54
2	D	281	ILE	CA-CB	-5.43	1.42	1.54
1	A	152	PHE	CD2-CE2	-5.04	1.29	1.39

All (35) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	247	ASP	CB-CG-OD2	9.71	127.04	118.30
1	C	127	ASP	CB-CG-OD2	9.23	126.61	118.30
2	B	283	ASP	CB-CG-OD2	8.61	126.05	118.30
2	B	345	ASP	CB-CG-OD2	8.50	125.95	118.30
1	A	86	ASP	CB-CG-OD2	7.71	125.24	118.30
1	A	270	ASP	CB-CG-OD2	7.68	125.21	118.30
2	B	205	ASP	CB-CG-OD2	7.55	125.09	118.30
2	B	305	ASP	CB-CG-OD2	7.53	125.07	118.30
1	C	210	ASP	CB-CG-OD2	7.32	124.88	118.30
1	C	256	ASP	CB-CG-OD2	7.18	124.76	118.30
1	C	206	ASP	CB-CG-OD2	7.12	124.71	118.30
1	C	169	ARG	NE-CZ-NH2	-6.96	116.82	120.30
2	D	177	ASP	CB-CG-OD2	6.95	124.56	118.30
1	C	86	ASP	CB-CG-OD2	6.86	124.47	118.30
2	B	393	ASP	CB-CG-OD2	6.70	124.33	118.30
1	A	206	ASP	CB-CG-OD2	6.61	124.25	118.30
1	A	247	ASP	CB-CG-OD2	6.60	124.24	118.30
1	C	92	ASP	CB-CG-OD2	6.58	124.22	118.30
1	A	210	ASP	CB-CG-OD2	6.50	124.16	118.30
2	B	181	ASP	CB-CG-OD2	6.26	123.94	118.30
1	A	185	ASP	CB-CG-OD2	6.10	123.79	118.30
1	C	76	LEU	CA-CB-CG	6.06	129.25	115.30
2	D	243	LEU	CA-CB-CG	6.05	129.22	115.30
2	D	216	ASP	CB-CG-OD2	6.01	123.71	118.30
1	A	258	ASP	CB-CG-OD2	5.87	123.58	118.30
2	D	343	ASP	CB-CG-OD2	5.54	123.28	118.30
1	C	258	ASP	CB-CG-OD2	5.52	123.27	118.30
2	B	177	ASP	CB-CG-OD1	5.49	123.24	118.30
1	A	92	ASP	CB-CG-OD2	5.48	123.23	118.30
2	D	345	ASP	CB-CG-OD2	5.40	123.16	118.30
1	A	38	ASP	CB-CG-OD2	5.38	123.14	118.30
1	C	223	ASP	CB-CG-OD2	5.33	123.10	118.30
1	C	124	LEU	CA-CB-CG	5.29	127.48	115.30
1	A	150	ARG	NE-CZ-NH1	5.21	122.91	120.30
2	D	305	ASP	CB-CG-OD2	5.04	122.84	118.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	159	TYR	Mainchain
1	C	160	TPO	Mainchain

## 5.2 Too-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 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	2388	0	2429	170	0
1	C	2388	0	2430	195	0
2	B	2083	0	2107	148	2
2	D	2083	0	2107	175	2
3	E	78	0	80	8	0
3	F	68	0	72	15	0
4	A	12	0	0	3	0
4	B	11	0	0	0	0
4	C	10	0	0	6	0
4	D	3	0	0	0	0
4	F	1	0	0	1	0
All	All	9125	0	9225	654	2

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 36.

All (654) 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:277:ALA:O	1:A:279:ALA:N	1.76	1.18
2:B:207:THR:OG1	2:B:210:MET:HG3	1.49	1.12
1:C:253:PRO:HB2	1:C:254:PRO:HD3	1.35	1.05
2:D:415:ASN:OD1	2:D:417:LYS:N	1.89	1.05
2:B:336:LEU:HD13	2:B:362:LEU:HD23	1.42	1.02
1:C:245:ARG:HG3	1:C:245:ARG:HH11	1.19	1.02
2:D:321:HIS:ND1	2:D:375:SER:OG	1.87	1.00
2:D:366:THR:HG23	2:D:427:PRO:HD3	1.44	0.99
1:C:88:LYS:HE3	1:C:131:GLN:NE2	1.77	0.98
1:C:227:TRP:O	1:C:230:VAL:HG23	1.66	0.95
2:D:175:VAL:O	2:D:177:ASP:N	2.00	0.93
1:A:0:SER:HA	4:A:2001:HOH:O	1.69	0.93
1:C:156:VAL:HG12	1:C:159:TYR:HE2	1.33	0.91
2:B:329:VAL:HG11	2:B:364:LEU:HD12	1.52	0.91
1:C:88:LYS:HB2	1:C:130:PRO:HB2	1.53	0.90
1:C:72:THR:HB	1:C:75:LYS:O	1.71	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:361:HIS:HD2	2:B:372:TRP:H	1.11	0.89
1:A:50:ARG:HH22	1:A:150:ARG:NH2	1.71	0.88
2:D:211:ARG:HH11	2:D:211:ARG:HG2	1.40	0.87
1:C:99:ILE:HG23	1:C:103:LEU:HD23	1.57	0.86
1:A:135:ILE:HG22	1:A:141:ILE:HG13	1.56	0.86
1:A:72:THR:O	1:A:74:ASN:N	2.07	0.86
1:A:88:LYS:HB2	1:A:130:PRO:HB2	1.56	0.85
1:A:116:ALA:HB2	1:A:277:ALA:HB1	1.59	0.85
1:A:7:VAL:HG11	1:A:20:LYS:HD3	1.59	0.85
1:C:248:PHE:HB3	1:C:260:ARG:HD2	1.60	0.84
1:A:129:LYS:NZ	1:A:165:THR:OG1	2.11	0.83
1:A:81:GLU:OE1	1:A:142:LYS:NZ	2.10	0.82
1:A:39:THR:HG21	2:B:289:LYS:HG2	1.59	0.82
2:B:266:LYS:NZ	2:B:295:GLU:OE1	2.11	0.82
1:A:50:ARG:NH2	1:A:150:ARG:NH2	2.26	0.81
3:F:659:ARG:NH2	3:F:663:GLU:HA	1.94	0.81
1:A:255:LEU:HD23	1:A:260:ARG:N	1.96	0.80
1:C:60:HIS:CD2	1:C:62:ASN:H	1.99	0.80
2:B:391:LEU:HD23	2:B:432:LEU:HD11	1.65	0.79
2:B:388:LYS:HB3	2:B:389:PRO:HD3	1.62	0.79
1:C:71:HIS:HE1	2:D:304:PHE:HE2	1.29	0.79
1:C:253:PRO:HB2	1:C:254:PRO:CD	2.11	0.79
1:A:266:MET:O	1:A:274:ARG:HD3	1.82	0.79
1:A:252:VAL:HG12	1:A:255:LEU:HB2	1.64	0.79
2:D:281:ILE:O	3:F:657:LYS:HA	1.83	0.79
1:C:268:HIS:NE2	1:C:273:LYS:HD2	1.99	0.78
2:D:329:VAL:HG22	2:D:367:VAL:HG21	1.64	0.78
1:C:119:HIS:HE1	1:C:185:ASP:OD2	1.65	0.78
1:C:245:ARG:HG3	1:C:245:ARG:NH1	1.98	0.78
1:C:117:PHE:O	1:C:120:SER:HB2	1.84	0.77
2:D:332:LEU:HD23	2:D:363:ALA:HA	1.65	0.77
2:B:336:LEU:CD1	2:B:362:LEU:HD23	2.14	0.76
1:C:83:LEU:HD11	1:C:142:LYS:HD2	1.66	0.76
1:C:49:ILE:O	1:C:53:SER:OG	2.03	0.76
1:C:21:ALA:HB3	1:C:30:VAL:HG22	1.67	0.76
1:C:245:ARG:HH11	1:C:245:ARG:CG	1.96	0.76
1:C:253:PRO:CB	1:C:254:PRO:HD3	2.16	0.75
2:B:319:PHE:O	2:B:322:GLN:HB2	1.85	0.75
1:A:64:VAL:HG23	1:A:143:LEU:O	1.86	0.75
1:A:154:VAL:O	2:B:316:THR:HG23	1.88	0.74
2:B:342:ILE:HD11	2:B:409:ILE:HD12	1.69	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:251:VAL:HG12	1:C:252:VAL:HG13	1.69	0.73
2:D:400:LYS:HA	2:D:403:GLN:HE21	1.51	0.73
1:A:96:LEU:HD12	1:A:96:LEU:H	1.54	0.73
1:C:60:HIS:HD2	1:C:62:ASN:H	1.36	0.73
2:D:285:THR:HG21	3:F:659:ARG:HG3	1.71	0.72
1:A:1:MET:O	4:A:2002:HOH:O	2.07	0.72
2:D:265:SER:O	2:D:267:PHE:N	2.22	0.72
2:D:347:TYR:OH	2:D:394:LEU:HA	1.89	0.72
1:C:296:LEU:O	4:C:2010:HOH:O	2.08	0.72
1:C:39:THR:HA	2:D:292:LEU:HD23	1.70	0.72
1:C:88:LYS:HE3	1:C:131:GLN:HE22	1.53	0.72
1:A:40:GLU:O	2:B:288:LYS:NZ	2.18	0.72
1:A:224:GLU:OE2	1:A:231:THR:OG1	2.07	0.71
1:A:247:ASP:OD2	1:A:249:SER:OG	2.06	0.71
1:C:50:ARG:NH2	1:C:160:TPO:O2P	2.22	0.71
1:A:178:LYS:HE2	1:A:179:TYR:CE1	2.25	0.71
1:A:172:GLU:OE1	1:A:172:GLU:N	2.22	0.71
1:C:156:VAL:HG12	1:C:159:TYR:CE2	2.23	0.71
2:D:400:LYS:HA	2:D:403:GLN:NE2	2.06	0.70
2:D:175:VAL:C	2:D:177:ASP:H	1.93	0.70
2:D:278:PHE:O	2:D:281:ILE:HG22	1.91	0.70
1:A:72:THR:HG23	1:A:72:THR:O	1.90	0.69
1:C:39:THR:O	2:D:292:LEU:CD2	2.40	0.69
1:C:157:ARG:NH1	2:D:268:GLU:OE2	2.22	0.69
2:B:398:TYR:CE2	2:B:426:PRO:HB3	2.27	0.69
1:A:154:VAL:O	2:B:316:THR:CG2	2.41	0.69
2:B:412:LYS:HD3	2:B:413:TYR:CE1	2.27	0.69
2:B:223:GLU:OE2	2:B:412:LYS:HE3	1.92	0.69
1:A:2:GLU:OE1	1:C:73:GLU:HG2	1.91	0.69
2:B:411:GLU:O	2:B:414:LYS:HB2	1.93	0.69
2:D:306:LEU:O	2:D:308:ALA:N	2.19	0.69
3:F:661:PHE:O	3:F:663:GLU:N	2.21	0.68
1:A:108:LEU:HD23	1:A:286:PHE:HZ	1.56	0.68
2:B:196:LYS:O	2:B:199:TYR:HB3	1.92	0.68
1:A:33:LYS:NZ	1:A:51:GLU:OE2	2.26	0.68
1:A:25:LEU:HD12	2:D:297:LEU:HD22	1.76	0.68
1:A:10:ILE:HG12	1:A:18:VAL:O	1.94	0.68
1:A:239:SER:O	1:A:240:PHE:O	2.12	0.68
3:F:662:GLY:O	3:F:663:GLU:HB2	1.94	0.67
1:C:54:LEU:O	1:C:57:GLU:HB3	1.95	0.67
1:C:37:LEU:O	1:C:38:ASP:CB	2.42	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:181:SER:OG	1:C:182:THR:N	2.27	0.67
1:C:81:GLU:HG3	1:C:81:GLU:O	1.95	0.67
2:D:221:VAL:HG13	2:D:281:ILE:CD1	2.25	0.67
1:C:160:TPO:N	1:C:160:TPO:O3P	2.28	0.67
1:C:37:LEU:O	1:C:38:ASP:HB2	1.94	0.67
1:C:181:SER:O	1:C:184:VAL:HG22	1.95	0.67
2:B:254:GLN:NE2	3:E:660:LEU:HG	2.09	0.66
2:B:361:HIS:CD2	2:B:372:TRP:H	2.03	0.66
3:F:658:ARG:HG2	3:F:660:LEU:HD23	1.77	0.66
2:D:363:ALA:O	2:D:367:VAL:HG22	1.96	0.66
1:A:157:ARG:NH2	2:B:268:GLU:OE1	2.24	0.66
1:C:115:LEU:HD11	1:C:119:HIS:CE1	2.30	0.66
1:A:239:SER:O	1:A:240:PHE:C	2.31	0.66
2:D:383:THR:N	2:D:386:SER:OG	2.28	0.66
2:B:203:GLN:NE2	2:B:246:MET:O	2.28	0.66
2:D:384:LEU:HG	2:D:432:LEU:HD22	1.78	0.66
1:A:105:LYS:NZ	1:A:288:ASP:OD1	2.27	0.65
2:B:200:MET:SD	2:B:206:ILE:HG13	2.36	0.65
1:C:101:LEU:HB3	1:C:102:PRO:HD3	1.78	0.65
1:C:112:LEU:CD2	1:C:189:LEU:HD13	2.26	0.65
1:C:39:THR:CB	2:D:289:LYS:HD3	2.27	0.65
1:C:74:ASN:O	1:C:75:LYS:HB3	1.95	0.65
1:C:52:ILE:O	1:C:56:LYS:HG2	1.97	0.65
2:B:344:ALA:O	2:B:348:LEU:HB2	1.96	0.65
1:C:245:ARG:NH1	1:C:245:ARG:CG	2.59	0.64
2:D:211:ARG:NH1	2:D:211:ARG:HG2	2.09	0.64
2:D:364:LEU:HG	2:D:370:GLN:HB2	1.79	0.64
1:C:68:ASP:O	1:C:79:VAL:HG23	1.98	0.64
2:B:361:HIS:O	2:B:362:LEU:C	2.35	0.64
2:B:388:LYS:HB3	2:B:389:PRO:CD	2.27	0.64
2:B:361:HIS:NE2	2:B:371:SER:OG	2.31	0.64
2:D:332:LEU:O	2:D:335:PHE:HB3	1.98	0.64
2:D:400:LYS:O	2:D:403:GLN:HG2	1.97	0.64
2:B:299:LEU:HD23	2:B:306:LEU:HD21	1.80	0.64
1:A:50:ARG:HH22	1:A:150:ARG:HH21	1.43	0.64
1:A:10:ILE:HD11	1:A:18:VAL:HG12	1.79	0.64
2:D:366:THR:CG2	2:D:427:PRO:HD3	2.23	0.64
1:C:99:ILE:HG22	1:C:104:ILE:HG13	1.80	0.64
2:B:223:GLU:CD	2:B:412:LYS:HE3	2.18	0.64
1:A:37:LEU:O	1:A:38:ASP:HB2	1.98	0.64
1:C:112:LEU:HD23	1:C:189:LEU:HD13	1.80	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:10:ILE:HD13	1:C:82:PHE:HE1	1.63	0.63
2:D:299:LEU:HD22	2:D:304:PHE:CE1	2.34	0.63
2:B:342:ILE:CD1	2:B:409:ILE:HD12	2.28	0.63
1:A:65:LYS:HB3	1:A:81:GLU:OE2	1.97	0.63
1:A:2:GLU:HG2	1:A:2:GLU:O	1.98	0.63
2:D:221:VAL:HG13	2:D:281:ILE:HD12	1.79	0.63
2:D:361:HIS:CD2	2:D:362:LEU:N	2.66	0.63
1:C:136:ASN:ND2	1:C:140:ALA:HB3	2.14	0.63
2:D:416:SER:O	2:D:419:HIS:N	2.31	0.63
1:A:39:THR:CG2	2:B:289:LYS:HG2	2.29	0.63
2:B:412:LYS:HD3	2:B:413:TYR:HE1	1.62	0.62
1:A:247:ASP:OD2	1:A:249:SER:N	2.32	0.62
1:C:210:ASP:O	1:C:214:ARG:HG3	1.99	0.62
1:C:42:GLU:O	2:D:266:LYS:NZ	2.24	0.62
1:C:231:THR:HG22	1:C:236:TYR:CE2	2.35	0.62
1:C:155:PRO:HD2	2:D:316:THR:HG22	1.80	0.62
1:A:251:VAL:HG12	1:A:252:VAL:HG23	1.81	0.62
1:C:248:PHE:CB	1:C:260:ARG:HD2	2.27	0.62
1:A:108:LEU:HD23	1:A:286:PHE:CZ	2.34	0.62
2:D:384:LEU:HG	2:D:432:LEU:CD2	2.29	0.62
2:D:402:PRO:HA	2:D:407:GLN:HE22	1.64	0.62
3:F:659:ARG:HH21	3:F:663:GLU:HA	1.63	0.62
1:C:88:LYS:HA	1:C:91:MET:HE2	1.82	0.61
1:A:67:LEU:HD12	1:A:79:VAL:HG12	1.82	0.61
1:C:35:ILE:HD12	1:C:78:LEU:HD21	1.80	0.61
2:D:177:ASP:HB3	2:D:178:TYR:CD2	2.35	0.61
1:C:39:THR:OG1	2:D:289:LYS:HD3	1.99	0.61
1:C:5:GLN:HE21	1:C:5:GLN:HA	1.65	0.61
2:B:236:VAL:HG21	2:B:341:LEU:HD22	1.82	0.61
1:C:268:HIS:CE1	1:C:273:LYS:HD2	2.35	0.61
1:C:126:ARG:NH2	1:C:160:TPO:O1P	2.30	0.61
2:B:234:LEU:HD23	2:B:310:THR:HG21	1.81	0.61
1:A:253:PRO:HB2	1:A:254:PRO:HD3	1.83	0.61
1:C:283:HIS:ND1	1:C:284:PRO:HD2	2.14	0.61
1:A:190:GLY:HA2	1:A:266:MET:CE	2.31	0.60
1:C:161:HIS:O	1:C:163:VAL:N	2.33	0.60
2:D:285:THR:HG22	3:F:659:ARG:HD2	1.83	0.60
1:A:119:HIS:HE1	1:A:185:ASP:OD2	1.84	0.60
2:D:216:ASP:HB2	2:D:406:GLN:HG2	1.83	0.60
1:A:51:GLU:O	1:A:55:LEU:HB2	2.02	0.60
2:D:254:GLN:HG3	2:D:254:GLN:O	2.01	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:277:ALA:O	1:A:278:LYS:C	2.37	0.60
1:A:96:LEU:N	1:A:96:LEU:HD12	2.17	0.60
2:B:203:GLN:NE2	2:B:247:SER:HA	2.16	0.60
1:A:116:ALA:HB2	1:A:277:ALA:CB	2.31	0.60
2:B:219:VAL:HG22	2:B:232:LEU:HD11	1.84	0.60
2:D:289:LYS:HD2	2:D:293:ARG:HH21	1.67	0.60
2:D:368:THR:CB	2:D:370:GLN:HE21	2.14	0.60
2:D:176:PRO:HA	2:D:179:HIS:CG	2.37	0.59
2:D:360:PHE:HD2	2:D:372:TRP:CZ3	2.20	0.59
1:C:230:VAL:HG12	1:C:236:TYR:CD1	2.38	0.59
1:A:190:GLY:HA2	1:A:266:MET:HE3	1.83	0.59
1:A:157:ARG:HH11	1:A:157:ARG:HG3	1.68	0.59
2:D:247:SER:O	2:D:247:SER:OG	2.16	0.58
1:C:136:ASN:HD21	1:C:140:ALA:HB3	1.66	0.58
2:D:402:PRO:HB3	2:D:410:ARG:CZ	2.33	0.58
1:A:90:PHE:CE2	1:A:99:ILE:HD12	2.39	0.58
2:D:265:SER:O	2:D:266:LYS:C	2.41	0.58
1:C:55:LEU:C	1:C:57:GLU:H	2.07	0.58
1:C:39:THR:CA	2:D:292:LEU:HD23	2.34	0.58
2:D:253:LEU:HD12	2:D:253:LEU:O	2.03	0.58
1:A:239:SER:C	1:A:240:PHE:O	2.39	0.58
2:B:428:GLU:O	2:B:428:GLU:HG2	2.04	0.58
3:F:658:ARG:NE	4:F:2001:HOH:O	2.20	0.57
2:D:178:TYR:O	2:D:180:GLU:N	2.38	0.57
1:A:61:PRO:O	1:A:142:LYS:HD3	2.05	0.57
2:B:203:GLN:HE22	2:B:247:SER:HA	1.67	0.57
1:C:110:GLN:HE22	1:C:140:ALA:HA	1.69	0.57
1:A:54:LEU:HD13	1:A:123:VAL:HG13	1.86	0.57
1:A:1:MET:CE	1:A:70:ILE:HD13	2.35	0.57
1:A:177:CYS:SG	1:A:178:LYS:N	2.77	0.57
1:C:218:THR:HA	1:C:246:GLN:HG3	1.86	0.57
2:D:263:LEU:HD23	2:D:295:GLU:OE2	2.04	0.57
1:C:128:LEU:HB2	4:C:2004:HOH:O	2.04	0.57
2:D:388:LYS:N	2:D:389:PRO:CD	2.67	0.57
2:D:338:GLU:OE2	2:D:412:LYS:NZ	2.33	0.57
2:B:216:ASP:OD1	2:B:406:GLN:HB3	2.04	0.57
1:C:230:VAL:HG12	1:C:236:TYR:CE1	2.40	0.57
2:B:283:ASP:O	2:B:283:ASP:OD1	2.23	0.57
1:C:65:LYS:NZ	1:C:67:LEU:HD23	2.20	0.57
1:C:129:LYS:HE2	1:C:132:ASN:ND2	2.20	0.56
2:B:338:GLU:OE2	2:B:412:LYS:NZ	2.33	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:401:ALA:N	2:B:402:PRO:CD	2.69	0.56
1:C:109:PHE:CE2	1:C:113:GLN:NE2	2.73	0.56
3:F:659:ARG:CZ	3:F:663:GLU:HA	2.34	0.56
1:C:283:HIS:CG	1:C:284:PRO:HD2	2.41	0.56
2:D:371:SER:O	2:D:372:TRP:C	2.44	0.56
1:A:84:HIS:CD2	1:A:296:LEU:HD13	2.41	0.56
1:C:21:ALA:HB3	1:C:30:VAL:CG2	2.34	0.56
2:B:391:LEU:HD23	2:B:432:LEU:CD1	2.32	0.56
1:C:108:LEU:CD2	1:C:193:PHE:CD2	2.88	0.56
2:B:365:TYR:O	2:B:369:GLY:HA2	2.04	0.56
2:D:234:LEU:O	2:D:235:ALA:C	2.40	0.56
1:A:256:ASP:O	1:A:260:ARG:HG3	2.05	0.56
1:C:7:VAL:HB	1:C:20:LYS:HB3	1.88	0.56
2:B:396:GLN:O	2:B:399:LEU:N	2.39	0.56
1:C:145:ASP:OD1	1:C:145:ASP:C	2.44	0.56
2:B:215:VAL:HG22	2:B:236:VAL:HG22	1.88	0.56
1:C:113:GLN:HA	1:C:281:LEU:HD11	1.88	0.56
2:D:254:GLN:HG2	2:D:286:TYR:HE2	1.71	0.55
1:C:268:HIS:CE1	1:C:273:LYS:HB3	2.42	0.55
2:D:220:GLU:HG3	2:D:408:SER:HB3	1.87	0.55
2:D:219:VAL:HG22	2:D:232:LEU:HD11	1.88	0.55
2:D:265:SER:O	2:D:268:GLU:N	2.40	0.55
2:B:187:ARG:NH1	2:B:187:ARG:HG3	2.20	0.55
1:A:124:LEU:HG	1:A:152:PHE:HD2	1.72	0.55
1:A:122:ARG:HA	1:A:152:PHE:CZ	2.41	0.55
2:D:416:SER:O	2:D:417:LYS:C	2.45	0.55
1:C:39:THR:O	2:D:292:LEU:HD23	2.06	0.55
2:B:200:MET:SD	2:B:206:ILE:CD1	2.95	0.55
2:D:321:HIS:HD1	2:D:375:SER:HG	0.57	0.55
1:A:42:GLU:O	2:B:266:LYS:NZ	2.38	0.55
1:C:178:LYS:HG2	1:C:179:TYR:CE1	2.42	0.55
2:D:336:LEU:HD13	2:D:362:LEU:HD23	1.88	0.55
2:D:319:PHE:CZ	2:D:330:GLU:HA	2.42	0.55
1:C:272:ASN:HB3	4:C:2009:HOH:O	2.07	0.55
2:D:314:PHE:O	2:D:315:LEU:C	2.44	0.55
2:D:227:LEU:N	2:D:227:LEU:HD23	2.22	0.55
1:C:35:ILE:O	1:C:35:ILE:HG22	2.06	0.54
1:C:101:LEU:HB3	1:C:102:PRO:CD	2.37	0.54
1:A:2:GLU:OE1	1:C:73:GLU:CG	2.55	0.54
1:A:1:MET:CE	1:A:70:ILE:CD1	2.86	0.54
2:D:317:GLN:NE2	2:D:379:LYS:NZ	2.56	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:175:VAL:N	2:D:176:PRO:CD	2.70	0.54
1:A:255:LEU:HD23	1:A:259:GLY:C	2.26	0.54
1:C:34:LYS:HB2	1:C:77:TYR:CE1	2.42	0.54
2:D:329:VAL:HG22	2:D:367:VAL:CG2	2.37	0.54
1:C:109:PHE:O	1:C:113:GLN:HB2	2.07	0.54
2:B:221:VAL:HG11	2:B:281:ILE:HD13	1.90	0.54
2:D:383:THR:N	2:D:386:SER:HG	2.04	0.54
1:C:193:PHE:CD1	1:C:193:PHE:C	2.82	0.54
1:A:226:VAL:O	1:A:226:VAL:HG22	2.07	0.54
1:A:110:GLN:HE22	1:A:140:ALA:HA	1.72	0.54
2:B:361:HIS:CD2	2:B:371:SER:OG	2.61	0.54
1:A:32:LEU:CD2	1:A:79:VAL:HG22	2.39	0.54
2:B:210:MET:HE1	2:B:250:ARG:HG2	1.90	0.53
1:C:50:ARG:O	1:C:54:LEU:HD12	2.08	0.53
1:A:172:GLU:O	1:A:177:CYS:HB2	2.08	0.53
1:A:171:PRO:HD2	1:A:172:GLU:OE1	2.07	0.53
2:D:392:MET:O	2:D:395:HIS:HB3	2.08	0.53
1:A:27:GLY:HA3	2:D:249:LEU:HD12	1.90	0.53
2:D:374:GLU:HA	2:D:377:ILE:HD12	1.90	0.53
1:A:122:ARG:HD2	1:A:122:ARG:O	2.08	0.53
2:D:175:VAL:C	2:D:177:ASP:N	2.56	0.53
2:B:185:TYR:O	2:B:188:GLU:HB3	2.09	0.53
2:B:294:MET:O	2:B:295:GLU:C	2.47	0.53
2:D:368:THR:HB	2:D:370:GLN:HE21	1.73	0.53
2:D:376:LEU:O	2:D:380:THR:OG1	2.16	0.53
2:B:221:VAL:CG1	2:B:281:ILE:HD13	2.39	0.53
2:D:415:ASN:OD1	2:D:416:SER:N	2.42	0.53
2:D:326:ASN:HB3	2:D:329:VAL:HG23	1.91	0.53
1:C:55:LEU:C	1:C:57:GLU:N	2.60	0.53
2:D:210:MET:CE	2:D:250:ARG:HB2	2.39	0.53
1:C:193:PHE:C	1:C:193:PHE:HD1	2.12	0.52
2:B:211:ARG:O	2:B:214:LEU:HB3	2.08	0.52
2:B:234:LEU:HD23	2:B:310:THR:CG2	2.40	0.52
2:B:203:GLN:HB3	2:B:206:ILE:HG12	1.91	0.52
1:A:211:GLN:O	1:A:215:ILE:HG13	2.09	0.52
1:C:63:ILE:O	1:C:64:VAL:C	2.47	0.52
1:A:181:SER:O	1:A:184:VAL:HG22	2.10	0.52
1:C:170:ALA:HB1	1:C:171:PRO:CD	2.39	0.52
3:E:659:ARG:HE	3:E:663:GLU:HA	1.73	0.52
1:C:156:VAL:CG1	1:C:159:TYR:HE2	2.14	0.52
2:D:221:VAL:HG22	2:D:281:ILE:CD1	2.39	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:39:THR:HB	2:D:289:LYS:HD3	1.91	0.52
1:A:42:GLU:HA	1:A:42:GLU:OE1	2.09	0.52
1:C:160:TPO:HG23	1:C:161:HIS:N	2.25	0.52
1:C:37:LEU:HD22	1:C:44:VAL:HA	1.91	0.52
1:A:236:TYR:C	1:A:236:TYR:CD2	2.82	0.52
2:B:330:GLU:O	2:B:333:ALA:HB3	2.10	0.52
2:D:216:ASP:CB	2:D:406:GLN:HG2	2.40	0.52
1:C:155:PRO:CD	2:D:316:THR:HG22	2.39	0.52
1:C:40:GLU:O	2:D:288:LYS:NZ	2.43	0.52
1:A:60:HIS:HD2	1:A:62:ASN:H	1.55	0.51
2:D:285:THR:CG2	3:F:659:ARG:HD2	2.40	0.51
1:A:101:LEU:HB3	1:A:102:PRO:HD3	1.92	0.51
2:B:196:LYS:HB2	2:B:196:LYS:NZ	2.25	0.51
1:C:178:LYS:HG2	1:C:179:TYR:CD1	2.45	0.51
1:C:266:MET:O	1:C:274:ARG:HD3	2.10	0.51
1:C:57:GLU:HG3	2:D:185:TYR:OH	2.11	0.51
2:B:262:LEU:O	2:B:265:SER:HB2	2.11	0.51
2:B:211:ARG:HD3	2:B:344:ALA:HB2	1.91	0.51
1:A:38:ASP:HB3	4:A:2004:HOH:O	2.10	0.51
2:B:189:MET:O	2:B:190:GLU:C	2.49	0.51
1:A:17:VAL:HG12	1:A:18:VAL:H	1.75	0.51
1:A:25:LEU:O	2:D:252:LYS:HG3	2.10	0.51
2:B:217:TRP:CE3	3:E:660:LEU:HD11	2.46	0.51
2:B:388:LYS:N	2:B:389:PRO:HD2	2.26	0.51
1:C:160:TPO:HA	2:D:270:ILE:HG23	1.92	0.51
1:A:52:ILE:O	1:A:53:SER:C	2.49	0.51
1:C:231:THR:HG22	1:C:236:TYR:CZ	2.46	0.51
3:E:657:LYS:O	3:E:658:ARG:HB2	2.12	0.50
2:B:249:LEU:HD12	1:C:27:GLY:HA3	1.92	0.50
1:C:101:LEU:N	1:C:102:PRO:HD2	2.26	0.50
2:D:221:VAL:HG22	2:D:281:ILE:HD11	1.93	0.50
1:C:128:LEU:CB	4:C:2004:HOH:O	2.59	0.50
2:D:350:TYR:CE1	2:D:390:CYS:HB2	2.47	0.50
1:A:132:ASN:OD1	1:A:145:ASP:HB3	2.12	0.50
1:C:123:VAL:HG12	1:C:124:LEU:N	2.25	0.50
1:A:266:MET:O	1:A:274:ARG:CD	2.58	0.50
2:D:306:LEU:C	2:D:308:ALA:H	2.12	0.50
2:D:205:ASP:O	2:D:206:ILE:CG2	2.59	0.50
2:B:342:ILE:HD11	2:B:409:ILE:CD1	2.39	0.50
2:B:398:TYR:CD2	2:B:426:PRO:HB3	2.46	0.50
2:B:187:ARG:HH11	2:B:187:ARG:CG	2.24	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:101:LEU:O	1:C:104:ILE:HB	2.12	0.50
2:B:278:PHE:O	2:B:282:THR:HG23	2.12	0.50
1:C:253:PRO:CB	1:C:254:PRO:CD	2.83	0.50
2:D:175:VAL:N	2:D:176:PRO:HD2	2.26	0.50
1:A:268:HIS:HB2	1:A:274:ARG:HA	1.92	0.50
2:D:339:LEU:HD23	2:D:409:ILE:HG21	1.92	0.50
2:B:322:GLN:CD	2:B:325:ALA:HA	2.33	0.50
1:C:108:LEU:HD11	1:C:112:LEU:HD21	1.93	0.50
1:A:40:GLU:H	2:B:292:LEU:HD23	1.75	0.50
1:A:115:LEU:HD21	1:A:185:ASP:HB3	1.93	0.50
1:C:284:PRO:C	1:C:286:PHE:N	2.62	0.49
2:D:395:HIS:O	2:D:398:TYR:HB3	2.12	0.49
1:C:197:VAL:HG21	1:C:255:LEU:HD13	1.94	0.49
1:A:174:LEU:HD13	1:A:212:LEU:HD23	1.93	0.49
2:D:361:HIS:HD2	2:D:391:LEU:HD11	1.76	0.49
1:A:124:LEU:HG	1:A:152:PHE:CD2	2.46	0.49
1:C:233:MET:O	1:C:234:PRO:C	2.50	0.49
2:D:200:MET:SD	2:D:206:ILE:HG13	2.52	0.49
2:D:327:CYS:SG	2:D:328:LYS:N	2.86	0.49
3:F:659:ARG:HH21	3:F:663:GLU:CA	2.25	0.49
1:C:60:HIS:HD2	1:C:62:ASN:N	2.08	0.49
2:B:409:ILE:O	2:B:412:LYS:HB3	2.13	0.49
1:A:37:LEU:O	1:A:38:ASP:CB	2.61	0.49
2:B:203:GLN:OE1	2:B:247:SER:HA	2.13	0.49
2:B:314:PHE:O	2:B:315:LEU:C	2.49	0.49
1:A:1:MET:C	1:A:3:ASN:H	2.16	0.49
1:C:241:PRO:HB2	1:C:243:TRP:CZ3	2.48	0.49
2:B:227:LEU:HD21	2:B:273:PRO:CG	2.43	0.49
1:C:39:THR:O	2:D:292:LEU:HD22	2.11	0.48
2:D:326:ASN:OD1	2:D:329:VAL:HG23	2.12	0.48
1:C:180:TYR:C	1:C:180:TYR:CD1	2.86	0.48
2:D:296:HIS:CD2	2:D:300:LYS:HE2	2.48	0.48
1:A:7:VAL:HG12	1:A:8:GLU:N	2.28	0.48
1:A:163:VAL:HG13	1:A:164:VAL:HG23	1.95	0.48
1:A:124:LEU:O	1:A:149:ALA:HA	2.13	0.48
2:B:336:LEU:O	2:B:337:GLY:C	2.51	0.48
1:C:260:ARG:O	1:C:264:SER:HB3	2.13	0.48
1:A:47:THR:O	1:A:51:GLU:N	2.40	0.48
2:B:278:PHE:HD1	2:B:281:ILE:HD11	1.78	0.48
1:C:57:GLU:CG	2:D:185:TYR:OH	2.61	0.48
2:D:255:LEU:HB2	2:D:286:TYR:CZ	2.47	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:209:ILE:CG2	1:C:210:ASP:N	2.76	0.48
2:D:392:MET:CE	2:D:430:LEU:HD12	2.44	0.48
1:A:284:PRO:O	1:A:287:GLN:HG2	2.14	0.48
2:D:246:MET:HG2	2:D:301:VAL:HG11	1.96	0.48
1:C:95:ALA:O	1:C:199:ARG:NH1	2.44	0.48
1:C:83:LEU:HA	1:C:83:LEU:HD23	1.49	0.48
2:B:346:PRO:O	2:B:348:LEU:N	2.47	0.48
1:C:284:PRO:O	1:C:286:PHE:N	2.47	0.48
1:C:123:VAL:CG1	1:C:124:LEU:N	2.76	0.48
2:D:378:ARG:CB	2:D:378:ARG:HH11	2.27	0.48
1:C:65:LYS:HZ3	1:C:67:LEU:HD23	1.77	0.48
2:D:260:ALA:O	2:D:261:MET:C	2.52	0.48
1:C:99:ILE:CG2	1:C:104:ILE:HG13	2.43	0.47
1:A:131:GLN:N	1:A:131:GLN:OE1	2.47	0.47
2:B:400:LYS:HG2	2:B:403:GLN:HE21	1.79	0.47
2:B:384:LEU:O	2:B:385:GLU:C	2.53	0.47
1:A:190:GLY:O	1:A:193:PHE:HB3	2.13	0.47
1:C:10:ILE:HD11	1:C:20:LYS:HA	1.96	0.47
2:B:198:GLY:O	2:B:201:LYS:HG3	2.14	0.47
1:A:266:MET:O	1:A:274:ARG:HG3	2.14	0.47
1:A:237:LYS:HG2	1:A:240:PHE:CZ	2.49	0.47
2:B:299:LEU:HD21	2:B:306:LEU:HD11	1.96	0.47
1:A:2:GLU:CG	1:A:2:GLU:O	2.63	0.47
1:A:17:VAL:C	1:A:18:VAL:HG23	2.35	0.47
2:B:329:VAL:HG11	2:B:364:LEU:CD1	2.35	0.47
1:A:171:PRO:HA	1:A:174:LEU:HB2	1.97	0.47
2:B:398:TYR:CZ	2:B:426:PRO:HB3	2.49	0.47
2:D:366:THR:HG23	2:D:427:PRO:CD	2.31	0.47
1:C:88:LYS:HB2	1:C:130:PRO:CB	2.36	0.47
1:C:103:LEU:O	1:C:104:ILE:C	2.53	0.47
2:B:428:GLU:O	2:B:429:THR:HG23	2.15	0.47
2:D:205:ASP:O	2:D:206:ILE:HG23	2.14	0.47
2:B:293:ARG:CG	1:C:2:GLU:OE2	2.63	0.47
2:D:254:GLN:HG2	2:D:286:TYR:CE2	2.49	0.47
1:A:11:GLY:O	1:A:18:VAL:HB	2.14	0.47
2:B:201:LYS:HB2	2:B:201:LYS:HE2	1.64	0.47
1:A:267:LEU:HA	1:A:267:LEU:HD23	1.71	0.47
2:D:252:LYS:O	2:D:255:LEU:N	2.47	0.47
2:D:226:LYS:HE3	2:D:226:LYS:HB3	1.52	0.47
1:C:156:VAL:HG22	4:C:2006:HOH:O	2.15	0.47
1:C:46:SER:O	1:C:50:ARG:HG3	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:33:LYS:NZ	1:A:51:GLU:CD	2.68	0.47
2:D:178:TYR:O	2:D:181:ASP:N	2.46	0.46
1:C:74:ASN:O	1:C:75:LYS:CB	2.63	0.46
2:B:398:TYR:O	2:B:398:TYR:CD1	2.68	0.46
1:A:259:GLY:O	1:A:260:ARG:C	2.52	0.46
2:D:360:PHE:CD2	2:D:372:TRP:CZ3	3.03	0.46
1:A:64:VAL:HG12	1:A:65:LYS:N	2.29	0.46
1:A:226:VAL:CG2	1:A:226:VAL:O	2.63	0.46
2:B:190:GLU:O	2:B:191:VAL:C	2.53	0.46
2:D:210:MET:HE3	2:D:250:ARG:HB2	1.97	0.46
1:C:241:PRO:HB2	1:C:243:TRP:CE3	2.50	0.46
1:C:106:SER:O	1:C:107:TYR:C	2.52	0.46
1:A:10:ILE:HG13	1:A:11:GLY:N	2.30	0.46
1:C:17:VAL:HG12	1:C:18:VAL:N	2.30	0.46
2:B:398:TYR:O	2:B:398:TYR:HD1	1.99	0.46
2:D:199:TYR:C	2:D:199:TYR:CD1	2.88	0.46
2:B:256:VAL:HG22	2:B:294:MET:CE	2.46	0.46
1:C:64:VAL:CG1	1:C:65:LYS:N	2.78	0.46
1:C:129:LYS:HE3	1:C:131:GLN:HG2	1.98	0.46
1:A:268:HIS:CD2	1:A:273:LYS:HB3	2.50	0.46
2:D:360:PHE:HD2	2:D:372:TRP:CE3	2.32	0.46
2:D:397:THR:O	2:D:398:TYR:C	2.55	0.46
2:D:231:THR:HG23	2:D:264:ALA:C	2.36	0.46
2:D:190:GLU:HG3	2:D:351:LEU:HD22	1.97	0.45
2:B:350:TYR:OH	2:B:389:PRO:O	2.32	0.45
1:C:125:HIS:O	1:C:126:ARG:HB2	2.16	0.45
1:C:108:LEU:CD1	1:C:112:LEU:HD21	2.46	0.45
1:C:170:ALA:HB1	1:C:171:PRO:HD2	1.97	0.45
1:A:165:THR:O	1:A:166:LEU:C	2.54	0.45
1:A:166:LEU:HD13	1:A:169:ARG:NH1	2.31	0.45
1:A:125:HIS:NE2	1:A:144:ALA:O	2.35	0.45
1:C:30:VAL:HB	1:C:80:PHE:O	2.17	0.45
1:C:284:PRO:O	1:C:285:PHE:C	2.55	0.45
2:D:239:ILE:HD11	2:D:257:GLY:HA2	1.99	0.45
1:A:203:PHE:O	1:A:211:GLN:NE2	2.46	0.45
1:C:39:THR:C	2:D:292:LEU:HD23	2.37	0.45
1:C:261:SER:O	1:C:262:LEU:C	2.54	0.45
2:D:288:LYS:HB3	2:D:288:LYS:HE2	1.56	0.45
2:B:296:HIS:O	2:B:297:LEU:C	2.55	0.45
2:D:360:PHE:CD2	2:D:372:TRP:HZ3	2.35	0.45
1:A:64:VAL:HG21	1:A:144:ALA:HB2	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:284:PRO:C	1:C:286:PHE:H	2.20	0.45
1:A:90:PHE:HE2	1:A:99:ILE:HD12	1.79	0.45
1:A:87:LEU:HG	1:A:87:LEU:O	2.17	0.45
2:B:219:VAL:HG21	2:B:409:ILE:CG1	2.47	0.45
2:D:423:LEU:O	2:D:424:LEU:C	2.49	0.45
2:B:394:LEU:HD12	2:B:394:LEU:HA	1.59	0.45
1:A:129:LYS:HA	1:A:192:ILE:HD11	1.99	0.45
2:D:252:LYS:O	2:D:253:LEU:C	2.54	0.45
2:D:253:LEU:HD12	2:D:253:LEU:C	2.35	0.45
2:B:423:LEU:O	2:B:424:LEU:C	2.54	0.45
1:A:252:VAL:CG1	1:A:255:LEU:HB2	2.42	0.44
2:B:200:MET:SD	2:B:206:ILE:CG1	3.05	0.44
1:A:45:PRO:O	1:A:48:ALA:HB3	2.16	0.44
1:A:248:PHE:CE2	1:A:264:SER:HB3	2.52	0.44
1:A:172:GLU:O	1:A:177:CYS:CB	2.65	0.44
1:A:142:LYS:O	1:A:143:LEU:C	2.55	0.44
1:C:55:LEU:O	1:C:57:GLU:N	2.50	0.44
2:B:312:ASN:OD1	2:B:334:MET:CE	2.65	0.44
2:B:358:ALA:HA	2:B:391:LEU:HD13	1.99	0.44
2:D:217:TRP:O	2:D:221:VAL:HG23	2.18	0.44
2:D:281:ILE:O	2:D:281:ILE:HG12	2.17	0.44
1:C:10:ILE:HD11	1:C:20:LYS:CA	2.47	0.44
2:D:318:TYR:HA	2:D:376:LEU:HD21	1.99	0.44
2:D:211:ARG:HH12	2:D:215:VAL:HG21	1.82	0.44
1:A:1:MET:C	1:A:3:ASN:N	2.71	0.44
2:B:199:TYR:CD1	2:B:199:TYR:C	2.91	0.44
2:D:361:HIS:CD2	2:D:391:LEU:HD11	2.51	0.44
1:A:111:LEU:HD21	1:A:133:LEU:HD22	2.00	0.44
2:B:212:ALA:O	2:B:213:ILE:C	2.54	0.44
2:D:201:LYS:HE3	2:D:202:LYS:NZ	2.32	0.44
1:A:50:ARG:NH2	1:A:150:ARG:CZ	2.80	0.44
1:C:119:HIS:CE1	1:C:185:ASP:OD2	2.57	0.44
2:D:292:LEU:HA	2:D:292:LEU:HD12	1.75	0.44
1:C:209:ILE:HG23	1:C:210:ASP:N	2.33	0.44
2:D:317:GLN:NE2	2:D:379:LYS:HZ1	2.16	0.44
1:A:109:PHE:O	1:A:113:GLN:HG3	2.18	0.44
2:D:342:ILE:HD11	2:D:409:ILE:HD12	2.00	0.44
2:B:385:GLU:O	2:B:386:SER:C	2.56	0.44
2:B:293:ARG:HG2	1:C:2:GLU:OE2	2.18	0.44
2:D:345:ASP:HA	2:D:346:PRO:HA	1.74	0.44
1:A:1:MET:HE3	1:A:70:ILE:CD1	2.48	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:71:HIS:CE1	2:B:304:PHE:CE1	3.05	0.44
1:A:268:HIS:CB	1:A:274:ARG:HA	2.48	0.44
2:B:187:ARG:HH11	2:B:187:ARG:HG3	1.82	0.44
1:C:227:TRP:HB3	1:C:230:VAL:CG2	2.48	0.44
1:C:115:LEU:CD1	1:C:119:HIS:CE1	3.00	0.44
1:C:48:ALA:O	1:C:49:ILE:C	2.53	0.44
2:B:214:LEU:HD12	2:B:214:LEU:O	2.17	0.44
1:C:233:MET:HE2	1:C:233:MET:HB2	1.69	0.44
1:C:12:GLU:HA	1:C:17:VAL:HA	2.00	0.44
1:C:17:VAL:HG12	1:C:18:VAL:H	1.81	0.44
1:A:71:HIS:HE1	2:B:304:PHE:CD1	2.36	0.44
2:D:278:PHE:O	2:D:281:ILE:CG2	2.62	0.43
2:D:350:TYR:CD1	2:D:390:CYS:HB2	2.53	0.43
1:A:111:LEU:HD23	1:A:111:LEU:HA	1.82	0.43
2:B:190:GLU:O	2:B:192:LYS:N	2.51	0.43
1:C:18:VAL:HA	1:C:32:LEU:O	2.18	0.43
1:C:71:HIS:CE1	2:D:304:PHE:HE2	2.21	0.43
1:C:112:LEU:HD13	1:C:280:ALA:HB3	2.00	0.43
2:D:242:PHE:O	2:D:246:MET:HB2	2.18	0.43
1:C:239:SER:O	1:C:240:PHE:C	2.57	0.43
1:C:261:SER:HB3	1:C:283:HIS:CE1	2.53	0.43
2:D:315:LEU:HD13	2:D:356:ALA:HB1	2.00	0.43
2:D:194:LYS:HA	2:D:195:PRO:HD3	1.87	0.43
2:B:354:VAL:O	2:B:357:GLY:N	2.52	0.43
2:B:288:LYS:O	2:B:289:LYS:C	2.56	0.43
2:B:203:GLN:CD	2:B:247:SER:HA	2.38	0.43
1:A:115:LEU:HD11	1:A:185:ASP:HB3	2.00	0.43
2:B:315:LEU:HD13	2:B:356:ALA:HB1	2.01	0.43
1:C:221:THR:OG1	1:C:241:PRO:O	2.24	0.43
1:A:72:THR:CG2	1:A:72:THR:O	2.60	0.43
2:B:203:GLN:HE22	2:B:246:MET:C	2.21	0.43
2:B:247:SER:OG	1:C:28:GLU:OE2	2.37	0.43
2:B:281:ILE:O	3:E:657:LYS:HA	2.18	0.43
1:A:203:PHE:HB2	1:A:211:GLN:HE22	1.84	0.43
3:E:661:PHE:O	3:E:663:GLU:N	2.52	0.43
2:B:401:ALA:N	2:B:402:PRO:HD3	2.33	0.43
2:B:374:GLU:O	2:B:374:GLU:HG3	2.19	0.43
1:A:46:SER:HB3	2:B:266:LYS:HG2	2.01	0.43
1:C:160:TPO:HA	2:D:270:ILE:CG2	2.49	0.43
2:B:249:LEU:HD12	1:C:27:GLY:CA	2.48	0.43
1:C:122:ARG:HA	1:C:152:PHE:CE1	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:277:ALA:O	1:A:279:ALA:CA	2.60	0.43
1:A:33:LYS:NZ	1:A:51:GLU:OE1	2.52	0.43
1:C:63:ILE:O	1:C:64:VAL:O	2.37	0.43
1:A:17:VAL:C	1:A:18:VAL:CG2	2.87	0.43
2:D:384:LEU:HA	2:D:384:LEU:HD12	1.69	0.43
2:B:395:HIS:O	2:B:396:GLN:C	2.58	0.42
2:D:232:LEU:O	2:D:232:LEU:HD22	2.19	0.42
2:B:366:THR:OG1	2:B:427:PRO:HD3	2.19	0.42
1:A:40:GLU:H	2:B:292:LEU:CD2	2.32	0.42
1:A:220:GLY:O	1:A:221:THR:C	2.55	0.42
3:F:661:PHE:C	3:F:663:GLU:H	2.16	0.42
1:A:1:MET:HE3	1:A:70:ILE:HD12	2.01	0.42
1:A:105:LYS:O	1:A:286:PHE:HE1	2.01	0.42
2:D:415:ASN:OD1	2:D:417:LYS:CB	2.67	0.42
1:A:57:GLU:OE2	2:B:189:MET:CE	2.67	0.42
1:C:121:HIS:O	1:C:122:ARG:HD2	2.18	0.42
1:C:227:TRP:CD2	1:C:230:VAL:HG22	2.55	0.42
2:D:350:TYR:CZ	2:D:390:CYS:HA	2.55	0.42
1:C:176:GLY:O	1:C:234:PRO:HG2	2.19	0.42
2:D:372:TRP:CH2	2:D:376:LEU:HD13	2.54	0.42
2:B:294:MET:O	2:B:298:VAL:HG23	2.20	0.42
1:A:247:ASP:OD2	1:A:249:SER:CB	2.67	0.42
1:A:174:LEU:C	1:A:176:GLY:H	2.23	0.42
2:D:372:TRP:CZ3	2:D:376:LEU:HD13	2.55	0.42
1:A:221:THR:HA	1:A:222:PRO:HD3	1.95	0.42
1:A:278:LYS:HE2	2:B:177:ASP:O	2.20	0.42
1:C:71:HIS:HE1	2:D:304:PHE:CE2	2.21	0.42
2:B:323:GLN:HA	2:B:324:PRO:HA	1.80	0.42
1:A:158:THR:HG23	1:A:178:LYS:O	2.20	0.42
2:B:233:HIS:CD2	2:B:311:VAL:HB	2.55	0.42
1:C:131:GLN:CD	1:C:131:GLN:H	2.22	0.42
1:A:252:VAL:HG21	1:A:263:LEU:CD2	2.50	0.42
2:B:322:GLN:O	2:B:324:PRO:HA	2.20	0.42
2:D:362:LEU:HA	2:D:362:LEU:HD12	1.81	0.42
2:D:317:GLN:NE2	2:D:379:LYS:HZ3	2.18	0.41
2:D:255:LEU:HB2	2:D:286:TYR:CE1	2.55	0.41
1:C:173:ILE:O	1:C:175:LEU:N	2.53	0.41
2:B:346:PRO:HG3	2:B:393:ASP:OD2	2.20	0.41
2:D:223:GLU:CD	2:D:412:LYS:HD2	2.40	0.41
2:D:344:ALA:O	2:D:348:LEU:HB2	2.20	0.41
1:A:42:GLU:OE2	2:B:274:GLU:HG2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:174:LEU:CD1	1:A:212:LEU:HD23	2.49	0.41
2:B:214:LEU:HD12	2:B:214:LEU:C	2.40	0.41
1:A:110:GLN:O	1:A:113:GLN:HB2	2.20	0.41
2:D:323:GLN:HA	2:D:323:GLN:OE1	2.20	0.41
1:C:91:MET:HB2	1:C:91:MET:HE2	1.87	0.41
2:D:254:GLN:CG	2:D:254:GLN:O	2.68	0.41
1:C:110:GLN:HB2	1:C:141:ILE:CG2	2.50	0.41
2:D:317:GLN:O	2:D:320:LEU:HB2	2.20	0.41
2:D:331:SER:HB2	2:D:421:VAL:HG11	2.01	0.41
2:B:376:LEU:O	2:B:380:THR:HG23	2.21	0.41
1:C:186:ILE:O	1:C:187:TRP:C	2.57	0.41
2:D:280:TYR:CE1	3:F:657:LYS:HD3	2.55	0.41
2:D:198:GLY:C	2:D:200:MET:N	2.74	0.41
2:D:190:GLU:O	2:D:194:LYS:HB3	2.21	0.41
1:C:23:ASN:CG	1:C:26:THR:OG1	2.58	0.41
1:C:270:ASP:C	1:C:270:ASP:OD1	2.59	0.41
1:C:88:LYS:HD3	1:C:92:ASP:OD2	2.20	0.41
1:C:157:ARG:O	1:C:158:THR:C	2.59	0.41
1:C:173:ILE:HG22	1:C:174:LEU:N	2.35	0.41
1:C:136:ASN:OD1	1:C:140:ALA:N	2.41	0.41
1:A:99:ILE:HG22	1:A:104:ILE:HG13	2.02	0.41
2:D:346:PRO:O	2:D:349:LYS:HG2	2.21	0.41
2:D:348:LEU:HA	2:D:348:LEU:HD12	1.78	0.41
2:B:388:LYS:O	2:B:392:MET:N	2.45	0.41
1:C:173:ILE:O	1:C:174:LEU:C	2.59	0.41
3:E:659:ARG:HH21	3:E:663:GLU:N	2.19	0.41
2:B:398:TYR:C	2:B:398:TYR:CD1	2.92	0.41
1:C:262:LEU:HD23	1:C:285:PHE:CD2	2.56	0.41
2:B:283:ASP:C	2:B:283:ASP:OD1	2.59	0.41
1:A:110:GLN:O	1:A:111:LEU:C	2.58	0.41
1:A:57:GLU:OE2	2:B:189:MET:HE2	2.20	0.41
2:B:423:LEU:C	2:B:424:LEU:O	2.57	0.41
1:A:69:VAL:HG22	1:A:71:HIS:CE1	2.56	0.41
3:E:655:SER:OG	3:E:655:SER:O	2.31	0.41
1:A:75:LYS:HZ2	1:A:75:LYS:HB2	1.85	0.41
1:A:75:LYS:NZ	1:A:77:TYR:OH	2.48	0.41
2:D:326:ASN:HB3	2:D:329:VAL:CG2	2.51	0.41
1:C:189:LEU:O	1:C:193:PHE:N	2.40	0.41
2:D:398:TYR:CD2	2:D:426:PRO:HB3	2.56	0.41
2:B:260:ALA:O	2:B:261:MET:C	2.55	0.41
2:B:194:LYS:HA	2:B:195:PRO:HD3	1.81	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C:2006:HOH:O	2:D:175:VAL:HG21	2.22	0.40
1:A:190:GLY:HA2	1:A:266:MET:HE1	2.02	0.40
1:C:173:ILE:HD11	1:C:184:VAL:HG11	2.04	0.40
1:A:157:ARG:HD3	2:B:228:GLN:OE1	2.21	0.40
1:C:189:LEU:HD23	1:C:189:LEU:HA	1.76	0.40
1:C:188:SER:O	1:C:192:ILE:HG13	2.22	0.40
1:A:115:LEU:HD13	1:A:128:LEU:HD11	2.03	0.40
1:C:188:SER:O	1:C:189:LEU:C	2.60	0.40
1:A:1:MET:CE	1:A:70:ILE:HD12	2.52	0.40
1:C:150:ARG:HH21	1:C:160:TPO:P	2.44	0.40
1:A:174:LEU:HB3	1:A:212:LEU:HD21	2.02	0.40
2:B:238:TYR:OH	2:B:306:LEU:HB3	2.21	0.40
2:D:342:ILE:HD13	2:D:342:ILE:HG21	1.91	0.40
1:A:71:HIS:CE1	2:B:304:PHE:HE1	2.39	0.40
3:F:662:GLY:O	3:F:663:GLU:CB	2.66	0.40
2:D:265:SER:C	2:D:267:PHE:N	2.74	0.40
1:C:191:CYS:O	1:C:195:GLU:HB2	2.22	0.40
2:B:176:PRO:HA	2:B:179:HIS:ND1	2.36	0.40
2:D:338:GLU:C	2:D:340:SER:N	2.72	0.40
2:B:216:ASP:CB	2:B:406:GLN:HG2	2.51	0.40
2:B:315:LEU:HD12	2:B:315:LEU:HA	1.94	0.40
1:A:41:THR:C	1:A:43:GLY:H	2.25	0.40
2:B:180:GLU:OE1	2:B:180:GLU:HA	2.21	0.40

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:379:LYS:O	2:D:378:ARG:NH2[2_665]	1.84	0.36
2:B:378:ARG:NH1	2:D:320:LEU:O[2_665]	2.18	0.02

## 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	294/303 (97%)	232 (79%)	47 (16%)	15 (5%)	2	8
1	C	294/303 (97%)	242 (82%)	37 (13%)	15 (5%)	2	8
2	B	256/259 (99%)	204 (80%)	42 (16%)	10 (4%)	4	12
2	D	256/259 (99%)	201 (78%)	48 (19%)	7 (3%)	6	21
3	E	8/11 (73%)	4 (50%)	2 (25%)	2 (25%)	0	0
3	F	6/11 (54%)	4 (67%)	1 (17%)	1 (17%)	0	0
All	All	1114/1146 (97%)	887 (80%)	177 (16%)	50 (4%)	3	10

All (50) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	14	THR
1	A	73	GLU
1	A	137	THR
1	A	277	ALA
1	A	278	LYS
2	B	197	VAL
1	C	14	THR
1	C	145	ASP
1	C	174	LEU
2	D	176	PRO
2	D	266	LYS
1	A	145	ASP
1	A	164	VAL
1	A	175	LEU
2	B	320	LEU
2	B	347	TYR
1	C	38	ASP
1	C	75	LYS
1	C	164	VAL
1	C	173	ILE
2	D	179	HIS
2	D	307	ALA
2	D	417	LYS
3	E	658	ARG
3	F	662	GLY
1	A	38	ASP
1	A	143	LEU
2	B	191	VAL

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Mol	Chain	Res	Type
2	B	364	LEU
1	C	41	THR
1	C	56	LYS
1	C	285	PHE
3	E	655	SER
1	A	193	PHE
1	A	256	ASP
2	B	385	GLU
2	B	396	GLN
1	C	64	VAL
1	C	120	SER
2	B	179	HIS
2	B	336	LEU
1	C	104	ILE
1	C	234	PRO
2	D	265	SER
2	B	327	CYS
2	D	201	LYS
1	A	104	ILE
1	A	147	GLY
1	A	240	PHE
1	C	275	ILE

### 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	261/265 (98%)	232 (89%)	29 (11%)	8	23
1	C	261/265 (98%)	226 (87%)	35 (13%)	5	14
2	B	232/233 (100%)	202 (87%)	30 (13%)	5	16
2	D	232/233 (100%)	197 (85%)	35 (15%)	3	10
3	E	7/7 (100%)	7 (100%)	0	100	100
3	F	6/7 (86%)	5 (83%)	1 (17%)	3	8
All	All	999/1010 (99%)	869 (87%)	130 (13%)	5	15

All (130) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	7	VAL
1	A	17	VAL
1	A	30	VAL
1	A	34	LYS
1	A	44	VAL
1	A	69	VAL
1	A	74	ASN
1	A	75	LYS
1	A	94	SER
1	A	96	LEU
1	A	120	SER
1	A	122	ARG
1	A	131	GLN
1	A	148	LEU
1	A	150	ARG
1	A	156	VAL
1	A	157	ARG
1	A	161	HIS
1	A	163	VAL
1	A	166	LEU
1	A	199	ARG
1	A	206	ASP
1	A	230	VAL
1	A	246	GLN
1	A	268	HIS
1	A	272	ASN
1	A	274	ARG
1	A	290	THR
1	A	291	LYS
2	B	177	ASP
2	B	187	ARG
2	B	196	LYS
2	B	199	TYR
2	B	201	LYS
2	B	202	LYS
2	B	209	SER
2	B	220	GLU
2	B	224	GLU
2	B	231	THR
2	B	232	LEU
2	B	266	LYS
2	B	288	LYS

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Mol	Chain	Res	Type
2	B	292	LEU
2	B	293	ARG
2	B	296	HIS
2	B	315	LEU
2	B	316	THR
2	B	331	SER
2	B	349	LYS
2	B	364	LEU
2	B	368	THR
2	B	380	THR
2	B	384	LEU
2	B	385	GLU
2	B	399	LEU
2	B	417	LYS
2	B	425	ASN
2	B	430	LEU
2	B	432	LEU
1	C	5	GLN
1	C	30	VAL
1	C	34	LYS
1	C	47	THR
1	C	55	LEU
1	C	56	LYS
1	C	66	LEU
1	C	67	LEU
1	C	76	LEU
1	C	78	LEU
1	C	88	LYS
1	C	94	SER
1	C	96	LEU
1	C	112	LEU
1	C	122	ARG
1	C	126	ARG
1	C	131	GLN
1	C	133	LEU
1	C	150	ARG
1	C	156	VAL
1	C	163	VAL
1	C	165	THR
1	C	181	SER
1	C	193	PHE
1	C	198	THR

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Mol	Chain	Res	Type
1	C	199	ARG
1	C	206	ASP
1	C	207	SER
1	C	226	VAL
1	C	243	TRP
1	C	245	ARG
1	C	246	GLN
1	C	248	PHE
1	C	250	LYS
1	C	257	GLU
2	D	175	VAL
2	D	176	PRO
2	D	179	HIS
2	D	181	ASP
2	D	188	GLU
2	D	194	LYS
2	D	202	LYS
2	D	211	ARG
2	D	226	LYS
2	D	232	LEU
2	D	243	LEU
2	D	246	MET
2	D	247	SER
2	D	254	GLN
2	D	280	TYR
2	D	285	THR
2	D	292	LEU
2	D	295	GLU
2	D	315	LEU
2	D	322	GLN
2	D	334	MET
2	D	338	GLU
2	D	348	LEU
2	D	349	LYS
2	D	361	HIS
2	D	367	VAL
2	D	375	SER
2	D	383	THR
2	D	384	LEU
2	D	386	SER
2	D	394	LEU
2	D	398	TYR

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Mol	Chain	Res	Type
2	D	403	GLN
2	D	410	ARG
2	D	429	THR
3	F	663	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (24) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	71	HIS
1	A	74	ASN
1	A	85	GLN
1	A	119	HIS
1	A	268	HIS
2	B	317	GLN
2	B	370	GLN
2	B	395	HIS
2	B	403	GLN
1	C	5	GLN
1	C	60	HIS
1	C	71	HIS
1	C	85	GLN
1	C	113	GLN
1	C	119	HIS
1	C	131	GLN
2	D	179	HIS
2	D	254	GLN
2	D	296	HIS
2	D	317	GLN
2	D	361	HIS
2	D	370	GLN
2	D	396	GLN
2	D	403	GLN

### 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	1.65	2 (25%)	7,14,16	1.25	1 (14%)
1	TPO	C	160	1	8,10,11	1.24	1 (12%)	7,14,16	3.13	4 (57%)

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 (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	160	TPO	P-O1P	2.06	1.58	1.51
1	A	160	TPO	P-O3P	2.67	1.64	1.54
1	A	160	TPO	P-O1P	3.36	1.62	1.51

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	160	TPO	C-CA-N	-4.06	101.35	109.83
1	C	160	TPO	O-C-CA	-2.84	117.94	125.44
1	A	160	TPO	CG2-CB-CA	2.07	117.38	113.17
1	C	160	TPO	O3P-P-O2P	2.54	117.05	107.38
1	C	160	TPO	OG1-P-O1P	5.61	121.11	107.11

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	C	160	TPO	7	0

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

## 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	296/303 (97%)	0.19	19 (6%) 23 14	13, 32, 60, 75	0
1	C	296/303 (97%)	0.17	17 (5%) 27 17	12, 32, 58, 71	0
2	B	258/259 (99%)	-0.02	10 (3%) 43 31	9, 25, 48, 59	0
2	D	258/259 (99%)	0.06	9 (3%) 48 35	11, 28, 47, 64	0
3	E	10/11 (90%)	0.90	3 (30%) 1 0	33, 41, 46, 46	0
3	F	8/11 (72%)	0.44	0 100 100	42, 45, 54, 57	0
All	All	1126/1146 (98%)	0.11	58 (5%) 31 20	9, 29, 54, 75	0

All (58) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	323	GLN	7.1
1	C	39	THR	5.2
1	A	39	THR	4.7
1	A	40	GLU	4.7
1	C	16	GLY	4.2
1	A	41	THR	4.1
2	B	324	PRO	3.9
1	A	16	GLY	3.8
1	A	247	ASP	3.6
2	D	432	LEU	3.5
1	A	95	ALA	3.3
1	C	40	GLU	3.3
1	A	250	LYS	3.2
2	D	176	PRO	3.2
1	C	287	GLN	3.2
2	B	176	PRO	3.1
2	D	429	THR	3.1
2	D	205	ASP	3.0
1	C	74	ASN	3.0

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	A	12	GLU	3.0
1	A	225	VAL	3.0
1	C	199	ARG	3.0
1	A	257	GLU	2.9
2	B	196	LYS	2.9
2	B	369	GLY	2.9
1	C	15	TYR	2.9
3	E	663	GLU	2.9
1	C	92	ASP	2.9
1	A	231	THR	2.9
1	A	178	LYS	2.8
2	B	177	ASP	2.8
2	B	416	SER	2.7
1	C	36	ARG	2.7
1	C	8	GLU	2.7
2	B	370	GLN	2.6
2	D	323	GLN	2.6
2	D	417	LYS	2.6
1	C	178	LYS	2.6
1	C	247	ASP	2.6
1	A	8	GLU	2.5
1	C	59	ASN	2.5
2	D	175	VAL	2.4
1	C	96	LEU	2.4
1	C	250	LYS	2.4
3	E	654	GLY	2.4
1	A	11	GLY	2.3
1	A	287	GLN	2.3
2	D	201	LYS	2.3
1	A	206	ASP	2.3
1	A	15	TYR	2.3
1	A	288	ASP	2.2
2	D	324	PRO	2.2
1	C	231	THR	2.2
1	C	97	THR	2.2
1	A	10	ILE	2.1
3	E	662	GLY	2.1
2	B	374	GLU	2.1
2	B	326	ASN	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, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
1	TPO	A	160	11/12	0.98	0.12	-	4,14,21,27	0
1	TPO	C	160	11/12	0.97	0.11	-	14,19,24,25	0

## 6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 6.4 Ligands [i](#)

There are no ligands in this entry.

## 6.5 Other polymers [i](#)

There are no such residues in this entry.