



Full wwPDB X-ray Structure Validation Report ⓘ

Jun 14, 2020 – 05:04 pm BST

PDB ID : 2PKQ
Title : Crystal structure of the photosynthetic A2B2-glyceraldehyde-3-phosphate dehydrogenase, complexed with NADP
Authors : Fermani, S.; Falini, G.; Ripamonti, A.
Deposited on : 2007-04-18
Resolution : 3.60 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

<https://www.wwpdb.org/validation/2017/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 : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.11
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

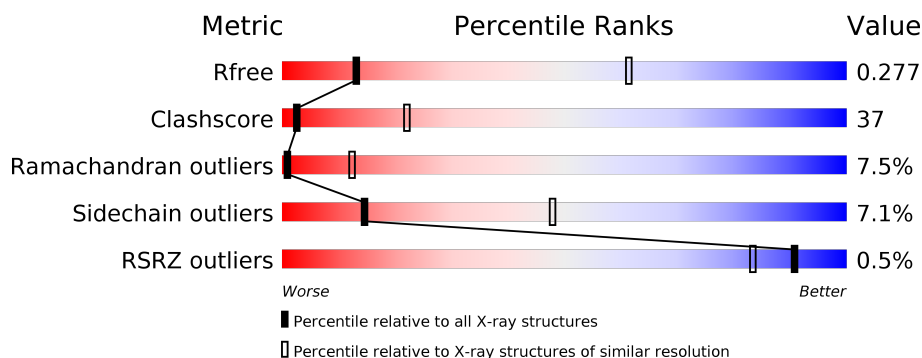
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.60 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}	130704	1257 (3.70-3.50)
Clashscore	141614	1353 (3.70-3.50)
Ramachandran outliers	138981	1307 (3.70-3.50)
Sidechain outliers	138945	1307 (3.70-3.50)
RSRZ outliers	127900	1161 (3.70-3.50)

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 respectively. 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	O	368	<div> <div>36%</div> <div>48%</div> <div>10%</div> <div>6%</div> </div>
1	Q	368	<div> <div>38%</div> <div>46%</div> <div>11%</div> <div>6%</div> </div>
1	T	368	<div> <div>38%</div> <div>46%</div> <div>10%</div> <div>5%</div> </div>
2	P	337	<div> <div>44%</div> <div>49%</div> <div>7%</div> </div>
2	R	337	<div> <div>45%</div> <div>49%</div> <div>6%</div> </div>
2	S	337	<div> <div>46%</div> <div>47%</div> <div>6%</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 criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	SO4	T	379	-	-	-	X

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 15840 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 Glyceraldehyde-3-phosphate dehydrogenase B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	O	346	Total	C	N	O	S	0	0	0
			2611	1657	452	491	11			
1	Q	347	Total	C	N	O	S	0	0	0
			2615	1658	453	494	10			
1	T	349	Total	C	N	O	S	0	0	0
			2625	1663	455	496	11			

- Molecule 2 is a protein called Glyceraldehyde-3-phosphate dehydrogenase A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	P	337	Total	C	N	O	S	0	0	0
			2544	1600	445	488	11			
2	R	337	Total	C	N	O	S	0	0	0
			2544	1600	445	488	11			
2	S	336	Total	C	N	O	S	0	0	0
			2538	1597	444	486	11			

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



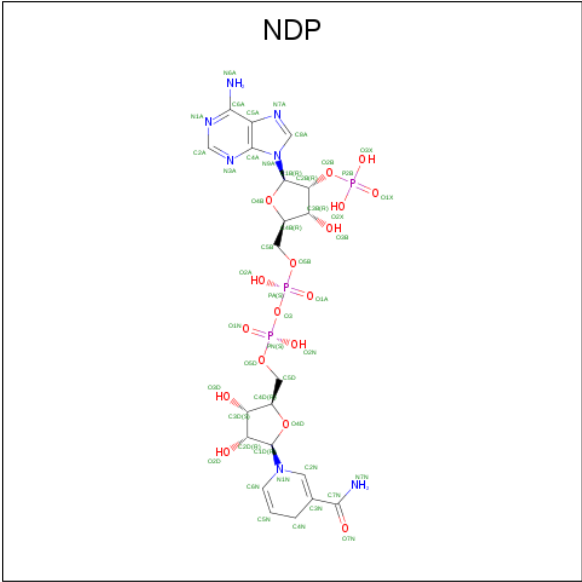
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	O	1	Total	O	S	0	0
			5	4	1		
3	P	1	Total	O	S	0	0
			5	4	1		
3	P	1	Total	O	S	0	0
			5	4	1		
3	Q	1	Total	O	S	0	0
			5	4	1		
3	Q	1	Total	O	S	0	0
			5	4	1		
3	Q	1	Total	O	S	0	0
			5	4	1		
3	R	1	Total	O	S	0	0
			5	4	1		
3	R	1	Total	O	S	0	0
			5	4	1		
3	R	1	Total	O	S	0	0
			5	4	1		
3	S	1	Total	O	S	0	0
			5	4	1		
3	S	1	Total	O	S	0	0
			5	4	1		
3	S	1	Total	O	S	0	0
			5	4	1		
3	T	1	Total	O	S	0	0
			5	4	1		
3	T	1	Total	O	S	0	0
			5	4	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	T	1	Total	O	S	0	0
			5	4	1		

- Molecule 4 is NADPH DIHYDRO-NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (three-letter code: NDP) (formula: C₂₁H₃₀N₇O₁₇P₃).

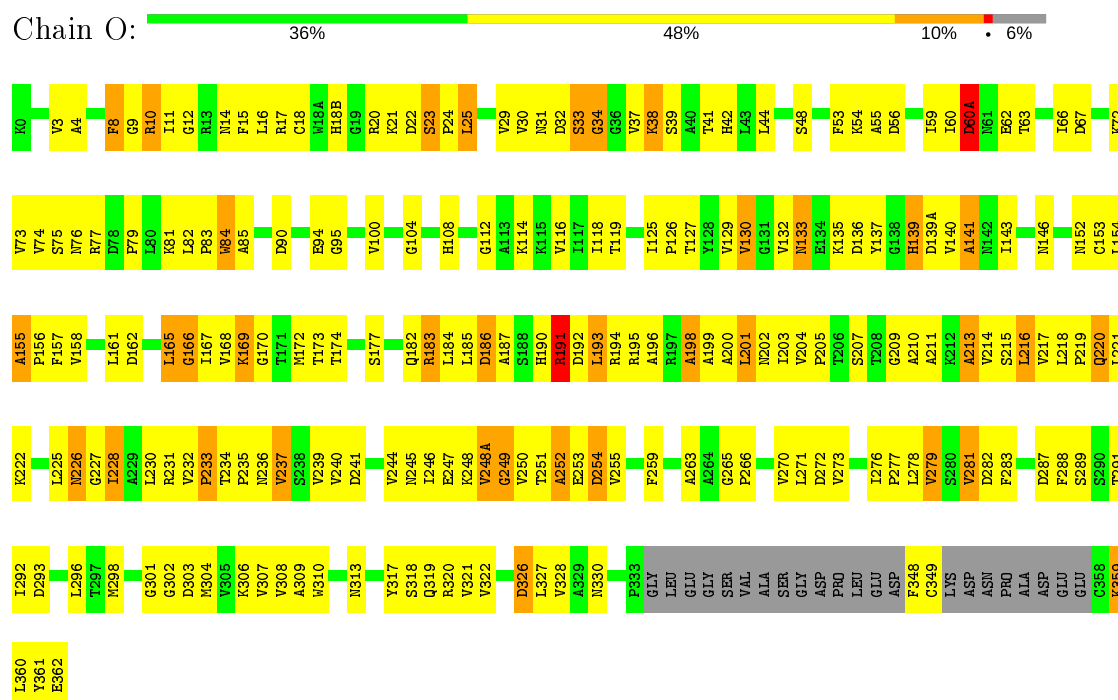


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	O	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
4	P	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
4	Q	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
4	R	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
4	S	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
4	T	1	Total	C	N	O	P	0	0
			48	21	7	17	3		

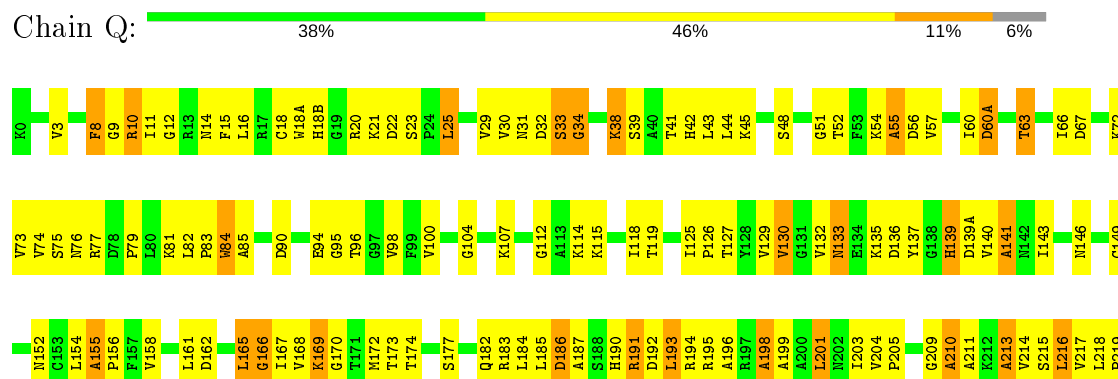
3 Residue-property plots

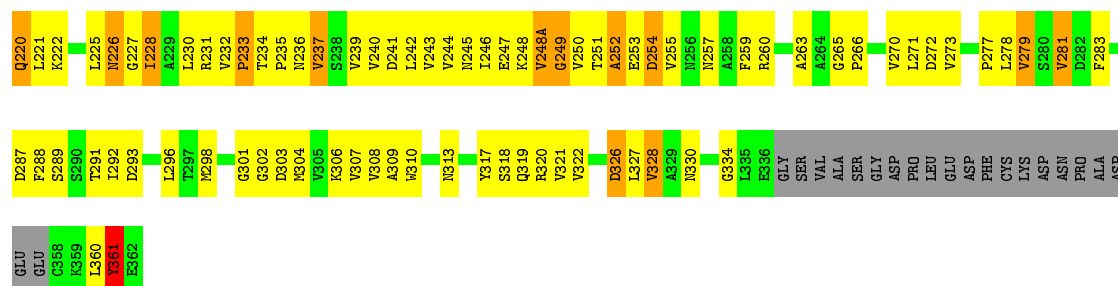
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are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

- Molecule 1: Glyceraldehyde-3-phosphate dehydrogenase B

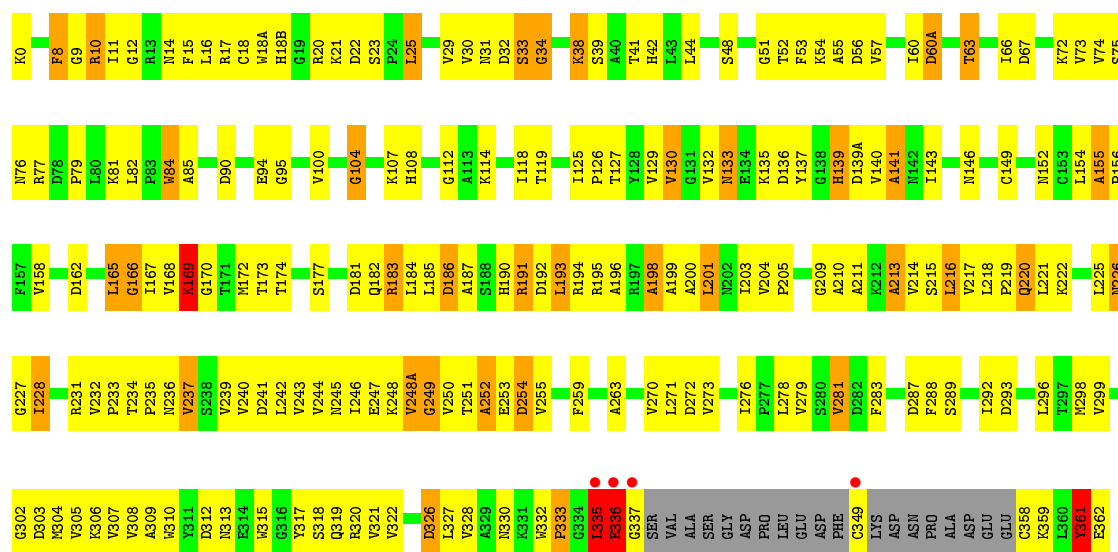


- Molecule 1: Glyceraldehyde-3-phosphate dehydrogenase B

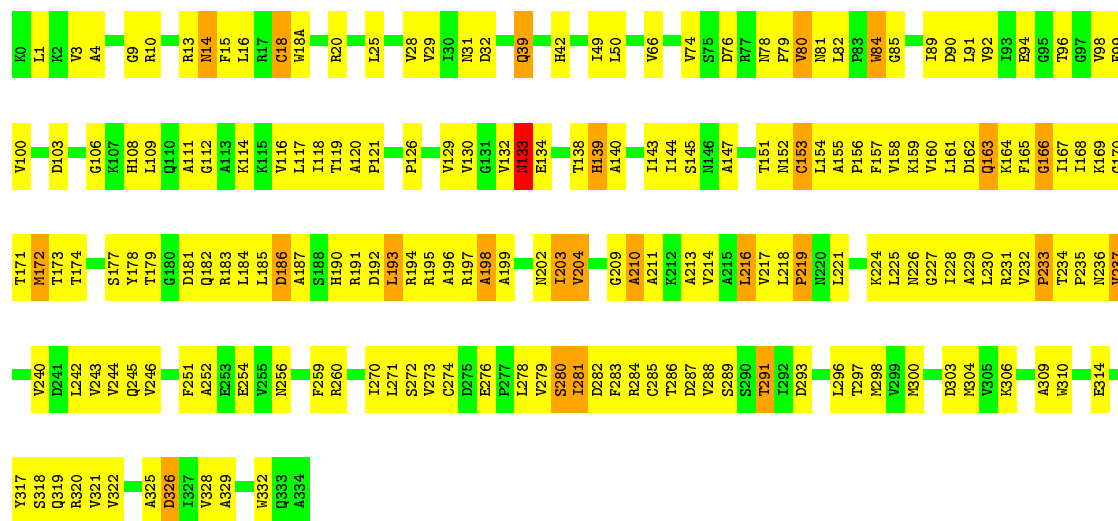




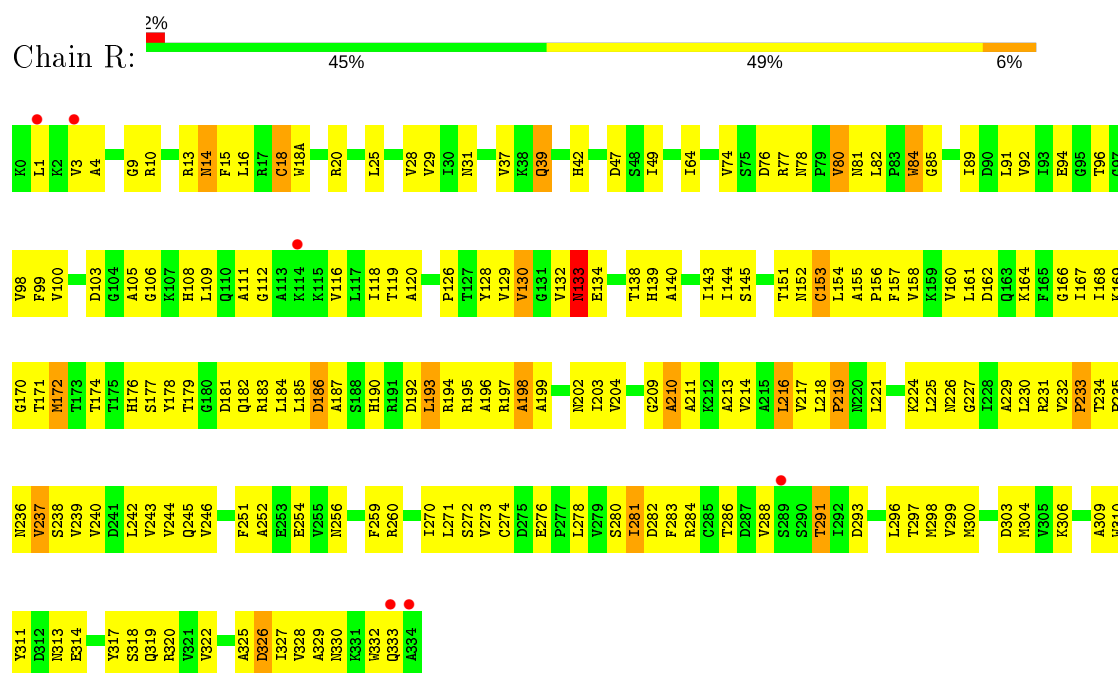
- Molecule 1: Glyceraldehyde-3-phosphate dehydrogenase B



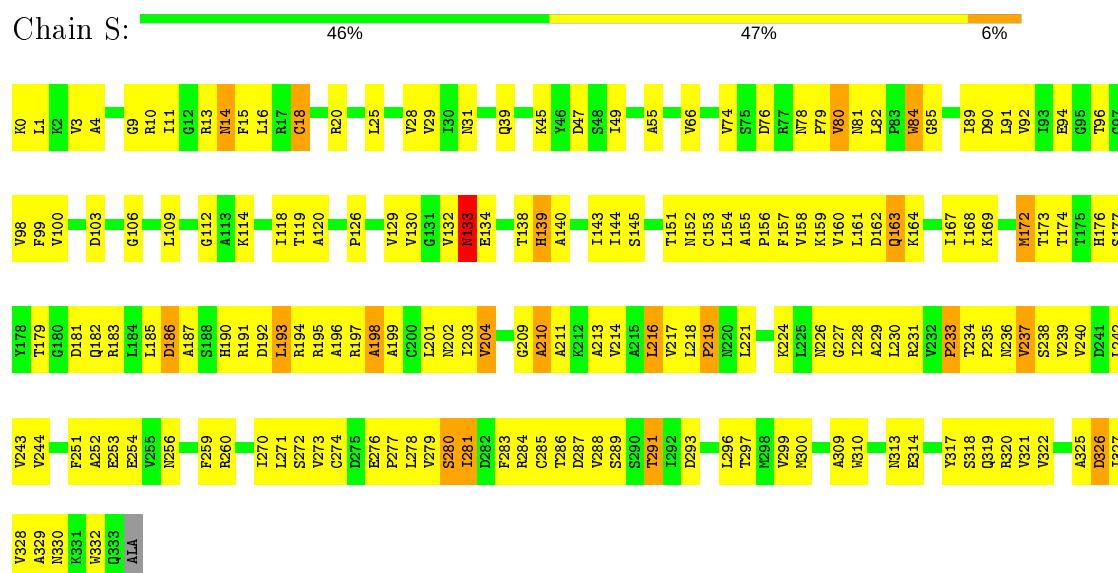
- Molecule 2: Glyceraldehyde-3-phosphate dehydrogenase A



- Molecule 2: Glyceraldehyde-3-phosphate dehydrogenase A



• Molecule 2: Glyceraldehyde-3-phosphate dehydrogenase A



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	186.15Å 215.69Å 81.47Å 90.00° 102.52° 90.00°	Depositor
Resolution (Å)	90.86 – 3.60 90.86 – 3.50	Depositor EDS
% Data completeness (in resolution range)	99.9 (90.86-3.60) 99.7 (90.86-3.50)	Depositor EDS
R_{merge}	0.36	Depositor
R_{sym}	0.36	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.52 (at 3.49Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.261 , 0.292 0.247 , 0.277	Depositor DCC
R_{free} test set	1802 reflections (4.58%)	wwPDB-VP
Wilson B-factor (Å ²)	66.2	Xtriage
Anisotropy	0.103	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 55.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.43$, $\langle L^2 \rangle = 0.25$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.86	EDS
Total number of atoms	15840	wwPDB-VP
Average B, all atoms (Å ²)	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.49% 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, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: NDP, SO4

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	O	0.46	0/2656	0.68	1/3605 (0.0%)
1	Q	0.46	0/2660	0.68	2/3612 (0.1%)
1	T	0.44	0/2669	0.67	1/3622 (0.0%)
2	P	0.46	0/2585	0.68	1/3509 (0.0%)
2	R	0.48	0/2585	0.68	1/3509 (0.0%)
2	S	0.48	0/2579	0.68	1/3502 (0.0%)
All	All	0.46	0/15734	0.68	7/21359 (0.0%)

There are no bond length outliers.

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	O	203	ILE	N-CA-C	-6.98	92.16	111.00
2	S	203	ILE	N-CA-C	-6.71	92.87	111.00
1	T	203	ILE	N-CA-C	-6.55	93.31	111.00
2	R	203	ILE	N-CA-C	-6.29	94.03	111.00
1	Q	203	ILE	N-CA-C	-6.26	94.11	111.00
2	P	203	ILE	N-CA-C	-6.25	94.13	111.00
1	Q	334	GLY	N-CA-C	-5.12	100.30	113.10

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	O	2611	0	2666	256	0
1	Q	2615	0	2675	244	0
1	T	2625	0	2680	217	0
2	P	2544	0	2580	189	0
2	R	2544	0	2580	183	0
2	S	2538	0	2575	149	0
3	O	5	0	0	0	0
3	P	10	0	0	0	0
3	Q	15	0	0	0	0
3	R	15	0	0	0	0
3	S	15	0	0	1	0
3	T	15	0	0	1	0
4	O	48	0	26	1	0
4	P	48	0	26	2	0
4	Q	48	0	26	1	0
4	R	48	0	26	1	0
4	S	48	0	26	2	0
4	T	48	0	26	8	0
All	All	15840	0	15912	1163	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 37.

All (1163) 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:T:248:LYS:HG2	1:T:248(A):VAL:HG12	1.37	1.05
1:T:183:ARG:HH22	1:T:362:GLU:HG3	1.19	1.03
2:P:211:ALA:HB1	2:P:226:ASN:HA	1.45	0.98
1:O:193:LEU:H	1:O:193:LEU:HD12	1.29	0.97
2:S:193:LEU:HD12	2:S:193:LEU:H	1.27	0.97
1:O:245:ASN:HD22	1:Q:245:ASN:HD22	1.04	0.97
2:P:193:LEU:HD12	2:P:193:LEU:H	1.28	0.96
2:R:193:LEU:HD12	2:R:193:LEU:H	1.28	0.95
1:O:204:VAL:HG22	1:Q:279:VAL:HG11	1.46	0.95
1:Q:248:LYS:HG2	1:Q:248(A):VAL:HG12	1.45	0.95
1:Q:271:LEU:HD11	1:Q:292:ILE:HD11	1.48	0.95
2:R:211:ALA:HB1	2:R:226:ASN:HA	1.48	0.94
1:T:248(A):VAL:HG13	1:T:249:GLY:H	1.31	0.93
1:O:248:LYS:HG2	1:O:248(A):VAL:HG12	1.47	0.93
1:T:193:LEU:H	1:T:193:LEU:HD12	1.33	0.92
1:T:271:LEU:HD11	1:T:292:ILE:HD11	1.48	0.92

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:228:ILE:H	1:O:228:ILE:HD13	1.35	0.91
1:Q:193:LEU:H	1:Q:193:LEU:HD12	1.32	0.91
2:S:211:ALA:HB1	2:S:226:ASN:HA	1.53	0.91
1:T:168:VAL:HG12	1:T:169:LYS:HG3	1.52	0.90
1:O:191:ARG:HH21	1:O:360:LEU:HD13	1.37	0.88
1:T:228:ILE:H	1:T:228:ILE:HD13	1.37	0.88
1:Q:248(A):VAL:HG13	1:Q:249:GLY:H	1.38	0.88
2:R:129:VAL:HG23	2:R:217:VAL:HG11	1.56	0.87
1:O:168:VAL:HG12	1:O:169:LYS:HG3	1.55	0.87
2:S:129:VAL:HG23	2:S:217:VAL:HG11	1.58	0.86
1:O:248(A):VAL:HG13	1:O:249:GLY:H	1.38	0.86
1:O:279:VAL:HG11	1:Q:204:VAL:HG22	1.58	0.86
1:Q:360:LEU:O	1:Q:361:TYR:HB2	1.73	0.85
1:O:271:LEU:HD11	1:O:292:ILE:HD11	1.58	0.85
1:O:359:LYS:HD3	1:O:360:LEU:H	1.40	0.84
1:Q:228:ILE:H	1:Q:228:ILE:HD13	1.40	0.84
2:S:154:LEU:O	2:S:158:VAL:HG23	1.79	0.83
1:T:190:HIS:HB3	1:T:196:ALA:HB2	1.61	0.83
2:P:202:ASN:ND2	2:R:281:ILE:HB	1.94	0.83
2:P:202:ASN:HD21	2:R:281:ILE:HB	1.44	0.82
2:P:25:LEU:HD21	2:P:326:ASP:HA	1.61	0.82
2:R:25:LEU:HD21	2:R:326:ASP:HA	1.61	0.81
2:S:25:LEU:HD21	2:S:326:ASP:HA	1.62	0.81
2:P:129:VAL:HG23	2:P:217:VAL:HG11	1.61	0.81
2:P:39:GLN:HE22	1:Q:190:HIS:H	1.29	0.81
1:Q:129:VAL:HG23	1:Q:217:VAL:HG11	1.63	0.81
1:Q:168:VAL:HG12	1:Q:169:LYS:HG3	1.62	0.81
1:Q:155:ALA:HB3	1:Q:156:PRO:HD3	1.63	0.80
1:T:248(A):VAL:HG22	1:T:249:GLY:N	1.96	0.80
1:O:249:GLY:HA2	1:O:302:GLY:O	1.82	0.80
1:T:155:ALA:HB3	1:T:156:PRO:HD3	1.63	0.80
2:P:190:HIS:HB3	2:P:196:ALA:HB2	1.64	0.79
1:O:155:ALA:HB3	1:O:156:PRO:HD3	1.64	0.79
1:T:33:SER:HA	1:T:75:SER:OG	1.83	0.78
1:Q:33:SER:HA	1:Q:75:SER:OG	1.83	0.78
1:Q:11:ILE:HD11	1:Q:317:TYR:HD2	1.49	0.78
1:T:251:THR:HG22	1:T:252:ALA:H	1.50	0.78
1:O:245:ASN:HD22	1:Q:245:ASN:ND2	1.82	0.77
1:O:38:LYS:HG3	1:O:39:SER:H	1.49	0.77
2:P:154:LEU:HD13	2:P:240:VAL:HG21	1.66	0.77
1:O:301:GLY:HA3	1:Q:169:LYS:HZ2	1.49	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:190:HIS:HB3	1:O:196:ALA:HB2	1.65	0.77
2:S:190:HIS:HB3	2:S:196:ALA:HB2	1.67	0.77
1:O:251:THR:HG22	1:O:252:ALA:H	1.50	0.76
1:T:335:LEU:CD2	1:T:336:GLU:H	1.98	0.76
1:O:74:VAL:HG12	1:O:75:SER:H	1.50	0.76
2:R:154:LEU:O	2:R:158:VAL:HG23	1.86	0.76
1:Q:165:LEU:HG	1:Q:246:ILE:HG12	1.66	0.76
1:O:245:ASN:ND2	1:Q:245:ASN:HD22	1.82	0.76
2:R:190:HIS:HB3	2:R:196:ALA:HB2	1.67	0.76
1:O:204:VAL:HG22	1:Q:279:VAL:CG1	2.16	0.76
1:O:82:LEU:HD13	1:O:84:TRP:CZ2	2.21	0.75
1:Q:251:THR:HG22	1:Q:252:ALA:H	1.49	0.75
1:T:129:VAL:HG23	1:T:217:VAL:HG11	1.68	0.75
1:T:154:LEU:O	1:T:158:VAL:HG23	1.87	0.75
1:T:183:ARG:HH12	1:T:362:GLU:HB2	1.51	0.75
1:T:74:VAL:HG12	1:T:75:SER:H	1.51	0.75
1:O:169:LYS:HZ2	1:Q:301:GLY:HA3	1.53	0.74
1:T:249:GLY:HA2	1:T:302:GLY:O	1.87	0.74
1:Q:213:ALA:HA	1:Q:216:LEU:HD23	1.69	0.74
1:Q:249:GLY:HA2	1:Q:302:GLY:O	1.87	0.74
1:Q:74:VAL:HG12	1:Q:75:SER:H	1.53	0.74
2:S:198:ALA:HB3	2:S:202:ASN:OD1	1.88	0.74
1:O:165:LEU:HG	1:O:246:ILE:HG12	1.69	0.73
2:P:198:ALA:HB3	2:P:202:ASN:OD1	1.88	0.73
2:P:154:LEU:O	2:P:158:VAL:HG23	1.89	0.73
2:R:126:PRO:HB2	2:R:144:ILE:HG22	1.71	0.72
1:Q:82:LEU:HD13	1:Q:84:TRP:CZ2	2.25	0.72
2:P:153:CYS:O	2:P:156:PRO:HD2	1.88	0.72
2:R:155:ALA:HB3	2:R:156:PRO:HD3	1.71	0.72
1:T:165:LEU:HG	1:T:246:ILE:HG12	1.69	0.72
1:Q:248(A):VAL:HG22	1:Q:249:GLY:N	2.04	0.72
1:Q:245:ASN:HA	1:Q:304:MET:HA	1.70	0.72
1:T:292:ILE:H	1:T:292:ILE:HD12	1.55	0.72
2:S:20:ARG:HH11	2:S:20:ARG:HG3	1.55	0.72
1:Q:154:LEU:O	1:Q:158:VAL:HG23	1.89	0.72
1:O:213:ALA:HA	1:O:216:LEU:HD23	1.69	0.71
1:O:301:GLY:HA3	1:Q:169:LYS:NZ	2.04	0.71
2:R:198:ALA:HB3	2:R:202:ASN:OD1	1.89	0.71
2:R:91:LEU:HD12	2:R:92:VAL:H	1.54	0.71
1:O:250:VAL:HA	1:T:337:GLY:HA3	1.71	0.71
1:T:245:ASN:HA	1:T:304:MET:HA	1.72	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:T:183:ARG:NH2	1:T:362:GLU:HG3	2.00	0.71
1:O:292:ILE:HD12	1:O:292:ILE:H	1.53	0.71
2:P:9:GLY:O	2:P:13:ARG:HG3	1.91	0.71
1:O:292:ILE:HD12	1:O:292:ILE:N	2.06	0.71
1:Q:38:LYS:HG3	1:Q:39:SER:H	1.54	0.71
2:R:82:LEU:HD13	2:R:84:TRP:CZ2	2.26	0.71
1:T:82:LEU:HD13	1:T:84:TRP:CZ2	2.26	0.71
1:Q:190:HIS:HB3	1:Q:196:ALA:HB2	1.73	0.70
2:P:91:LEU:HD12	2:P:92:VAL:H	1.57	0.70
1:O:11:ILE:HD11	1:O:317:TYR:HD2	1.57	0.70
1:O:184:LEU:HD13	2:R:184:LEU:HD13	1.74	0.70
2:R:320:ARG:NE	2:R:320:ARG:HA	2.07	0.70
1:O:192:ASP:HB3	1:O:195:ARG:HD2	1.72	0.70
2:P:320:ARG:HA	2:P:320:ARG:NE	2.06	0.70
1:T:292:ILE:N	1:T:292:ILE:HD12	2.07	0.69
2:S:126:PRO:HB2	2:S:144:ILE:HG22	1.74	0.69
1:Q:292:ILE:HD12	1:Q:292:ILE:H	1.56	0.69
2:S:260:ARG:HG2	2:S:273:VAL:HG21	1.74	0.69
1:O:177:SER:HB3	1:O:234:THR:O	1.92	0.69
1:T:241:ASP:OD1	1:T:306:LYS:HE3	1.91	0.69
1:T:38:LYS:HG3	1:T:39:SER:H	1.58	0.69
1:O:169:LYS:NZ	1:Q:301:GLY:HA3	2.07	0.69
1:T:44:LEU:HD21	1:T:66:ILE:HD11	1.72	0.69
1:O:221:LEU:HD23	1:O:225:LEU:HD11	1.74	0.69
1:O:241:ASP:OD1	1:O:306:LYS:HE3	1.91	0.69
1:O:248(A):VAL:HA	1:T:333:PRO:HB3	1.74	0.69
1:O:245:ASN:HA	1:O:304:MET:HA	1.73	0.69
1:Q:292:ILE:HD12	1:Q:292:ILE:N	2.07	0.69
2:P:229:ALA:O	2:P:230:LEU:HD23	1.92	0.69
1:O:146:ASN:HD22	1:O:321:VAL:HA	1.57	0.69
2:S:182:GLN:HE22	2:S:231:ARG:HB3	1.57	0.69
2:P:126:PRO:HB2	2:P:144:ILE:HG22	1.75	0.69
1:T:30:VAL:HB	1:T:73:VAL:HG22	1.75	0.68
1:Q:221:LEU:HD23	1:Q:225:LEU:HD11	1.75	0.68
2:S:153:CYS:O	2:S:156:PRO:HD2	1.93	0.68
1:O:248(A):VAL:HG22	1:O:249:GLY:N	2.08	0.68
1:T:221:LEU:HD23	1:T:225:LEU:HD11	1.75	0.68
1:O:154:LEU:O	1:O:158:VAL:HG23	1.93	0.68
1:Q:44:LEU:HD21	1:Q:66:ILE:HD11	1.76	0.68
1:O:33:SER:HA	1:O:75:SER:OG	1.94	0.68
2:P:210:ALA:O	2:P:214:VAL:HG23	1.93	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:T:293:ASP:CB	1:T:296:LEU:HD12	2.24	0.68
2:R:229:ALA:O	2:R:230:LEU:HD23	1.94	0.67
1:Q:250:VAL:HB	1:Q:254:ASP:OD2	1.93	0.67
1:T:335:LEU:HD23	1:T:336:GLU:H	1.58	0.67
1:O:74:VAL:HG12	1:O:75:SER:N	2.08	0.67
1:O:226:ASN:OD1	1:Q:298:MET:SD	2.52	0.67
2:R:91:LEU:HD12	2:R:92:VAL:N	2.09	0.67
1:T:250:VAL:HB	1:T:254:ASP:OD2	1.94	0.67
2:P:178:TYR:HE1	1:Q:185:LEU:HD21	1.59	0.67
1:O:193:LEU:CD1	1:O:193:LEU:H	2.06	0.67
2:S:9:GLY:O	2:S:13:ARG:HG3	1.95	0.67
2:P:155:ALA:HB3	2:P:156:PRO:HD3	1.75	0.67
1:Q:177:SER:HB3	1:Q:234:THR:O	1.94	0.67
1:Q:74:VAL:HG12	1:Q:75:SER:N	2.10	0.66
1:Q:146:ASN:HD22	1:Q:321:VAL:HA	1.60	0.66
1:Q:241:ASP:OD1	1:Q:306:LYS:HE3	1.96	0.66
2:S:320:ARG:HA	2:S:320:ARG:NE	2.10	0.66
1:T:74:VAL:HG12	1:T:75:SER:N	2.10	0.66
1:O:228:ILE:HD12	1:Q:306:LYS:HE2	1.77	0.66
2:P:91:LEU:HD12	2:P:92:VAL:N	2.10	0.66
1:Q:48:SER:HA	2:R:281:ILE:HG21	1.78	0.66
1:T:177:SER:HB3	1:T:234:THR:O	1.96	0.66
2:S:251:PHE:CE1	2:S:254:GLU:HB2	2.31	0.66
2:P:251:PHE:CE1	2:P:254:GLU:HB2	2.31	0.65
1:O:228:ILE:H	1:O:228:ILE:CD1	2.10	0.65
2:P:202:ASN:HD22	2:R:281:ILE:H	1.45	0.65
1:T:273:VAL:HG22	1:T:292:ILE:HD13	1.77	0.65
2:R:251:PHE:CE1	2:R:254:GLU:HB2	2.31	0.65
1:T:192:ASP:HB3	1:T:195:ARG:HD2	1.77	0.65
1:O:190:HIS:H	2:R:39:GLN:HE22	1.43	0.65
2:S:91:LEU:HD12	2:S:92:VAL:H	1.62	0.65
1:Q:192:ASP:HB3	1:Q:195:ARG:HD2	1.79	0.65
2:S:154:LEU:HD13	2:S:240:VAL:HG21	1.78	0.65
1:Q:320:ARG:NE	1:Q:320:ARG:HA	2.12	0.65
2:S:10:ARG:O	2:S:14:ASN:HB2	1.97	0.65
1:O:129:VAL:HG23	1:O:217:VAL:HG11	1.78	0.64
1:T:232:VAL:HG23	1:T:234:THR:HG22	1.78	0.64
2:P:242:LEU:HD12	2:P:243:VAL:H	1.60	0.64
2:R:15:PHE:CE1	2:R:322:VAL:HG22	2.31	0.64
2:R:210:ALA:O	2:R:214:VAL:HG23	1.98	0.64
1:Q:182:GLN:HB3	1:Q:199:ALA:HB2	1.80	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Q:225:LEU:O	1:Q:226:ASN:HB2	1.97	0.64
1:Q:293:ASP:CB	1:Q:296:LEU:HD12	2.28	0.64
2:R:154:LEU:HD13	2:R:240:VAL:HG21	1.79	0.64
2:S:133:ASN:HD22	2:S:133:ASN:C	2.01	0.64
2:R:242:LEU:HD12	2:R:243:VAL:H	1.63	0.64
1:T:246:ILE:HG13	1:T:247:GLU:H	1.63	0.64
1:O:100:VAL:HA	1:O:118:ILE:HD13	1.79	0.64
2:R:126:PRO:HD2	2:R:143:ILE:O	1.97	0.64
2:R:181:ASP:CG	2:R:195:ARG:HH11	2.01	0.64
1:O:273:VAL:HG22	1:O:292:ILE:HD13	1.80	0.64
2:P:82:LEU:HD13	2:P:84:TRP:CZ2	2.32	0.64
1:Q:232:VAL:HG23	1:Q:234:THR:HG22	1.78	0.64
2:R:20:ARG:HG3	2:R:20:ARG:HH11	1.62	0.64
2:R:18:CYS:SG	2:R:319:GLN:HG2	2.38	0.64
2:R:260:ARG:HG2	2:R:273:VAL:HG21	1.80	0.64
1:T:213:ALA:HA	1:T:216:LEU:HD23	1.78	0.64
2:P:133:ASN:C	2:P:133:ASN:HD22	2.00	0.64
2:R:182:GLN:HE22	2:R:231:ARG:HB3	1.63	0.64
2:P:177:SER:HB3	2:P:234:THR:O	1.98	0.63
1:T:146:ASN:HD22	1:T:321:VAL:HA	1.62	0.63
2:P:10:ARG:O	2:P:14:ASN:HB2	1.98	0.63
1:O:279:VAL:CG1	1:Q:204:VAL:HG22	2.28	0.63
1:O:194:ARG:NH1	1:Q:278:LEU:O	2.31	0.63
1:T:11:ILE:HD11	1:T:317:TYR:HD2	1.64	0.63
1:T:293:ASP:HB3	1:T:296:LEU:HD12	1.81	0.63
1:O:246:ILE:HG13	1:O:247:GLU:H	1.63	0.63
1:O:193:LEU:N	1:O:193:LEU:HD12	2.10	0.63
2:P:126:PRO:HD2	2:P:143:ILE:O	1.99	0.63
2:S:229:ALA:O	2:S:230:LEU:HD23	1.99	0.63
1:T:246:ILE:HG22	1:T:303:ASP:O	1.99	0.63
1:O:349:CYS:SG	1:O:360:LEU:HG	2.38	0.62
2:P:182:GLN:HE22	2:P:231:ARG:HB3	1.64	0.62
1:O:204:VAL:HB	1:O:231:ARG:HB2	1.80	0.62
2:P:184:LEU:HD13	1:Q:184:LEU:HD13	1.80	0.62
2:P:260:ARG:HG2	2:P:273:VAL:HG21	1.80	0.62
2:R:9:GLY:O	2:R:13:ARG:HG3	1.98	0.62
1:Q:170:GLY:HA3	1:Q:244:VAL:HG12	1.80	0.62
2:R:14:ASN:HB3	2:R:318:SER:OG	1.99	0.62
2:S:91:LEU:HD12	2:S:92:VAL:N	2.14	0.62
1:T:29:VAL:HA	1:T:72:LYS:O	1.99	0.62
2:S:293:ASP:CG	2:S:296:LEU:HD12	2.21	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:T:191:ARG:HB2	1:T:191:ARG:NH1	2.15	0.61
1:O:251:THR:HB	1:O:254:ASP:OD1	2.00	0.61
1:O:250:VAL:HB	1:O:254:ASP:OD2	2.00	0.61
1:O:44:LEU:HD21	1:O:66:ILE:HD11	1.82	0.61
2:P:9:GLY:HA3	4:P:364:NDP:O5B	2.01	0.61
1:T:204:VAL:HB	1:T:231:ARG:HB2	1.83	0.61
1:O:25:LEU:N	1:O:25:LEU:HD22	2.14	0.61
1:O:29:VAL:HA	1:O:72:LYS:O	2.00	0.61
1:O:306:LYS:HE2	1:Q:228:ILE:HD12	1.82	0.61
2:P:168:ILE:HG22	2:P:169:LYS:HG2	1.82	0.61
2:S:82:LEU:HD13	2:S:84:TRP:CZ2	2.36	0.61
1:T:85:ALA:HB2	1:T:112:GLY:HA3	1.82	0.61
1:Q:246:ILE:HG13	1:Q:247:GLU:H	1.65	0.61
2:R:153:CYS:O	2:R:156:PRO:HD2	2.00	0.61
2:S:132:VAL:O	2:S:133:ASN:HB3	2.01	0.61
1:T:225:LEU:O	1:T:226:ASN:HB2	2.00	0.61
2:P:183:ARG:HD2	2:P:187:ALA:HB3	1.83	0.61
1:Q:29:VAL:HA	1:Q:72:LYS:O	2.00	0.61
1:O:191:ARG:NH1	1:O:191:ARG:HB2	2.16	0.61
1:O:48:SER:HA	2:P:281:ILE:HG21	1.83	0.61
1:O:31:ASN:OD1	1:O:75:SER:HA	2.00	0.61
1:Q:100:VAL:HA	1:Q:118:ILE:HD13	1.82	0.61
2:P:281:ILE:HB	2:R:202:ASN:ND2	2.15	0.61
1:T:246:ILE:HG13	1:T:247:GLU:N	2.16	0.61
2:R:120:ALA:O	2:R:145:SER:HB2	2.01	0.60
1:O:146:ASN:ND2	1:O:321:VAL:HA	2.16	0.60
2:P:20:ARG:HH11	2:P:20:ARG:HG3	1.66	0.60
1:O:201:LEU:HD23	1:O:201:LEU:N	2.16	0.60
1:Q:273:VAL:HG22	1:Q:292:ILE:HD13	1.83	0.60
2:S:155:ALA:HB3	2:S:156:PRO:HD3	1.83	0.60
1:T:133:ASN:C	1:T:133:ASN:HD22	2.04	0.60
1:T:251:THR:HG22	1:T:252:ALA:N	2.16	0.60
2:S:18:CYS:SG	2:S:319:GLN:HG2	2.42	0.60
2:S:210:ALA:O	2:S:214:VAL:HG23	2.02	0.60
2:P:181:ASP:CG	2:P:195:ARG:HH11	2.04	0.60
1:Q:293:ASP:HB3	1:Q:296:LEU:HD12	1.84	0.60
1:Q:30:VAL:HB	1:Q:73:VAL:HG22	1.84	0.60
2:R:183:ARG:HD2	2:R:187:ALA:HB3	1.84	0.60
1:Q:246:ILE:HG22	1:Q:303:ASP:O	2.00	0.60
2:S:20:ARG:NH1	2:S:20:ARG:HG3	2.14	0.60
1:Q:154:LEU:HG	1:Q:158:VAL:CG2	2.32	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:228:ILE:CD1	1:Q:306:LYS:HE2	2.32	0.59
2:R:177:SER:HB3	2:R:234:THR:O	2.02	0.59
1:Q:31:ASN:OD1	1:Q:75:SER:HA	2.02	0.59
2:R:221:LEU:HA	2:R:224:LYS:HD2	1.84	0.59
2:S:209:GLY:O	2:S:211:ALA:N	2.35	0.59
1:O:185:LEU:HD21	2:R:178:TYR:HE1	1.67	0.59
1:T:358:CYS:SG	1:T:359:LYS:N	2.76	0.59
2:R:256:ASN:HD21	2:R:297:THR:CB	2.16	0.59
1:O:170:GLY:HA3	1:O:244:VAL:HG12	1.85	0.59
1:O:232:VAL:HG23	1:O:234:THR:HG22	1.85	0.59
1:O:30:VAL:HB	1:O:73:VAL:HG22	1.84	0.59
1:Q:129:VAL:CG2	1:Q:217:VAL:HG11	2.31	0.59
1:Q:154:LEU:HG	1:Q:158:VAL:HG21	1.85	0.59
1:Q:85:ALA:HB2	1:Q:112:GLY:HA3	1.84	0.59
1:O:133:ASN:HD22	1:O:133:ASN:C	2.05	0.59
2:P:78:ASN:OD1	2:P:80:VAL:HG22	2.02	0.59
2:R:172:MET:O	2:R:227:GLY:HA3	2.03	0.59
1:T:154:LEU:HG	1:T:158:VAL:CG2	2.33	0.59
1:T:320:ARG:HA	1:T:320:ARG:NE	2.17	0.59
1:Q:25:LEU:N	1:Q:25:LEU:HD22	2.17	0.59
2:R:281:ILE:O	2:R:284:ARG:HG2	2.02	0.59
1:O:177:SER:HA	1:O:234:THR:HG23	1.84	0.59
1:O:236:ASN:O	1:O:237:VAL:HB	2.02	0.59
1:Q:193:LEU:H	1:Q:193:LEU:CD1	2.09	0.59
2:R:10:ARG:O	2:R:14:ASN:HB2	2.02	0.59
1:T:66:ILE:O	1:T:67:ASP:HB2	2.02	0.59
1:Q:191:ARG:HB2	1:Q:191:ARG:NH1	2.18	0.59
2:R:168:ILE:HG22	2:R:169:LYS:HG2	1.85	0.59
2:S:177:SER:HB3	2:S:234:THR:O	2.02	0.59
1:O:225:LEU:O	1:O:226:ASN:HB2	2.02	0.58
1:Q:15:PHE:CE1	1:Q:322:VAL:HG22	2.37	0.58
1:T:248(A):VAL:HG13	1:T:249:GLY:N	2.12	0.58
2:P:218:LEU:HB3	2:P:221:LEU:HD23	1.85	0.58
2:P:221:LEU:HA	2:P:224:LYS:HD2	1.85	0.58
1:Q:184:LEU:O	1:Q:185:LEU:HD23	2.04	0.58
1:Q:191:ARG:HD2	1:Q:361:TYR:CD2	2.37	0.58
1:Q:246:ILE:HG13	1:Q:247:GLU:N	2.18	0.58
1:T:177:SER:HA	1:T:234:THR:HG23	1.86	0.58
1:T:193:LEU:N	1:T:193:LEU:HD12	2.13	0.58
1:O:85:ALA:HB2	1:O:112:GLY:HA3	1.86	0.58
2:S:281:ILE:HG21	1:T:48:SER:HA	1.84	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Q:251:THR:HG22	1:Q:252:ALA:N	2.17	0.58
2:R:78:ASN:OD1	2:R:80:VAL:HG22	2.04	0.58
1:T:154:LEU:HG	1:T:158:VAL:HG21	1.85	0.58
1:Q:204:VAL:HB	1:Q:231:ARG:HB2	1.86	0.58
1:Q:248:LYS:HG2	1:Q:248(A):VAL:N	2.19	0.58
1:T:25:LEU:HD22	1:T:25:LEU:N	2.18	0.58
1:T:31:ASN:OD1	1:T:75:SER:HA	2.03	0.58
1:O:293:ASP:CB	1:O:296:LEU:HD12	2.33	0.58
2:P:293:ASP:CG	2:P:296:LEU:HD12	2.25	0.58
1:Q:165:LEU:HD23	1:Q:246:ILE:HD13	1.86	0.58
2:R:293:ASP:CG	2:R:296:LEU:HD12	2.24	0.58
1:Q:193:LEU:N	1:Q:193:LEU:HD12	2.12	0.58
1:O:246:ILE:HG13	1:O:247:GLU:N	2.18	0.57
2:P:96:THR:OG1	2:P:98:VAL:HG22	2.04	0.57
1:Q:162:ASP:HB2	1:Q:167:ILE:HD12	1.86	0.57
1:Q:25:LEU:HD21	1:Q:326:ASP:HA	1.85	0.57
1:T:84:TRP:HE1	1:T:108:HIS:HD1	1.50	0.57
2:R:133:ASN:HD22	2:R:133:ASN:C	2.07	0.57
1:O:125:ILE:HG23	1:O:143:ILE:O	2.03	0.57
2:P:226:ASN:O	2:R:298:MET:HE1	2.04	0.57
1:T:182:GLN:HB3	1:T:199:ALA:HB2	1.86	0.57
1:O:246:ILE:HG22	1:O:303:ASP:O	2.04	0.57
1:O:251:THR:HG22	1:O:252:ALA:N	2.18	0.57
1:T:218:LEU:HB3	1:T:221:LEU:HD13	1.85	0.57
2:P:171:THR:HB	2:R:306:LYS:HE2	1.87	0.57
2:R:1:LEU:HD22	2:R:329:ALA:HA	1.87	0.57
2:R:84:TRP:HE3	2:R:84:TRP:HA	1.69	0.57
2:P:271:LEU:HG	2:P:272:SER:N	2.19	0.57
1:T:129:VAL:CG2	1:T:217:VAL:HG11	2.34	0.57
1:O:211:ALA:O	1:O:214:VAL:HG23	2.04	0.57
1:O:228:ILE:HG21	1:Q:296:LEU:CD2	2.35	0.57
2:R:251:PHE:CZ	2:R:254:GLU:HB2	2.39	0.57
2:S:168:ILE:HG22	2:S:169:LYS:HG2	1.87	0.57
2:S:139:HIS:HE1	2:S:332:TRP:CE3	2.22	0.57
2:P:256:ASN:HD21	2:P:297:THR:CB	2.16	0.57
1:O:306:LYS:HE2	1:Q:228:ILE:CD1	2.34	0.57
2:R:20:ARG:HG3	2:R:20:ARG:NH1	2.19	0.57
1:O:177:SER:CB	1:O:234:THR:O	2.53	0.56
1:T:168:VAL:HG12	1:T:169:LYS:CG	2.28	0.56
1:T:259:PHE:O	1:T:263:ALA:N	2.38	0.56
1:Q:133:ASN:HD22	1:Q:133:ASN:C	2.09	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:R:132:VAL:O	2:R:133:ASN:HB3	2.04	0.56
1:T:132:VAL:HG12	1:T:133:ASN:N	2.20	0.56
1:O:248:LYS:HG2	1:O:248(A):VAL:N	2.20	0.56
1:O:361:TYR:O	1:O:362:GLU:HB2	2.04	0.56
1:Q:66:ILE:O	1:Q:67:ASP:HB2	2.04	0.56
2:P:84:TRP:HA	2:P:84:TRP:CE3	2.40	0.56
1:O:193:LEU:HD23	2:R:42:HIS:CG	2.39	0.56
2:R:84:TRP:CE3	2:R:84:TRP:HA	2.39	0.56
2:S:78:ASN:OD1	2:S:80:VAL:HG22	2.04	0.56
1:O:182:GLN:HB3	1:O:199:ALA:HB2	1.86	0.56
1:O:232:VAL:O	1:O:234:THR:HG22	2.06	0.56
1:O:154:LEU:HG	1:O:158:VAL:HG21	1.88	0.56
2:P:134:GLU:N	2:P:134:GLU:OE1	2.33	0.56
1:Q:139:HIS:O	1:Q:139(A):ASP:HB2	2.05	0.56
2:P:225:LEU:C	2:R:300:MET:HE1	2.26	0.56
2:P:156:PRO:O	2:P:160:VAL:HG23	2.06	0.56
2:P:182:GLN:OE1	2:P:231:ARG:HD2	2.06	0.56
1:Q:170:GLY:HA3	1:Q:244:VAL:HA	1.86	0.56
1:Q:165:LEU:C	1:Q:246:ILE:HD11	2.26	0.56
1:T:228:ILE:CD1	1:T:228:ILE:H	2.15	0.56
1:O:170:GLY:HA3	1:O:244:VAL:HA	1.87	0.56
1:O:348:PHE:CE1	1:O:359:LYS:HE3	2.41	0.56
1:O:162:ASP:HB2	1:O:167:ILE:HD12	1.88	0.56
1:O:60:ILE:HB	1:O:63:THR:O	2.06	0.56
2:P:281:ILE:HB	2:R:202:ASN:HD21	1.71	0.56
2:S:18:CYS:HG	2:S:319:GLN:HG2	1.70	0.56
1:T:25:LEU:HD21	1:T:326:ASP:HA	1.86	0.56
2:R:209:GLY:O	2:R:211:ALA:N	2.39	0.55
1:T:251:THR:HB	1:T:254:ASP:OD1	2.06	0.55
1:T:15:PHE:CE1	1:T:322:VAL:HG22	2.41	0.55
1:T:77:ARG:O	1:T:79:PRO:HD3	2.04	0.55
2:P:132:VAL:O	2:P:133:ASN:HB3	2.03	0.55
2:P:228:ILE:CD1	2:R:296:LEU:HD22	2.36	0.55
1:O:293:ASP:HB3	1:O:296:LEU:HD12	1.88	0.55
2:P:251:PHE:CZ	2:P:254:GLU:HB2	2.41	0.55
2:S:84:TRP:CE3	2:S:84:TRP:HA	2.41	0.55
2:S:84:TRP:HE3	2:S:84:TRP:HA	1.72	0.55
2:P:120:ALA:O	2:P:145:SER:HB2	2.05	0.55
1:T:60:ILE:HB	1:T:63:THR:O	2.06	0.55
1:T:170:GLY:HA3	1:T:244:VAL:HA	1.89	0.55
1:O:165:LEU:C	1:O:246:ILE:HD11	2.27	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:P:84:TRP:HA	2:P:84:TRP:HE3	1.72	0.55
1:Q:174:THR:O	1:Q:174:THR:HG23	2.07	0.55
1:Q:251:THR:HB	1:Q:254:ASP:OD1	2.07	0.55
1:T:236:ASN:O	1:T:237:VAL:HB	2.07	0.55
1:Q:177:SER:HA	1:Q:234:THR:HG23	1.88	0.55
2:R:49:ILE:HD11	2:R:235:PRO:HB2	1.89	0.55
2:S:193:LEU:H	2:S:193:LEU:CD1	2.05	0.55
1:O:168:VAL:HG12	1:O:169:LYS:CG	2.32	0.55
2:P:139:HIS:HE1	2:P:332:TRP:CE3	2.25	0.55
2:R:156:PRO:O	2:R:160:VAL:HG23	2.06	0.55
1:O:66:ILE:O	1:O:67:ASP:HB2	2.05	0.55
2:R:256:ASN:ND2	2:R:297:THR:HG21	2.22	0.55
1:Q:246:ILE:N	1:Q:303:ASP:O	2.39	0.54
2:S:256:ASN:HD21	2:S:297:THR:CB	2.19	0.54
1:T:125:ILE:HG23	1:T:143:ILE:O	2.07	0.54
2:R:25:LEU:HD11	2:R:325:ALA:HB1	1.89	0.54
2:S:120:ALA:O	2:S:145:SER:HB2	2.07	0.54
2:S:133:ASN:ND2	2:S:133:ASN:C	2.61	0.54
2:S:183:ARG:HD2	2:S:187:ALA:HB3	1.89	0.54
1:T:174:THR:O	1:T:174:THR:HG23	2.06	0.54
1:T:165:LEU:C	1:T:246:ILE:HD11	2.28	0.54
1:T:183:ARG:HH12	1:T:362:GLU:CB	2.18	0.54
1:O:174:THR:HG23	1:O:174:THR:O	2.06	0.54
2:P:171:THR:CB	2:R:306:LYS:HE2	2.37	0.54
2:S:281:ILE:O	2:S:284:ARG:HG2	2.07	0.54
1:Q:232:VAL:O	1:Q:234:THR:HG22	2.08	0.54
1:Q:272:ASP:HB2	1:Q:288:PHE:CE2	2.43	0.54
2:S:96:THR:OG1	2:S:98:VAL:HG22	2.08	0.54
1:O:320:ARG:NE	1:O:320:ARG:HA	2.23	0.54
2:P:18:CYS:SG	2:P:319:GLN:HG2	2.48	0.54
1:O:228:ILE:HG21	1:Q:296:LEU:HD22	1.90	0.54
2:S:242:LEU:HD12	2:S:243:VAL:H	1.72	0.54
1:T:100:VAL:HA	1:T:118:ILE:HD13	1.90	0.54
1:T:248:LYS:HG2	1:T:248(A):VAL:N	2.22	0.54
1:O:233:PRO:HB2	1:Q:233:PRO:HB2	1.90	0.54
2:P:20:ARG:NH1	2:P:20:ARG:HG3	2.23	0.54
1:Q:232:VAL:O	1:Q:234:THR:N	2.41	0.54
1:Q:236:ASN:O	1:Q:237:VAL:HB	2.07	0.54
2:S:172:MET:O	2:S:227:GLY:HA3	2.08	0.54
1:T:201:LEU:N	1:T:201:LEU:HD23	2.23	0.54
1:Q:228:ILE:N	1:Q:228:ILE:HD13	2.17	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Q:146:ASN:ND2	1:Q:321:VAL:HA	2.23	0.54
1:T:246:ILE:N	1:T:303:ASP:O	2.41	0.54
1:T:191:ARG:HD2	1:T:361:TYR:CD2	2.43	0.54
1:O:25:LEU:CD2	1:O:25:LEU:N	2.71	0.53
1:O:209:GLY:O	1:O:211:ALA:N	2.41	0.53
1:O:60:ILE:HG22	1:O:60(A):ASP:N	2.23	0.53
1:T:170:GLY:HA3	1:T:244:VAL:HG12	1.90	0.53
1:T:146:ASN:ND2	1:T:321:VAL:HA	2.22	0.53
2:P:281:ILE:O	2:P:284:ARG:HG2	2.09	0.53
2:P:28:VAL:HG23	2:P:29:VAL:HG12	1.90	0.53
2:P:80:VAL:HG23	2:P:81:ASN:OD1	2.08	0.53
2:R:286:THR:HG22	2:R:288:VAL:HG22	1.90	0.53
1:Q:218:LEU:HB3	1:Q:221:LEU:HD13	1.91	0.53
2:S:9:GLY:HA3	4:S:367:NDP:O5B	2.09	0.53
1:T:193:LEU:H	1:T:193:LEU:CD1	2.10	0.53
1:O:272:ASP:HB2	1:O:288:PHE:CE2	2.44	0.53
1:Q:18:CYS:O	1:Q:20:ARG:HG2	2.09	0.53
2:R:80:VAL:HG23	2:R:81:ASN:OD1	2.08	0.53
2:S:286:THR:HG22	2:S:288:VAL:HG22	1.90	0.53
2:S:84:TRP:CE3	2:S:89:ILE:HG13	2.44	0.53
1:T:187:ALA:O	1:T:196:ALA:HB1	2.08	0.53
2:P:42:HIS:CG	1:Q:193:LEU:HD23	2.43	0.53
2:P:94:GLU:OE1	2:P:99:PHE:HB2	2.09	0.53
2:S:251:PHE:CZ	2:S:254:GLU:HB2	2.44	0.53
1:O:259:PHE:O	1:O:263:ALA:N	2.41	0.53
1:T:20:ARG:HH21	1:T:319:GLN:HE22	1.54	0.53
2:P:31:ASN:OD1	2:P:74:VAL:HG23	2.08	0.53
2:R:157:PHE:HB2	2:R:259:PHE:CE1	2.43	0.53
1:T:149:CYS:HB3	4:T:368:NDP:H41N	1.90	0.53
1:O:248:LYS:HG2	1:O:248(A):VAL:H	1.74	0.53
1:O:77:ARG:O	1:O:79:PRO:HD3	2.09	0.53
1:Q:177:SER:CB	1:Q:234:THR:O	2.56	0.53
2:S:221:LEU:HA	2:S:224:LYS:HD2	1.91	0.53
1:T:232:VAL:O	1:T:234:THR:N	2.42	0.53
2:P:172:MET:O	2:P:227:GLY:HA3	2.08	0.53
1:Q:259:PHE:O	1:Q:263:ALA:N	2.41	0.53
2:R:256:ASN:HD21	2:R:297:THR:HG21	1.73	0.53
2:S:126:PRO:HD2	2:S:143:ILE:O	2.08	0.53
1:Q:228:ILE:H	1:Q:228:ILE:CD1	2.18	0.52
2:S:157:PHE:HB2	2:S:259:PHE:CE1	2.44	0.52
1:T:18:CYS:O	1:T:20:ARG:HG2	2.08	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:T:232:VAL:O	1:T:234:THR:HG22	2.09	0.52
1:O:18:CYS:O	1:O:20:ARG:HG2	2.09	0.52
2:P:286:THR:HG22	2:P:288:VAL:HG22	1.91	0.52
2:P:18:CYS:HG	2:P:319:GLN:HG2	1.74	0.52
1:Q:248:LYS:HG2	1:Q:248(A):VAL:H	1.74	0.52
2:R:128:TYR:HA	2:R:133:ASN:HD21	1.74	0.52
2:R:14:ASN:ND2	2:R:314:GLU:HB3	2.24	0.52
1:O:25:LEU:HD21	1:O:326:ASP:HA	1.91	0.52
2:P:14:ASN:HB3	2:P:318:SER:OG	2.10	0.52
1:T:177:SER:CB	1:T:234:THR:O	2.57	0.52
2:P:170:GLY:HA2	2:R:304:MET:SD	2.50	0.52
1:Q:168:VAL:HG12	1:Q:169:LYS:CG	2.36	0.52
1:Q:225:LEU:O	1:Q:226:ASN:CB	2.57	0.52
2:R:218:LEU:HB3	2:R:221:LEU:HD23	1.92	0.52
2:S:156:PRO:O	2:S:160:VAL:HG23	2.10	0.52
2:S:209:GLY:C	2:S:211:ALA:N	2.63	0.52
2:S:218:LEU:HB3	2:S:221:LEU:HD23	1.92	0.52
2:P:151:THR:OG1	2:P:210:ALA:HA	2.10	0.52
1:Q:154:LEU:C	1:Q:158:VAL:HG23	2.30	0.52
1:Q:209:GLY:O	1:Q:211:ALA:N	2.42	0.52
2:S:253:GLU:OE1	3:S:380:SO4:S	2.68	0.52
2:P:133:ASN:C	2:P:133:ASN:ND2	2.62	0.52
2:P:245:GLN:OE1	2:R:245:GLN:OE1	2.27	0.52
1:O:165:LEU:HD23	1:O:246:ILE:HD13	1.91	0.52
2:R:28:VAL:HG23	2:R:29:VAL:HG12	1.91	0.52
2:R:18:CYS:HG	2:R:319:GLN:HG2	1.74	0.52
2:S:192:ASP:O	2:S:194:ARG:N	2.43	0.52
1:O:20:ARG:HH21	1:O:319:GLN:HE22	1.58	0.52
1:O:15:PHE:CE1	1:O:322:VAL:HG22	2.45	0.52
2:P:202:ASN:HD21	2:R:281:ILE:CB	2.19	0.52
1:Q:192:ASP:O	1:Q:194:ARG:N	2.43	0.52
1:O:54:LYS:O	1:O:55:ALA:HB2	2.09	0.52
2:S:94:GLU:OE1	2:S:99:PHE:HB2	2.10	0.52
1:T:11:ILE:CG2	1:T:12:GLY:N	2.72	0.52
1:T:162:ASP:HB2	1:T:167:ILE:HD12	1.92	0.52
1:O:232:VAL:O	1:O:234:THR:N	2.43	0.52
1:O:79:PRO:HA	1:O:82:LEU:HG	1.90	0.52
2:S:134:GLU:OE1	2:S:134:GLU:N	2.33	0.52
1:O:139:HIS:O	1:O:139(A):ASP:HB2	2.10	0.51
1:O:246:ILE:N	1:O:303:ASP:O	2.43	0.51
2:P:167:ILE:HG23	2:P:244:VAL:HB	1.91	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:T:60:ILE:HG22	1:T:60(A):ASP:N	2.25	0.51
2:P:306:LYS:HE2	2:R:171:THR:HB	1.92	0.51
1:Q:130:VAL:HB	1:Q:320:ARG:HD3	1.92	0.51
2:R:271:LEU:HG	2:R:272:SER:N	2.24	0.51
1:O:154:LEU:HG	1:O:158:VAL:CG2	2.41	0.51
1:T:293:ASP:CG	1:T:296:LEU:HD12	2.30	0.51
1:O:140:VAL:O	1:O:141:ALA:O	2.28	0.51
1:O:194:ARG:NH2	1:Q:277:PRO:HA	2.26	0.51
1:O:298:MET:O	1:O:298:MET:HG3	2.11	0.51
2:R:270:ILE:O	2:R:288:VAL:HB	2.10	0.51
2:S:14:ASN:ND2	2:S:314:GLU:HB3	2.24	0.51
2:S:80:VAL:HG23	2:S:81:ASN:OD1	2.11	0.51
2:R:213:ALA:O	2:R:216:LEU:HB2	2.11	0.51
2:R:84:TRP:CE3	2:R:89:ILE:HG13	2.46	0.51
1:T:139:HIS:O	1:T:139(A):ASP:HB2	2.10	0.51
1:T:154:LEU:C	1:T:158:VAL:HG23	2.30	0.51
1:O:191:ARG:HH11	1:O:191:ARG:HB2	1.75	0.51
2:R:25:LEU:HD21	2:R:326:ASP:CA	2.38	0.51
1:T:104:GLY:O	1:T:107:LYS:HG3	2.10	0.51
1:T:272:ASP:HB2	1:T:288:PHE:CE2	2.46	0.51
2:S:161:LEU:HD13	2:S:244:VAL:HG21	1.92	0.51
1:Q:60:ILE:HB	1:Q:63:THR:O	2.11	0.51
1:O:218:LEU:HB3	1:O:221:LEU:HD13	1.92	0.51
1:O:228:ILE:N	1:O:228:ILE:HD13	2.13	0.51
1:O:283:PHE:CE2	1:O:310:TRP:CG	2.99	0.51
1:Q:25:LEU:CD2	1:Q:25:LEU:N	2.74	0.51
1:Q:77:ARG:O	1:Q:79:PRO:HD3	2.11	0.51
2:P:209:GLY:O	2:P:211:ALA:N	2.44	0.50
2:P:25:LEU:HD11	2:P:325:ALA:HB1	1.92	0.50
2:P:283:PHE:CE2	2:P:310:TRP:CD1	3.00	0.50
2:S:204:VAL:HB	2:S:231:ARG:HB2	1.92	0.50
2:S:271:LEU:HG	2:S:272:SER:N	2.27	0.50
2:S:28:VAL:HG23	2:S:29:VAL:HG12	1.93	0.50
1:T:191:ARG:HB2	1:T:191:ARG:HH11	1.75	0.50
1:O:12:GLY:O	1:O:15:PHE:HB3	2.12	0.50
2:P:192:ASP:O	2:P:194:ARG:N	2.43	0.50
2:S:25:LEU:HD21	2:S:326:ASP:CA	2.39	0.50
2:S:98:VAL:HG23	2:S:99:PHE:N	2.26	0.50
1:T:11:ILE:HG23	1:T:12:GLY:N	2.26	0.50
1:Q:248(A):VAL:HG13	1:Q:249:GLY:N	2.19	0.50
1:O:361:TYR:O	1:O:361:TYR:HD1	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:P:213:ALA:O	2:P:216:LEU:HB2	2.12	0.50
1:Q:272:ASP:HB2	1:Q:288:PHE:CD2	2.47	0.50
1:T:234:THR:O	1:T:234:THR:HG23	2.12	0.50
1:O:298:MET:SD	1:Q:226:ASN:OD1	2.70	0.50
1:Q:132:VAL:HG12	1:Q:133:ASN:N	2.27	0.50
2:S:15:PHE:CE1	2:S:322:VAL:HG22	2.46	0.50
1:O:283:PHE:CE2	1:O:310:TRP:CD1	2.99	0.50
1:O:32:ASP:O	1:O:34:GLY:N	2.44	0.50
1:Q:270:VAL:HG13	1:Q:289:SER:HB2	1.94	0.50
2:R:179:THR:OG1	2:R:231:ARG:NH1	2.44	0.50
2:S:185:LEU:O	2:S:186:ASP:C	2.50	0.50
1:O:95:GLY:HA2	1:O:119:THR:OG1	2.11	0.50
2:P:98:VAL:HG23	2:P:99:PHE:N	2.26	0.50
1:Q:84:TRP:HA	1:Q:84:TRP:CE3	2.46	0.50
2:R:139:HIS:HE1	2:R:332:TRP:CE3	2.30	0.50
1:O:168:VAL:HB	1:O:245:ASN:O	2.11	0.50
1:O:219:PRO:HD2	1:O:220:GLN:NE2	2.27	0.50
1:O:318:SER:O	1:O:322:VAL:HG23	2.12	0.50
1:Q:79:PRO:HA	1:Q:82:LEU:HG	1.92	0.50
1:O:272:ASP:HB2	1:O:288:PHE:CD2	2.47	0.49
2:R:192:ASP:O	2:R:194:ARG:N	2.45	0.49
2:P:300:MET:HE1	2:R:225:LEU:C	2.32	0.49
2:S:20:ARG:HE	2:S:319:GLN:HE22	1.60	0.49
1:T:271:LEU:HG	1:T:272:ASP:N	2.27	0.49
1:O:234:THR:HG23	1:O:234:THR:O	2.12	0.49
1:O:25:LEU:CD2	1:O:25:LEU:H	2.23	0.49
1:T:79:PRO:HA	1:T:82:LEU:HG	1.94	0.49
1:O:184:LEU:O	1:O:185:LEU:HD23	2.12	0.49
1:O:348:PHE:N	1:O:360:LEU:HD22	2.27	0.49
2:P:82:LEU:O	2:P:111:ALA:HB1	2.12	0.49
1:Q:12:GLY:O	1:Q:15:PHE:HB3	2.12	0.49
2:R:10:ARG:NH1	2:R:47:ASP:OD2	2.43	0.49
1:T:251:THR:O	1:T:255:VAL:HG23	2.12	0.49
1:O:187:ALA:O	1:O:196:ALA:HB1	2.12	0.49
1:O:359:LYS:CD	1:O:360:LEU:H	2.19	0.49
2:P:84:TRP:CE3	2:P:89:ILE:HG13	2.46	0.49
1:Q:293:ASP:HB3	1:Q:296:LEU:HB2	1.93	0.49
1:T:130:VAL:HB	1:T:320:ARG:HD3	1.95	0.49
1:O:200:ALA:C	1:O:201:LEU:HD23	2.33	0.49
1:O:251:THR:O	1:O:255:VAL:HG23	2.12	0.49
1:Q:140:VAL:O	1:Q:141:ALA:O	2.29	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:R:96:THR:OG1	2:R:98:VAL:HG22	2.12	0.49
2:S:172:MET:HE2	2:S:173:THR:N	2.28	0.49
2:S:139:HIS:CE1	2:S:332:TRP:CE3	3.01	0.49
1:T:54:LYS:O	1:T:55:ALA:HB2	2.12	0.49
2:P:185:LEU:O	2:P:186:ASP:C	2.50	0.49
2:P:228:ILE:HD13	2:R:296:LEU:HD22	1.95	0.49
1:Q:251:THR:O	1:Q:255:VAL:HG23	2.12	0.49
2:S:49:ILE:HD11	2:S:235:PRO:HB2	1.93	0.49
1:Q:54:LYS:O	1:Q:55:ALA:HB2	2.12	0.49
2:R:82:LEU:O	2:R:111:ALA:HB1	2.12	0.49
1:O:173:THR:HG22	1:O:174:THR:N	2.27	0.49
1:O:248(A):VAL:HG13	1:O:249:GLY:N	2.18	0.49
1:Q:165:LEU:HB3	1:Q:246:ILE:HD11	1.94	0.49
1:Q:149:CYS:SG	4:Q:365:NDP:H41N	2.53	0.49
2:S:322:VAL:O	2:S:326:ASP:HB2	2.12	0.49
1:T:9:GLY:O	1:T:11:ILE:N	2.46	0.49
1:O:166:GLY:O	1:O:246:ILE:HD12	2.13	0.49
1:O:252:ALA:O	1:O:254:ASP:N	2.46	0.49
2:P:193:LEU:HD12	2:P:193:LEU:N	2.12	0.49
1:Q:25:LEU:CD2	1:Q:25:LEU:H	2.26	0.49
1:T:129:VAL:O	1:T:130:VAL:C	2.51	0.49
1:O:270:VAL:HG13	1:O:289:SER:HB2	1.95	0.49
2:P:15:PHE:CE1	2:P:322:VAL:HG22	2.47	0.49
2:R:151:THR:OG1	2:R:210:ALA:HA	2.13	0.49
2:R:185:LEU:O	2:R:186:ASP:C	2.51	0.49
1:T:162:ASP:CA	1:T:167:ILE:HG13	2.43	0.49
1:T:25:LEU:CD2	1:T:25:LEU:N	2.75	0.49
2:P:3:VAL:HG12	2:P:4:ALA:N	2.27	0.48
1:T:186:ASP:HA	1:T:196:ALA:O	2.13	0.48
1:T:225:LEU:O	1:T:226:ASN:CB	2.61	0.48
1:O:250:VAL:HA	1:T:337:GLY:CA	2.42	0.48
2:P:270:ILE:O	2:P:288:VAL:HB	2.13	0.48
1:Q:173:THR:HG22	1:Q:174:THR:N	2.26	0.48
2:S:132:VAL:HG12	2:S:132:VAL:O	2.13	0.48
2:S:190:HIS:ND1	2:S:191:ARG:N	2.61	0.48
1:T:318:SER:O	1:T:322:VAL:HG23	2.13	0.48
1:T:95:GLY:HA2	1:T:119:THR:OG1	2.14	0.48
1:O:130:VAL:HB	1:O:320:ARG:HD3	1.94	0.48
1:Q:239:VAL:CG2	1:Q:308:VAL:HG13	2.43	0.48
1:Q:32:ASP:O	1:Q:34:GLY:N	2.45	0.48
2:R:85:GLY:CA	2:R:112:GLY:HA3	2.42	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:R:94:GLU:OE1	2:R:99:PHE:HB2	2.14	0.48
1:T:239:VAL:CG2	1:T:308:VAL:HG13	2.44	0.48
1:O:132:VAL:HG12	1:O:133:ASN:N	2.27	0.48
2:P:193:LEU:CD1	2:P:193:LEU:H	2.06	0.48
1:Q:95:GLY:HA2	1:Q:119:THR:OG1	2.12	0.48
2:R:182:GLN:OE1	2:R:231:ARG:HD2	2.12	0.48
2:R:283:PHE:CE2	2:R:310:TRP:CD1	3.00	0.48
2:R:328:VAL:O	2:R:332:TRP:HB2	2.12	0.48
1:T:252:ALA:O	1:T:254:ASP:N	2.47	0.48
1:T:293:ASP:HB3	1:T:296:LEU:HB2	1.94	0.48
1:O:225:LEU:O	1:O:226:ASN:CB	2.61	0.48
1:O:244:VAL:O	1:O:244:VAL:HG23	2.14	0.48
1:O:307:VAL:HG12	1:O:308:VAL:N	2.29	0.48
2:P:218:LEU:HB3	2:P:221:LEU:CD2	2.44	0.48
2:P:166:GLY:O	2:P:246:VAL:HA	2.14	0.48
1:Q:239:VAL:HB	1:Q:310:TRP:CZ3	2.49	0.48
1:Q:242:LEU:HD11	1:Q:244:VAL:HG13	1.95	0.48
1:Q:20:ARG:HH21	1:Q:319:GLN:HE22	1.62	0.48
1:T:184:LEU:O	1:T:185:LEU:HD23	2.13	0.48
2:P:49:ILE:HD11	2:P:235:PRO:HB2	1.96	0.48
2:S:85:GLY:CA	2:S:112:GLY:HA3	2.43	0.48
2:R:133:ASN:ND2	2:R:133:ASN:C	2.67	0.48
2:S:239:VAL:HB	2:S:310:TRP:CE3	2.49	0.48
2:S:25:LEU:CD2	2:S:326:ASP:HA	2.41	0.48
1:T:149:CYS:HB3	4:T:368:NDP:C4N	2.43	0.48
1:O:186:ASP:HA	1:O:196:ALA:O	2.14	0.48
1:O:165:LEU:HB3	1:O:246:ILE:HD11	1.94	0.48
2:P:14:ASN:OD1	2:P:50:LEU:HD11	2.14	0.48
2:R:158:VAL:HG13	2:R:167:ILE:CD1	2.44	0.48
2:S:270:ILE:O	2:S:288:VAL:HB	2.14	0.48
2:S:79:PRO:O	2:S:81:ASN:N	2.46	0.48
1:O:359:LYS:H	1:O:359:LYS:HD2	1.79	0.47
1:O:191:ARG:CG	1:O:361:TYR:HD2	2.27	0.47
2:S:182:GLN:OE1	2:S:231:ARG:HD2	2.14	0.47
2:S:25:LEU:HD22	2:S:25:LEU:N	2.29	0.47
1:T:228:ILE:N	1:T:228:ILE:HD13	2.16	0.47
1:T:25:LEU:H	1:T:25:LEU:CD2	2.27	0.47
1:Q:240:VAL:CG2	1:Q:309:ALA:HB3	2.44	0.47
1:Q:252:ALA:O	1:Q:254:ASP:N	2.47	0.47
2:S:236:ASN:O	2:S:237:VAL:HB	2.14	0.47
2:S:283:PHE:CE2	2:S:310:TRP:CD1	3.01	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:248(A):VAL:CA	1:T:333:PRO:HB3	2.42	0.47
1:O:235:PRO:O	1:O:236:ASN:HB2	2.14	0.47
1:Q:125:ILE:HG23	1:Q:143:ILE:O	2.14	0.47
1:Q:298:MET:HG3	1:Q:298:MET:O	2.14	0.47
2:R:20:ARG:HE	2:R:319:GLN:HE22	1.63	0.47
1:T:133:ASN:C	1:T:133:ASN:ND2	2.67	0.47
1:T:270:VAL:HG13	1:T:289:SER:HB2	1.96	0.47
1:O:125:ILE:HG23	1:O:143:ILE:HG22	1.95	0.47
2:S:181:ASP:CG	2:S:195:ARG:HH11	2.18	0.47
2:S:25:LEU:HD11	2:S:325:ALA:HB1	1.96	0.47
1:T:20:ARG:HH21	1:T:319:GLN:NE2	2.12	0.47
2:R:100:VAL:HA	2:R:118:ILE:HD13	1.96	0.47
2:S:106:GLY:O	2:S:109:LEU:N	2.47	0.47
2:S:151:THR:OG1	2:S:210:ALA:HA	2.14	0.47
1:Q:168:VAL:HB	1:Q:245:ASN:O	2.15	0.47
2:R:209:GLY:C	2:R:211:ALA:N	2.68	0.47
2:R:31:ASN:OD1	2:R:74:VAL:HG23	2.15	0.47
1:T:211:ALA:O	1:T:214:VAL:HG23	2.15	0.47
1:O:192:ASP:O	1:O:194:ARG:N	2.48	0.47
1:Q:10:ARG:O	1:Q:14:ASN:HB2	2.14	0.47
2:S:272:SER:O	2:S:291:THR:HA	2.14	0.47
2:P:157:PHE:HB2	2:P:259:PHE:CE1	2.50	0.47
2:P:25:LEU:HD22	2:P:25:LEU:N	2.29	0.47
1:Q:226:ASN:OD1	1:Q:227:GLY:N	2.48	0.47
1:Q:271:LEU:HG	1:Q:272:ASP:N	2.29	0.47
2:S:179:THR:OG1	2:S:231:ARG:NH1	2.47	0.47
1:T:140:VAL:O	1:T:141:ALA:O	2.32	0.47
1:T:154:LEU:O	1:T:155:ALA:C	2.53	0.47
1:T:12:GLY:O	1:T:15:PHE:HB3	2.14	0.47
1:T:271:LEU:HG	1:T:272:ASP:H	1.80	0.47
1:O:11:ILE:HG23	1:O:12:GLY:N	2.29	0.47
1:O:129:VAL:O	1:O:130:VAL:C	2.52	0.47
1:O:135:LYS:O	1:O:137:TYR:N	2.48	0.47
1:O:183:ARG:HG2	1:O:187:ALA:HB3	1.97	0.47
1:O:9:GLY:O	1:O:11:ILE:N	2.48	0.47
1:Q:327:LEU:O	1:Q:330:ASN:N	2.48	0.47
2:R:129:VAL:HB	2:R:132:VAL:HB	1.96	0.47
1:T:312:ASP:OD1	1:T:315:TRP:N	2.48	0.47
1:T:14:ASN:HB3	1:T:318:SER:OG	2.14	0.47
1:O:293:ASP:HB3	1:O:296:LEU:HB2	1.96	0.47
2:P:129:VAL:H	2:P:133:ASN:HD21	1.63	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:P:179:THR:OG1	2:P:231:ARG:NH1	2.47	0.47
1:Q:11:ILE:CG2	1:Q:12:GLY:N	2.77	0.47
1:Q:14:ASN:HB3	1:Q:318:SER:OG	2.15	0.47
2:P:161:LEU:HD13	2:P:244:VAL:HG21	1.97	0.46
2:P:256:ASN:ND2	2:P:297:THR:HG21	2.31	0.46
1:Q:129:VAL:O	1:Q:130:VAL:C	2.52	0.46
1:Q:165:LEU:CG	1:Q:246:ILE:HG12	2.43	0.46
1:Q:240:VAL:O	1:Q:308:VAL:HA	2.14	0.46
1:Q:307:VAL:HG12	1:Q:308:VAL:N	2.31	0.46
2:R:272:SER:O	2:R:291:THR:HA	2.15	0.46
1:T:135:LYS:O	1:T:137:TYR:N	2.48	0.46
1:T:84:TRP:CE3	1:T:84:TRP:HA	2.49	0.46
2:P:120:ALA:HB1	2:P:121:PRO:CD	2.46	0.46
2:P:202:ASN:HD22	2:R:281:ILE:N	2.11	0.46
2:P:273:VAL:HG12	2:P:274:CYS:N	2.28	0.46
2:R:16:LEU:O	2:R:16:LEU:HD23	2.15	0.46
2:S:16:LEU:O	2:S:16:LEU:HD23	2.14	0.46
1:T:166:GLY:O	1:T:246:ILE:HD12	2.15	0.46
1:O:226:ASN:OD1	1:O:227:GLY:N	2.48	0.46
2:P:158:VAL:HG13	2:P:167:ILE:CD1	2.46	0.46
2:P:16:LEU:O	2:P:16:LEU:HD23	2.15	0.46
2:P:79:PRO:O	2:P:81:ASN:N	2.48	0.46
1:Q:191:ARG:HB2	1:Q:191:ARG:HH11	1.80	0.46
2:R:240:VAL:CG1	2:R:309:ALA:HB3	2.45	0.46
1:T:32:ASP:O	1:T:34:GLY:N	2.44	0.46
1:Q:283:PHE:CE2	1:Q:310:TRP:CG	3.04	0.46
1:Q:318:SER:O	1:Q:322:VAL:HG23	2.15	0.46
2:S:138:THR:O	2:S:140:ALA:N	2.48	0.46
2:S:193:LEU:N	2:S:193:LEU:HD12	2.12	0.46
1:T:191:ARG:HD2	1:T:361:TYR:CE2	2.51	0.46
1:T:220:GLN:CD	1:T:220:GLN:H	2.19	0.46
1:O:11:ILE:CG2	1:O:12:GLY:N	2.78	0.46
1:O:23:SER:HA	1:O:24:PRO:HD3	1.82	0.46
1:O:74:VAL:CG1	1:O:75:SER:N	2.78	0.46
1:O:90:ASP:HA	1:O:114:LYS:CG	2.45	0.46
2:P:210:ALA:HA	2:P:213:ALA:HB3	1.98	0.46
2:P:271:LEU:HG	2:P:272:SER:H	1.80	0.46
2:P:39:GLN:HE21	2:P:39:GLN:HB3	1.58	0.46
1:Q:76:ASN:ND2	1:Q:81:LYS:HD2	2.30	0.46
2:R:25:LEU:CD2	2:R:326:ASP:HA	2.39	0.46
1:T:125:ILE:HA	1:T:126:PRO:HD3	1.76	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:T:242:LEU:HD11	1:T:244:VAL:HG13	1.97	0.46
1:T:276:ILE:O	1:T:278:LEU:HG	2.16	0.46
1:O:211:ALA:HB1	1:O:226:ASN:HA	1.98	0.46
1:O:239:VAL:CG2	1:O:308:VAL:HG13	2.46	0.46
1:Q:215:SER:HB3	1:Q:222:LYS:HA	1.98	0.46
2:R:167:ILE:HG23	2:R:244:VAL:HB	1.97	0.46
2:R:276:GLU:O	2:R:278:LEU:HG	2.16	0.46
2:S:289:SER:OG	2:S:320:ARG:HD2	2.15	0.46
2:S:1:LEU:HD22	2:S:329:ALA:HA	1.98	0.46
1:O:236:ASN:O	1:O:237:VAL:CB	2.64	0.46
1:O:82:LEU:HA	1:O:83:PRO:HD3	1.68	0.46
1:Q:60:ILE:HG22	1:Q:60(A):ASP:N	2.31	0.46
2:S:3:VAL:HG12	2:S:4:ALA:N	2.30	0.46
1:T:272:ASP:HB2	1:T:288:PHE:CD2	2.50	0.46
1:O:84:TRP:CE3	1:O:84:TRP:HA	2.50	0.46
2:P:154:LEU:HD21	2:P:172:MET:HG2	1.97	0.46
2:P:169:LYS:HE3	2:R:303:ASP:OD1	2.16	0.46
1:Q:125:ILE:HG23	1:Q:143:ILE:HG22	1.97	0.46
1:T:299:VAL:HG22	1:T:305:VAL:HG22	1.97	0.46
2:P:322:VAL:O	2:P:326:ASP:HB2	2.15	0.46
1:O:204:VAL:HA	1:Q:279:VAL:HG12	1.97	0.46
2:P:280:SER:O	2:P:282:ASP:N	2.49	0.46
1:O:205:PRO:HA	1:O:230:LEU:HD23	1.97	0.45
1:Q:198:ALA:CB	1:Q:201:LEU:HG	2.46	0.45
1:Q:204:VAL:HA	1:Q:205:PRO:HD3	1.77	0.45
1:Q:240:VAL:HG22	1:Q:309:ALA:HB3	1.98	0.45
2:P:202:ASN:ND2	2:R:281:ILE:H	2.14	0.45
2:S:138:THR:C	2:S:140:ALA:H	2.20	0.45
2:S:162:ASP:C	2:S:164:LYS:H	2.18	0.45
1:T:168:VAL:O	1:T:169:LYS:HB3	2.15	0.45
1:T:9:GLY:O	1:T:10:ARG:C	2.54	0.45
2:P:172:MET:HE2	2:P:173:THR:N	2.31	0.45
2:P:20:ARG:HE	2:P:319:GLN:HE22	1.63	0.45
1:Q:11:ILE:HG23	1:Q:12:GLY:N	2.30	0.45
1:T:298:MET:O	1:T:298:MET:HG3	2.16	0.45
1:O:154:LEU:O	1:O:155:ALA:C	2.55	0.45
1:O:198:ALA:CB	1:O:201:LEU:HG	2.46	0.45
1:O:327:LEU:O	1:O:330:ASN:N	2.48	0.45
1:T:307:VAL:HG12	1:T:308:VAL:N	2.32	0.45
1:O:162:ASP:CA	1:O:167:ILE:HG13	2.45	0.45
2:P:106:GLY:O	2:P:109:LEU:N	2.49	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:P:85:GLY:CA	2:P:112:GLY:HA3	2.46	0.45
2:P:317:TYR:O	2:P:320:ARG:HB2	2.16	0.45
2:P:303:ASP:OD1	2:R:169:LYS:HE3	2.17	0.45
1:T:168:VAL:HB	1:T:245:ASN:O	2.17	0.45
1:T:76:ASN:ND2	1:T:81:LYS:HD2	2.31	0.45
1:O:154:LEU:C	1:O:158:VAL:HG23	2.35	0.45
1:O:291:THR:O	1:O:310:TRP:N	2.40	0.45
2:P:165:PHE:O	2:P:246:VAL:HB	2.17	0.45
1:Q:211:ALA:HB1	1:Q:226:ASN:HA	1.99	0.45
1:O:202:ASN:OD1	1:Q:281:VAL:HB	2.17	0.45
1:Q:84:TRP:HA	1:Q:84:TRP:HE3	1.80	0.45
1:Q:9:GLY:O	1:Q:11:ILE:N	2.49	0.45
2:R:98:VAL:HG23	2:R:99:PHE:N	2.31	0.45
2:S:172:MET:HE3	2:S:240:VAL:HG23	1.98	0.45
1:T:9:GLY:C	4:T:368:NDP:O2A	2.55	0.45
1:O:133:ASN:ND2	1:O:133:ASN:C	2.70	0.45
1:Q:271:LEU:HG	1:Q:272:ASP:H	1.82	0.45
1:Q:289:SER:OG	1:Q:320:ARG:HD2	2.17	0.45
2:S:10:ARG:NH1	2:S:47:ASP:OD2	2.46	0.45
1:O:283:PHE:CZ	1:O:310:TRP:CD1	3.04	0.45
1:O:74:VAL:CG1	1:O:75:SER:H	2.27	0.45
2:P:218:LEU:HD23	2:P:218:LEU:HA	1.75	0.45
2:P:139:HIS:CE1	2:P:332:TRP:CE3	3.04	0.45
1:Q:190:HIS:CE1	1:Q:195:ARG:HD2	2.52	0.45
1:Q:55:ALA:O	1:Q:57:VAL:HG23	2.16	0.45
2:R:108:HIS:HB2	2:R:116:VAL:HG21	1.99	0.45
2:R:322:VAL:O	2:R:326:ASP:HB2	2.17	0.45
2:S:328:VAL:O	2:S:332:TRP:HB2	2.16	0.45
1:O:125:ILE:HA	1:O:126:PRO:HD3	1.77	0.45
1:O:76:ASN:ND2	1:O:81:LYS:HD2	2.32	0.45
1:O:9:GLY:O	1:O:10:ARG:C	2.55	0.45
1:Q:104:GLY:O	1:Q:107:LYS:HG3	2.17	0.45
1:Q:135:LYS:O	1:Q:137:TYR:N	2.50	0.45
1:Q:186:ASP:HA	1:Q:196:ALA:O	2.17	0.45
2:R:217:VAL:C	2:R:219:PRO:HD3	2.38	0.45
1:T:173:THR:HG22	1:T:174:THR:N	2.32	0.45
1:T:192:ASP:O	1:T:194:ARG:N	2.49	0.45
1:T:239:VAL:HB	1:T:310:TRP:CZ3	2.51	0.45
1:T:41:THR:O	1:T:42:HIS:C	2.55	0.45
1:O:155:ALA:HB3	1:O:156:PRO:CD	2.43	0.45
1:Q:192:ASP:C	1:Q:194:ARG:H	2.21	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Q:239:VAL:HG23	1:Q:309:ALA:O	2.17	0.45
2:R:77:ARG:HA	4:R:366:NDP:H62A	1.82	0.45
1:T:165:LEU:HB3	1:T:246:ILE:HD11	1.99	0.45
1:O:248(A):VAL:HA	1:T:333:PRO:CB	2.44	0.45
1:O:289:SER:OG	1:O:320:ARG:HD2	2.17	0.45
2:P:328:VAL:O	2:P:332:TRP:HB2	2.17	0.45
1:Q:283:PHE:CE2	1:Q:310:TRP:CD1	3.05	0.45
1:Q:291:THR:O	1:Q:310:TRP:N	2.39	0.45
2:R:256:ASN:HD21	2:R:297:THR:CG2	2.29	0.45
2:S:158:VAL:HG13	2:S:167:ILE:CD1	2.47	0.45
2:S:14:ASN:HB3	2:S:318:SER:OG	2.17	0.45
1:T:10:ARG:HB2	4:T:368:NDP:O2N	2.17	0.45
1:O:20:ARG:HH21	1:O:319:GLN:NE2	2.15	0.44
2:P:16:LEU:O	2:P:18(A):TRP:HB3	2.17	0.44
2:P:174:THR:HG23	2:P:229:ALA:CB	2.48	0.44
2:S:202:ASN:O	2:S:233:PRO:HD3	2.18	0.44
1:Q:3:VAL:HG21	1:Q:25:LEU:HD12	1.99	0.44
2:P:226:ASN:C	2:R:298:MET:HE1	2.38	0.44
2:S:11:ILE:HD11	4:S:367:NDP:H42N	1.98	0.44
1:O:191:ARG:HD2	1:O:361:TYR:CD2	2.52	0.44
2:P:279:VAL:HG23	2:R:202:ASN:ND2	2.33	0.44
1:T:204:VAL:HA	1:T:205:PRO:HD3	1.80	0.44
1:T:209:GLY:O	1:T:211:ALA:N	2.50	0.44
1:T:283:PHE:CE2	1:T:310:TRP:CD1	3.06	0.44
1:O:228:ILE:N	1:O:228:ILE:CD1	2.76	0.44
2:P:14:ASN:ND2	2:P:314:GLU:HB3	2.32	0.44
2:P:1:LEU:HD22	2:P:329:ALA:HA	1.98	0.44
2:P:236:ASN:O	2:P:237:VAL:HB	2.18	0.44
1:Q:154:LEU:HA	1:Q:154:LEU:HD12	1.79	0.44
1:Q:191:ARG:HD2	1:Q:361:TYR:CE2	2.53	0.44
1:Q:187:ALA:O	1:Q:196:ALA:HB1	2.17	0.44
1:T:11:ILE:HG21	4:T:368:NDP:H51N	1.98	0.44
1:O:10:ARG:O	1:O:14:ASN:HB2	2.17	0.44
2:P:228:ILE:HD12	2:R:296:LEU:HD22	2.00	0.44
2:P:25:LEU:CD2	2:P:326:ASP:HA	2.40	0.44
1:Q:90:ASP:HA	1:Q:114:LYS:HG2	1.99	0.44
2:R:134:GLU:OE1	2:R:134:GLU:N	2.38	0.44
2:S:228:ILE:HG13	2:S:229:ALA:N	2.31	0.44
2:S:293:ASP:HB3	2:S:296:LEU:HD12	1.99	0.44
1:T:181:ASP:HB2	1:T:361:TYR:HE1	1.83	0.44
1:T:84:TRP:HE3	1:T:84:TRP:HA	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:239:VAL:HB	1:O:310:TRP:CZ3	2.52	0.44
1:O:276:ILE:O	1:O:278:LEU:HG	2.18	0.44
1:O:348:PHE:N	1:O:360:LEU:CD2	2.81	0.44
2:P:276:GLU:O	2:P:278:LEU:HG	2.17	0.44
2:P:272:SER:O	2:P:291:THR:HA	2.17	0.44
2:R:197:ARG:O	2:R:199:ALA:N	2.51	0.44
1:T:190:HIS:CE1	1:T:195:ARG:HD2	2.53	0.44
2:P:15:PHE:CE1	2:P:321:VAL:HG12	2.53	0.44
2:S:182:GLN:HE22	2:S:231:ARG:CB	2.29	0.44
2:S:197:ARG:O	2:S:199:ALA:N	2.50	0.44
1:T:283:PHE:CE2	1:T:310:TRP:CG	3.06	0.44
1:O:135:LYS:C	1:O:137:TYR:H	2.21	0.44
1:O:221:LEU:O	1:O:222:LYS:C	2.56	0.44
1:Q:154:LEU:O	1:Q:155:ALA:C	2.56	0.44
1:T:55:ALA:O	1:T:57:VAL:HG23	2.17	0.44
2:R:106:GLY:O	2:R:109:LEU:N	2.49	0.44
2:R:193:LEU:CD1	2:R:193:LEU:H	2.06	0.44
1:T:327:LEU:O	1:T:330:ASN:N	2.50	0.44
1:O:220:GLN:CD	1:O:220:GLN:H	2.20	0.43
1:Q:220:GLN:H	1:Q:220:GLN:CD	2.21	0.43
2:R:176:HIS:HA	2:R:238:SER:HB3	2.00	0.43
2:R:161:LEU:HD13	2:R:244:VAL:HG21	1.98	0.43
2:S:100:VAL:HA	2:S:118:ILE:HD13	2.00	0.43
2:S:81:ASN:O	2:S:82:LEU:C	2.57	0.43
1:T:10:ARG:O	1:T:14:ASN:HB2	2.18	0.43
1:O:14:ASN:HB3	1:O:318:SER:OG	2.18	0.43
1:O:361:TYR:O	1:O:361:TYR:CD1	2.71	0.43
2:P:209:GLY:C	2:P:211:ALA:N	2.71	0.43
1:Q:125:ILE:HA	1:Q:126:PRO:HD3	1.75	0.43
1:Q:205:PRO:HA	1:Q:230:LEU:HD23	1.99	0.43
2:P:197:ARG:NH1	2:R:282:ASP:OD2	2.51	0.43
2:S:31:ASN:OD1	2:S:74:VAL:HG23	2.17	0.43
1:T:248:LYS:HG2	1:T:248(A):VAL:H	1.81	0.43
1:O:62:GLU:O	1:O:63:THR:OG1	2.35	0.43
2:P:162:ASP:C	2:P:164:LYS:H	2.21	0.43
2:P:217:VAL:C	2:P:219:PRO:HD3	2.39	0.43
2:P:256:ASN:HD21	2:P:297:THR:HG21	1.83	0.43
2:P:32:ASP:HA	4:P:364:NDP:N3A	2.34	0.43
1:T:165:LEU:HD23	1:T:246:ILE:HD13	2.01	0.43
1:O:168:VAL:O	1:O:169:LYS:HB3	2.18	0.43
1:O:204:VAL:HA	1:O:205:PRO:HD3	1.78	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:265:GLY:HA3	1:O:266:PRO:HD3	1.84	0.43
1:O:289:SER:HG	1:O:320:ARG:HD2	1.83	0.43
1:O:41:THR:O	1:O:42:HIS:C	2.56	0.43
1:Q:257:ASN:HA	1:Q:260:ARG:HD2	2.00	0.43
2:R:273:VAL:HG12	2:R:274:CYS:N	2.33	0.43
2:S:217:VAL:C	2:S:219:PRO:HD3	2.38	0.43
2:S:167:ILE:HG23	2:S:244:VAL:HB	1.99	0.43
2:S:20:ARG:HH12	2:S:322:VAL:HG12	1.82	0.43
1:T:135:LYS:C	1:T:137:TYR:H	2.20	0.43
1:T:149:CYS:SG	4:T:368:NDP:H41N	2.59	0.43
1:T:17:ARG:NE	1:T:53:PHE:CD1	2.87	0.43
1:Q:166:GLY:O	1:Q:246:ILE:HD12	2.18	0.43
2:R:154:LEU:HD21	2:R:172:MET:HG2	2.00	0.43
1:T:235:PRO:O	1:T:236:ASN:HB2	2.17	0.43
1:O:84:TRP:HE3	1:O:84:TRP:HA	1.83	0.43
2:P:228:ILE:HG13	2:P:229:ALA:N	2.34	0.43
2:P:233:PRO:HB2	2:R:233:PRO:HB2	1.99	0.43
2:P:317:TYR:O	2:P:320:ARG:N	2.51	0.43
1:Q:235:PRO:O	1:Q:236:ASN:HB2	2.17	0.43
1:Q:242:LEU:HD12	1:Q:243:VAL:H	1.83	0.43
2:P:306:LYS:HE2	2:R:171:THR:CB	2.48	0.43
2:S:276:GLU:O	2:S:278:LEU:HG	2.19	0.43
2:P:3:VAL:HG21	2:P:25:LEU:HD12	2.01	0.43
1:Q:162:ASP:CA	1:Q:167:ILE:HG13	2.48	0.43
1:Q:248:LYS:CG	1:Q:248(A):VAL:H	2.32	0.43
2:R:181:ASP:CG	2:R:195:ARG:NH1	2.70	0.43
2:R:25:LEU:N	2:R:25:LEU:HD22	2.34	0.43
2:R:18:CYS:SG	2:R:319:GLN:OE1	2.74	0.43
1:T:18(A):TRP:O	1:T:20:ARG:HB2	2.18	0.43
1:T:335:LEU:HD22	1:T:336:GLU:H	1.78	0.43
1:O:165:LEU:CG	1:O:246:ILE:HG12	2.45	0.43
2:P:298:MET:HE1	2:R:226:ASN:O	2.19	0.43
1:T:155:ALA:HB3	1:T:156:PRO:CD	2.42	0.43
1:O:10:ARG:HB2	4:O:363:NDP:O2N	2.19	0.43
1:O:161:LEU:HB2	1:O:167:ILE:HD11	2.00	0.43
1:O:37:VAL:HG11	1:O:59:ILE:HG23	2.00	0.43
2:P:159:LYS:O	2:P:163:GLN:HB3	2.19	0.43
2:P:232:VAL:HA	2:P:233:PRO:HD3	1.90	0.43
2:P:66:VAL:O	2:P:66:VAL:HG12	2.19	0.43
1:Q:191:ARG:HD2	1:Q:361:TYR:HD2	1.80	0.43
2:R:129:VAL:H	2:R:133:ASN:HD21	1.66	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:R:154:LEU:HD12	2:R:157:PHE:CZ	2.54	0.43
2:R:193:LEU:HD12	2:R:193:LEU:N	2.12	0.43
2:R:218:LEU:HB3	2:R:221:LEU:CD2	2.49	0.43
2:R:271:LEU:HG	2:R:272:SER:H	1.84	0.43
2:R:320:ARG:HE	2:R:320:ARG:HA	1.83	0.43
1:T:349:CYS:HB3	1:T:359:LYS:H	1.84	0.43
1:O:348:PHE:CD1	1:O:349:CYS:N	2.82	0.43
1:Q:211:ALA:O	1:Q:214:VAL:HG23	2.18	0.43
1:Q:82:LEU:HA	1:Q:83:PRO:HD3	1.72	0.43
2:R:239:VAL:HB	2:R:310:TRP:CE3	2.54	0.43
2:S:213:ALA:O	2:S:216:LEU:HB2	2.19	0.43
1:O:125:ILE:CG2	1:O:143:ILE:HG22	2.48	0.42
2:P:108:HIS:HB2	2:P:116:VAL:HG21	2.00	0.42
2:P:25:LEU:HD21	2:P:326:ASP:CA	2.39	0.42
2:R:236:ASN:O	2:R:237:VAL:HB	2.18	0.42
2:R:327:ILE:O	2:R:330:ASN:O	2.37	0.42
2:S:218:LEU:HB3	2:S:221:LEU:CD2	2.49	0.42
2:S:284:ARG:O	2:S:285:CYS:C	2.57	0.42
2:P:84:TRP:CE3	2:P:84:TRP:CA	3.02	0.42
1:Q:168:VAL:O	1:Q:169:LYS:HB3	2.18	0.42
2:R:153:CYS:SG	2:R:311:TYR:CD1	3.12	0.42
1:T:8:PHE:CB	1:T:32:ASP:HB2	2.49	0.42
1:O:215:SER:HB3	1:O:222:LYS:HA	2.00	0.42
2:P:221:LEU:N	2:P:221:LEU:HD22	2.34	0.42
2:P:229:ALA:C	2:P:230:LEU:HD23	2.39	0.42
1:Q:293:ASP:CG	1:Q:296:LEU:HD12	2.40	0.42
1:Q:90:ASP:HA	1:Q:114:LYS:CG	2.48	0.42
1:Q:9:GLY:O	1:Q:10:ARG:C	2.57	0.42
2:R:3:VAL:HG12	2:R:4:ALA:N	2.34	0.42
2:R:89:ILE:HG21	2:R:92:VAL:HG23	2.01	0.42
1:T:125:ILE:HG23	1:T:143:ILE:HG22	2.02	0.42
1:T:244:VAL:HG23	1:T:244:VAL:O	2.19	0.42
1:O:90:ASP:HA	1:O:114:LYS:HG2	2.01	0.42
2:P:240:VAL:CG1	2:P:309:ALA:HB3	2.49	0.42
1:Q:221:LEU:O	1:Q:222:LYS:C	2.57	0.42
1:Q:234:THR:HG23	1:Q:234:THR:O	2.19	0.42
2:S:25:LEU:HD23	2:S:326:ASP:OD1	2.19	0.42
1:T:192:ASP:C	1:T:194:ARG:H	2.22	0.42
1:T:215:SER:HB3	1:T:222:LYS:HA	2.01	0.42
1:O:248:LYS:CG	1:O:248(A):VAL:H	2.32	0.42
2:P:138:THR:O	2:P:140:ALA:N	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:P:279:VAL:O	2:P:280:SER:C	2.57	0.42
2:R:162:ASP:C	2:R:164:LYS:H	2.23	0.42
1:O:192:ASP:C	1:O:194:ARG:H	2.23	0.42
2:P:132:VAL:O	2:P:132:VAL:HG12	2.18	0.42
1:Q:265:GLY:HA3	1:Q:266:PRO:HD3	1.84	0.42
1:Q:74:VAL:CG1	1:Q:75:SER:H	2.29	0.42
1:Q:84:TRP:CA	1:Q:84:TRP:CE3	3.03	0.42
2:R:174:THR:HG23	2:R:229:ALA:CB	2.50	0.42
1:T:185:LEU:HD23	1:T:185:LEU:HA	1.85	0.42
1:T:226:ASN:OD1	1:T:227:GLY:N	2.52	0.42
1:T:228:ILE:CD1	1:T:228:ILE:N	2.80	0.42
1:T:33:SER:HA	1:T:75:SER:HG	1.82	0.42
1:T:41:THR:HG21	3:T:383:SO4:O2	2.19	0.42
1:O:240:VAL:O	1:O:308:VAL:HA	2.19	0.42
2:P:289:SER:OG	2:P:320:ARG:HD2	2.19	0.42
1:Q:133:ASN:C	1:Q:133:ASN:ND2	2.72	0.42
1:Q:201:LEU:N	1:Q:201:LEU:HD23	2.35	0.42
2:R:138:THR:C	2:R:140:ALA:H	2.23	0.42
2:R:299:VAL:CG1	2:R:300:MET:N	2.83	0.42
2:R:20:ARG:HH12	2:R:322:VAL:HG12	1.84	0.42
2:R:139:HIS:CE1	2:R:332:TRP:CE3	3.07	0.42
2:S:174:THR:HG23	2:S:229:ALA:CB	2.50	0.42
2:P:138:THR:C	2:P:140:ALA:H	2.23	0.42
2:P:89:ILE:HG21	2:P:92:VAL:HG23	2.02	0.42
2:P:232:VAL:HG11	2:R:232:VAL:HG21	2.02	0.42
2:R:84:TRP:CE3	2:R:84:TRP:CA	3.02	0.42
2:S:293:ASP:CB	2:S:296:LEU:HD12	2.49	0.42
1:T:162:ASP:HA	1:T:167:ILE:HG13	2.01	0.42
1:T:8:PHE:HB2	1:T:32:ASP:HB2	2.02	0.42
1:O:170:GLY:HA2	1:Q:304:MET:SD	2.60	0.42
1:O:215:SER:O	1:O:217:VAL:N	2.52	0.42
1:O:271:LEU:HG	1:O:272:ASP:N	2.34	0.42
1:O:296:LEU:CD2	1:Q:228:ILE:HG21	2.50	0.42
2:S:279:VAL:O	2:S:280:SER:C	2.58	0.42
1:Q:161:LEU:HB2	1:Q:167:ILE:HD11	2.01	0.42
1:Q:219:PRO:HD2	1:Q:220:GLN:NE2	2.35	0.42
2:R:105:ALA:HB2	2:R:118:ILE:HD11	2.02	0.42
2:S:138:THR:C	2:S:140:ALA:N	2.73	0.42
1:T:165:LEU:HD12	1:T:248:LYS:HD3	2.02	0.42
1:O:108:HIS:HB2	1:O:116:VAL:HG21	2.01	0.41
2:P:163:GLN:HG2	2:P:163:GLN:O	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:S:273:VAL:HG12	2:S:274:CYS:N	2.35	0.41
2:S:317:TYR:O	2:S:320:ARG:HB2	2.20	0.41
1:T:90:ASP:HA	1:T:114:LYS:CG	2.50	0.41
1:O:192:ASP:CB	1:O:195:ARG:HD2	2.46	0.41
1:Q:198:ALA:HB3	1:Q:201:LEU:HG	2.01	0.41
1:Q:41:THR:O	1:Q:42:HIS:C	2.58	0.41
2:R:210:ALA:HA	2:R:213:ALA:HB3	2.02	0.41
2:R:221:LEU:HD22	2:R:221:LEU:N	2.34	0.41
2:R:202:ASN:O	2:R:233:PRO:HD3	2.20	0.41
2:S:90:ASP:HA	2:S:114:LYS:HD2	2.02	0.41
1:T:217:VAL:O	1:T:218:LEU:HD12	2.20	0.41
1:O:135:LYS:C	1:O:137:TYR:N	2.74	0.41
1:O:281:VAL:O	1:O:281:VAL:HG12	2.21	0.41
2:P:172:MET:HE3	2:P:240:VAL:HG23	2.02	0.41
2:P:190:HIS:CB	2:P:196:ALA:HB2	2.43	0.41
1:Q:18(A):TRP:O	1:Q:20:ARG:HB2	2.20	0.41
2:R:181:ASP:OD1	2:R:195:ARG:HD3	2.21	0.41
2:R:256:ASN:HD22	2:R:256:ASN:N	2.17	0.41
2:R:39:GLN:HE21	2:R:39:GLN:HB3	1.58	0.41
2:S:45:LYS:NZ	2:S:55:ALA:O	2.49	0.41
1:O:161:LEU:HA	1:O:161:LEU:HD23	1.90	0.41
1:O:239:VAL:HG23	1:O:309:ALA:O	2.20	0.41
2:P:198:ALA:O	2:P:199:ALA:HB3	2.20	0.41
2:P:256:ASN:N	2:P:256:ASN:HD22	2.18	0.41
1:Q:135:LYS:C	1:Q:137:TYR:H	2.22	0.41
1:Q:248:LYS:CG	1:Q:248(A):VAL:N	2.82	0.41
1:Q:8:PHE:HB2	1:Q:32:ASP:HB2	2.02	0.41
1:Q:96:THR:OG1	1:Q:98:VAL:HG23	2.20	0.41
2:S:18:CYS:SG	2:S:319:GLN:OE1	2.78	0.41
2:S:79:PRO:O	2:S:80:VAL:C	2.59	0.41
1:T:11:ILE:CG2	4:T:368:NDP:H51N	2.50	0.41
1:T:200:ALA:C	1:T:201:LEU:HD23	2.40	0.41
1:O:129:VAL:CG2	1:O:217:VAL:HG11	2.45	0.41
1:O:277:PRO:HA	1:Q:194:ARG:NH2	2.35	0.41
2:P:100:VAL:HA	2:P:118:ILE:HD13	2.02	0.41
2:P:190:HIS:ND1	2:P:191:ARG:N	2.68	0.41
2:P:202:ASN:ND2	2:R:281:ILE:CB	2.75	0.41
2:P:90:ASP:HA	2:P:114:LYS:HD2	2.03	0.41
1:Q:283:PHE:CZ	1:Q:310:TRP:CD1	3.08	0.41
1:Q:271:LEU:CD1	1:Q:292:ILE:HD11	2.35	0.41
1:Q:8:PHE:CB	1:Q:32:ASP:HB2	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:R:138:THR:O	2:R:140:ALA:N	2.54	0.41
2:R:242:LEU:HD12	2:R:243:VAL:N	2.32	0.41
2:R:37:VAL:HG13	2:R:64:ILE:CG2	2.50	0.41
2:S:132:VAL:CG1	2:S:132:VAL:O	2.69	0.41
2:S:198:ALA:O	2:S:199:ALA:HB3	2.20	0.41
2:S:327:ILE:O	2:S:330:ASN:O	2.39	0.41
1:O:3:VAL:HG12	1:O:4:ALA:N	2.35	0.41
1:Q:281:VAL:O	1:Q:281:VAL:CG1	2.69	0.41
2:R:129:VAL:O	2:R:130:VAL:C	2.59	0.41
2:S:15:PHE:CE1	2:S:321:VAL:HG12	2.56	0.41
2:S:159:LYS:O	2:S:163:GLN:HB3	2.20	0.41
1:O:198:ALA:HB3	1:O:201:LEU:HG	2.02	0.41
2:P:204:VAL:HB	2:P:231:ARG:HB2	2.01	0.41
2:P:203:ILE:HG12	2:P:232:VAL:HG12	2.03	0.41
1:Q:115:LYS:HE3	1:Q:137:TYR:OH	2.21	0.41
1:Q:43:LEU:HD23	1:Q:43:LEU:HA	1.78	0.41
2:R:218:LEU:HD23	2:R:218:LEU:HA	1.77	0.41
2:R:293:ASP:OD1	2:R:296:LEU:HD12	2.20	0.41
2:R:94:GLU:OE2	2:R:94:GLU:HA	2.21	0.41
2:S:18:CYS:HG	2:S:319:GLN:CG	2.33	0.41
2:S:209:GLY:O	2:S:210:ALA:C	2.59	0.41
2:S:176:HIS:HA	2:S:238:SER:HB3	2.02	0.41
2:S:299:VAL:CG1	2:S:300:MET:N	2.84	0.41
1:T:135:LYS:C	1:T:137:TYR:N	2.73	0.41
1:T:281:VAL:CG1	1:T:281:VAL:O	2.68	0.41
1:T:359:LYS:HE3	1:T:359:LYS:HB2	1.76	0.41
1:O:162:ASP:HA	1:O:167:ILE:HG13	2.02	0.41
1:O:248:LYS:CG	1:O:248(A):VAL:N	2.83	0.41
2:P:29:VAL:HG21	2:P:84:TRP:HZ3	1.85	0.41
1:Q:307:VAL:CG1	1:Q:308:VAL:N	2.84	0.41
2:S:240:VAL:CG1	2:S:309:ALA:HB3	2.50	0.41
1:T:149:CYS:HB3	4:T:368:NDP:C5N	2.51	0.41
1:T:242:LEU:HD12	1:T:243:VAL:H	1.86	0.41
1:O:293:ASP:CG	1:O:296:LEU:HD12	2.42	0.41
2:P:304:MET:SD	2:R:170:GLY:HA2	2.61	0.41
1:Q:170:GLY:CA	1:Q:244:VAL:HG12	2.48	0.41
2:R:29:VAL:HG21	2:R:84:TRP:HZ3	1.86	0.41
1:O:17:ARG:NE	1:O:53:PHE:CD1	2.89	0.41
2:P:182:GLN:HE21	2:P:204:VAL:HG21	1.86	0.41
2:R:172:MET:HE3	2:R:240:VAL:HG23	2.01	0.41
1:T:198:ALA:HB3	1:T:201:LEU:HG	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:T:281:VAL:O	1:T:281:VAL:HG12	2.21	0.41
1:O:154:LEU:HD12	1:O:157:PHE:CE2	2.56	0.41
2:P:161:LEU:HD23	2:P:161:LEU:HA	1.90	0.41
1:Q:281:VAL:O	1:Q:281:VAL:HG12	2.20	0.41
1:Q:45:LYS:O	1:Q:52:THR:HA	2.21	0.41
1:Q:74:VAL:CG1	1:Q:75:SER:N	2.80	0.41
2:R:16:LEU:O	2:R:18(A):TRP:HB3	2.20	0.41
2:S:192:ASP:C	2:S:194:ARG:H	2.25	0.41
2:S:317:TYR:O	2:S:320:ARG:N	2.52	0.41
2:S:66:VAL:O	2:S:66:VAL:HG12	2.20	0.41
1:T:219:PRO:HD2	1:T:220:GLN:NE2	2.36	0.41
2:P:284:ARG:O	2:P:285:CYS:C	2.60	0.40
2:R:182:GLN:HE22	2:R:231:ARG:CB	2.31	0.40
1:O:194:ARG:CZ	1:Q:277:PRO:HA	2.51	0.40
1:O:278:LEU:HB3	1:O:282:ASP:OD2	2.21	0.40
1:O:8:PHE:HB2	1:O:32:ASP:HB2	2.04	0.40
1:Q:209:GLY:C	1:Q:211:ALA:N	2.74	0.40
2:R:166:GLY:O	2:R:246:VAL:HA	2.21	0.40
2:S:198:ALA:HB1	2:S:201:LEU:HG	2.03	0.40
1:T:51:GLY:O	1:T:52:THR:C	2.60	0.40
2:P:138:THR:C	2:P:140:ALA:N	2.75	0.40
2:P:20:ARG:HH12	2:P:322:VAL:HG12	1.86	0.40
1:Q:165:LEU:HD23	1:Q:246:ILE:CD1	2.51	0.40
1:Q:51:GLY:O	1:Q:52:THR:C	2.60	0.40
1:T:332:TRP:HA	1:T:333:PRO:HD3	1.95	0.40
1:O:248(A):VAL:HG11	1:T:336:GLU:O	2.21	0.40
1:O:240:VAL:CG2	1:O:309:ALA:HB3	2.52	0.40
1:Q:31:ASN:HA	1:Q:74:VAL:O	2.21	0.40
2:R:317:TYR:O	2:R:320:ARG:HB2	2.21	0.40
2:S:20:ARG:HH11	2:S:20:ARG:CG	2.27	0.40
2:S:236:ASN:O	2:S:237:VAL:CB	2.70	0.40
1:O:3:VAL:HG21	1:O:25:LEU:HD12	2.04	0.40
2:P:117:LEU:C	2:P:117:LEU:HD23	2.42	0.40
1:Q:209:GLY:O	1:Q:210:ALA:C	2.60	0.40
1:Q:236:ASN:O	1:Q:237:VAL:CB	2.69	0.40
1:Q:327:LEU:O	1:Q:328:VAL:C	2.59	0.40
2:R:185:LEU:O	2:R:187:ALA:N	2.54	0.40
2:S:320:ARG:HA	2:S:320:ARG:HE	1.84	0.40
1:T:248:LYS:CG	1:T:248(A):VAL:N	2.83	0.40
1:T:240:VAL:CG2	1:T:309:ALA:HB3	2.52	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	O	340/368 (92%)	238 (70%)	69 (20%)	33 (10%)	0	8
1	Q	343/368 (93%)	237 (69%)	75 (22%)	31 (9%)	1	9
1	T	344/368 (94%)	237 (69%)	72 (21%)	35 (10%)	0	7
2	P	335/337 (99%)	265 (79%)	51 (15%)	19 (6%)	1	18
2	R	335/337 (99%)	265 (79%)	55 (16%)	15 (4%)	2	23
2	S	334/337 (99%)	265 (79%)	50 (15%)	19 (6%)	1	18
All	All	2031/2115 (96%)	1507 (74%)	372 (18%)	152 (8%)	1	12

All (152) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	O	10	ARG
1	O	141	ALA
1	O	193	LEU
1	O	248(A)	VAL
2	P	133	ASN
2	P	198	ALA
2	P	280	SER
1	Q	10	ARG
1	Q	141	ALA
1	Q	193	LEU
1	Q	248(A)	VAL
1	Q	252	ALA
1	Q	361	TYR
2	R	133	ASN
2	R	198	ALA
2	R	280	SER
2	S	133	ASN
2	S	198	ALA
2	S	280	SER
1	T	10	ARG

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Mol	Chain	Res	Type
1	T	141	ALA
1	T	193	LEU
1	T	248(A)	VAL
1	T	252	ALA
1	T	361	TYR
1	O	18(B)	HIS
1	O	165	LEU
1	O	198	ALA
1	O	210	ALA
1	O	226	ASN
1	O	233	PRO
1	O	252	ALA
1	O	253	GLU
2	P	80	VAL
2	P	186	ASP
2	P	193	LEU
2	P	210	ALA
2	P	281	ILE
1	Q	18(B)	HIS
1	Q	165	LEU
1	Q	198	ALA
1	Q	210	ALA
1	Q	226	ASN
1	Q	233	PRO
1	Q	253	GLU
2	R	186	ASP
2	R	193	LEU
2	R	210	ALA
2	S	80	VAL
2	S	186	ASP
2	S	193	LEU
2	S	210	ALA
2	S	281	ILE
1	T	18(B)	HIS
1	T	165	LEU
1	T	226	ASN
1	T	233	PRO
1	T	253	GLU
1	O	22	ASP
1	O	33	SER
1	O	136	ASP
1	O	213	ALA

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Mol	Chain	Res	Type
1	O	216	LEU
2	P	130	VAL
2	P	233	PRO
2	P	237	VAL
2	P	252	ALA
1	Q	22	ASP
1	Q	136	ASP
1	Q	186	ASP
1	Q	237	VAL
2	R	130	VAL
2	R	233	PRO
2	R	237	VAL
2	R	252	ALA
2	S	130	VAL
2	S	233	PRO
2	S	237	VAL
2	S	252	ALA
2	S	313	ASN
1	T	22	ASP
1	T	33	SER
1	T	136	ASP
1	T	198	ALA
1	T	210	ALA
1	T	213	ALA
1	T	237	VAL
1	T	249	GLY
1	T	335	LEU
1	O	34	GLY
1	O	139	HIS
1	O	237	VAL
1	O	249	GLY
2	P	163	GLN
2	P	287	ASP
1	Q	33	SER
1	Q	38	LYS
1	Q	139	HIS
1	Q	213	ALA
1	Q	249	GLY
2	R	80	VAL
2	R	281	ILE
2	R	313	ASN
2	S	139	HIS

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Mol	Chain	Res	Type
2	S	287	ASP
1	T	38	LYS
1	T	139	HIS
1	T	186	ASP
1	T	216	LEU
1	O	21	LYS
1	O	38	LYS
1	O	60(A)	ASP
1	O	186	ASP
1	O	191	ARG
1	Q	21	LYS
1	Q	34	GLY
2	S	119	THR
2	S	163	GLN
2	S	219	PRO
1	T	21	LYS
1	T	34	GLY
1	T	169	LYS
1	O	207	SER
1	O	281	VAL
2	P	119	THR
2	P	139	HIS
2	P	147	ALA
2	P	219	PRO
1	Q	55	ALA
1	Q	166	GLY
1	Q	216	LEU
2	R	119	THR
2	R	219	PRO
1	T	166	GLY
1	T	336	GLU
1	O	166	GLY
1	Q	328	VAL
1	O	104	GLY
1	O	130	VAL
1	Q	130	VAL
1	T	104	GLY
1	T	130	VAL
1	T	333	PRO
1	O	155	ALA
1	O	328	VAL
2	P	166	GLY

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Mol	Chain	Res	Type
1	Q	155	ALA
1	Q	281	VAL
1	T	281	VAL
1	T	328	VAL
1	T	155	ALA
2	S	277	PRO

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	O	287/304 (94%)	262 (91%)	25 (9%)	10	41
1	Q	287/304 (94%)	262 (91%)	25 (9%)	10	41
1	T	288/304 (95%)	260 (90%)	28 (10%)	8	36
2	P	279/279 (100%)	265 (95%)	14 (5%)	24	59
2	R	279/279 (100%)	264 (95%)	15 (5%)	22	57
2	S	279/279 (100%)	265 (95%)	14 (5%)	24	59
All	All	1699/1749 (97%)	1578 (93%)	121 (7%)	14	48

All (121) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	O	8	PHE
1	O	16	LEU
1	O	23	SER
1	O	25	LEU
1	O	56	ASP
1	O	60(A)	ASP
1	O	84	TRP
1	O	94	GLU
1	O	127	THR
1	O	133	ASN
1	O	152	ASN
1	O	153	CYS

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Mol	Chain	Res	Type
1	O	169	LYS
1	O	172	MET
1	O	183	ARG
1	O	191	ARG
1	O	201	LEU
1	O	220	GLN
1	O	228	ILE
1	O	254	ASP
1	O	279	VAL
1	O	287	ASP
1	O	313	ASN
1	O	326	ASP
1	O	359	LYS
2	P	14	ASN
2	P	18	CYS
2	P	39	GLN
2	P	76	ASP
2	P	84	TRP
2	P	103	ASP
2	P	133	ASN
2	P	152	ASN
2	P	153	CYS
2	P	172	MET
2	P	204	VAL
2	P	216	LEU
2	P	291	THR
2	P	326	ASP
1	Q	8	PHE
1	Q	16	LEU
1	Q	23	SER
1	Q	25	LEU
1	Q	56	ASP
1	Q	60(A)	ASP
1	Q	63	THR
1	Q	84	TRP
1	Q	94	GLU
1	Q	127	THR
1	Q	133	ASN
1	Q	152	ASN
1	Q	169	LYS
1	Q	172	MET
1	Q	183	ARG

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Mol	Chain	Res	Type
1	Q	191	ARG
1	Q	201	LEU
1	Q	220	GLN
1	Q	228	ILE
1	Q	254	ASP
1	Q	279	VAL
1	Q	287	ASP
1	Q	313	ASN
1	Q	326	ASP
1	Q	361	TYR
2	R	14	ASN
2	R	18	CYS
2	R	39	GLN
2	R	76	ASP
2	R	84	TRP
2	R	103	ASP
2	R	133	ASN
2	R	152	ASN
2	R	153	CYS
2	R	172	MET
2	R	204	VAL
2	R	216	LEU
2	R	291	THR
2	R	326	ASP
2	R	333	GLN
2	S	0	LYS
2	S	14	ASN
2	S	18	CYS
2	S	39	GLN
2	S	76	ASP
2	S	84	TRP
2	S	103	ASP
2	S	133	ASN
2	S	152	ASN
2	S	172	MET
2	S	204	VAL
2	S	216	LEU
2	S	291	THR
2	S	326	ASP
1	T	0	LYS
1	T	8	PHE
1	T	16	LEU

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Mol	Chain	Res	Type
1	T	23	SER
1	T	25	LEU
1	T	56	ASP
1	T	60(A)	ASP
1	T	63	THR
1	T	84	TRP
1	T	94	GLU
1	T	127	THR
1	T	133	ASN
1	T	152	ASN
1	T	169	LYS
1	T	172	MET
1	T	183	ARG
1	T	191	ARG
1	T	201	LEU
1	T	220	GLN
1	T	228	ILE
1	T	254	ASP
1	T	279	VAL
1	T	287	ASP
1	T	313	ASN
1	T	326	ASP
1	T	335	LEU
1	T	336	GLU
1	T	361	TYR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (44) such sidechains are listed below:

Mol	Chain	Res	Type
1	O	146	ASN
1	O	220	GLN
1	O	319	GLN
1	O	330	ASN
2	P	39	GLN
2	P	133	ASN
2	P	139	HIS
2	P	152	ASN
2	P	176	HIS
2	P	182	GLN
2	P	202	ASN
2	P	256	ASN
2	P	319	GLN

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Mol	Chain	Res	Type
2	P	333	GLN
1	Q	133	ASN
1	Q	146	ASN
1	Q	220	GLN
1	Q	245	ASN
1	Q	319	GLN
1	Q	330	ASN
2	R	39	GLN
2	R	42	HIS
2	R	133	ASN
2	R	139	HIS
2	R	152	ASN
2	R	182	GLN
2	R	202	ASN
2	R	256	ASN
2	R	319	GLN
2	R	333	GLN
2	S	39	GLN
2	S	133	ASN
2	S	139	HIS
2	S	152	ASN
2	S	182	GLN
2	S	245	GLN
2	S	256	ASN
2	S	319	GLN
1	T	133	ASN
1	T	146	ASN
1	T	220	GLN
1	T	245	ASN
1	T	319	GLN
1	T	330	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

21 ligands 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
3	SO4	Q	382	-	4,4,4	0.28	0	6,6,6	0.07	0
4	NDP	P	364	-	45,52,52	1.56	7 (15%)	53,80,80	1.16	5 (9%)
3	SO4	R	374	-	4,4,4	0.18	0	6,6,6	0.19	0
3	SO4	S	380	-	4,4,4	0.27	0	6,6,6	0.08	0
4	NDP	T	368	-	45,52,52	1.57	7 (15%)	53,80,80	1.16	5 (9%)
4	NDP	S	367	-	45,52,52	1.55	7 (15%)	53,80,80	1.16	6 (11%)
3	SO4	T	378	-	4,4,4	0.21	0	6,6,6	0.12	0
3	SO4	S	376	-	4,4,4	0.21	0	6,6,6	0.19	0
3	SO4	T	383	-	4,4,4	0.31	0	6,6,6	0.21	0
3	SO4	Q	384	-	4,4,4	0.23	0	6,6,6	0.09	0
3	SO4	P	372	-	4,4,4	0.19	0	6,6,6	0.12	0
4	NDP	O	363	-	45,52,52	1.57	7 (15%)	53,80,80	1.16	5 (9%)
3	SO4	T	379	-	4,4,4	0.23	0	6,6,6	0.10	0
3	SO4	S	377	-	4,4,4	0.19	0	6,6,6	0.07	0
3	SO4	P	371	-	4,4,4	0.32	0	6,6,6	0.12	0
3	SO4	R	381	-	4,4,4	0.33	0	6,6,6	0.21	0
3	SO4	R	375	-	4,4,4	0.33	0	6,6,6	0.07	0
4	NDP	R	366	-	45,52,52	1.56	7 (15%)	53,80,80	1.16	5 (9%)
4	NDP	Q	365	-	45,52,52	1.57	7 (15%)	53,80,80	1.16	5 (9%)
3	SO4	O	370	-	4,4,4	0.27	0	6,6,6	0.09	0
3	SO4	Q	373	-	4,4,4	0.33	0	6,6,6	0.16	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
4	NDP	P	364	-	-	6/30/77/77	0/5/5/5
4	NDP	T	368	-	-	8/30/77/77	0/5/5/5
4	NDP	R	366	-	-	7/30/77/77	0/5/5/5
4	NDP	O	363	-	-	8/30/77/77	0/5/5/5
4	NDP	Q	365	-	-	8/30/77/77	0/5/5/5
4	NDP	S	367	-	-	6/30/77/77	0/5/5/5

All (42) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	Q	365	NDP	C4N-C3N	-4.91	1.40	1.49
4	O	363	NDP	C4N-C3N	-4.91	1.40	1.49
4	T	368	NDP	C4N-C3N	-4.90	1.40	1.49
4	R	366	NDP	C4N-C3N	-4.90	1.40	1.49
4	S	367	NDP	C4N-C3N	-4.89	1.40	1.49
4	P	364	NDP	C4N-C3N	-4.89	1.40	1.49
4	O	363	NDP	P2B-O1X	3.61	1.62	1.50
4	T	368	NDP	P2B-O1X	3.60	1.62	1.50
4	R	366	NDP	P2B-O1X	3.59	1.62	1.50
4	Q	365	NDP	P2B-O1X	3.59	1.62	1.50
4	S	367	NDP	P2B-O1X	3.58	1.62	1.50
4	P	364	NDP	P2B-O1X	3.56	1.62	1.50
4	T	368	NDP	C6N-C5N	3.42	1.39	1.33
4	R	366	NDP	C6N-C5N	3.38	1.39	1.33
4	O	363	NDP	C6N-C5N	3.38	1.39	1.33
4	Q	365	NDP	C6N-C5N	3.38	1.39	1.33
4	S	367	NDP	C6N-C5N	3.37	1.39	1.33
4	P	364	NDP	C6N-C5N	3.37	1.39	1.33
4	R	366	NDP	C7N-C3N	3.28	1.55	1.48
4	T	368	NDP	C7N-C3N	3.28	1.55	1.48
4	S	367	NDP	C7N-C3N	3.28	1.55	1.48
4	P	364	NDP	C7N-C3N	3.27	1.55	1.48
4	O	363	NDP	C7N-C3N	3.26	1.55	1.48
4	Q	365	NDP	C7N-C3N	3.24	1.55	1.48
4	T	368	NDP	C4N-C5N	-3.23	1.40	1.48
4	O	363	NDP	C4N-C5N	-3.22	1.40	1.48
4	Q	365	NDP	C4N-C5N	-3.22	1.40	1.48
4	R	366	NDP	C4N-C5N	-3.20	1.40	1.48
4	P	364	NDP	C4N-C5N	-3.19	1.40	1.48
4	S	367	NDP	C4N-C5N	-3.18	1.40	1.48
4	Q	365	NDP	C2N-C3N	2.11	1.40	1.34
4	O	363	NDP	C2N-C3N	2.09	1.40	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	T	368	NDP	C2N-C3N	2.09	1.40	1.34
4	R	366	NDP	C2N-C3N	2.08	1.40	1.34
4	P	364	NDP	C2N-C3N	2.07	1.40	1.34
4	S	367	NDP	C2N-C3N	2.06	1.40	1.34
4	T	368	NDP	C5A-N7A	-2.05	1.32	1.39
4	Q	365	NDP	C5A-N7A	-2.04	1.32	1.39
4	P	364	NDP	C5A-N7A	-2.04	1.32	1.39
4	S	367	NDP	C5A-N7A	-2.03	1.32	1.39
4	O	363	NDP	C5A-N7A	-2.03	1.32	1.39
4	R	366	NDP	C5A-N7A	-2.02	1.32	1.39

All (31) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	Q	365	NDP	C4A-C5A-N7A	3.17	112.71	109.40
4	T	368	NDP	C4A-C5A-N7A	3.15	112.68	109.40
4	O	363	NDP	C4A-C5A-N7A	3.15	112.68	109.40
4	R	366	NDP	C4A-C5A-N7A	3.13	112.67	109.40
4	P	364	NDP	C4A-C5A-N7A	3.13	112.67	109.40
4	S	367	NDP	C4A-C5A-N7A	3.11	112.64	109.40
4	R	366	NDP	N3A-C2A-N1A	-3.08	123.86	128.68
4	S	367	NDP	N3A-C2A-N1A	-3.08	123.86	128.68
4	Q	365	NDP	N3A-C2A-N1A	-3.08	123.87	128.68
4	O	363	NDP	N3A-C2A-N1A	-3.07	123.88	128.68
4	T	368	NDP	N3A-C2A-N1A	-3.07	123.88	128.68
4	P	364	NDP	N3A-C2A-N1A	-3.06	123.89	128.68
4	Q	365	NDP	O4B-C1B-C2B	-3.02	101.35	106.59
4	T	368	NDP	O4B-C1B-C2B	-3.01	101.36	106.59
4	O	363	NDP	O4B-C1B-C2B	-3.01	101.37	106.59
4	P	364	NDP	O4B-C1B-C2B	-2.96	101.45	106.59
4	R	366	NDP	O4B-C1B-C2B	-2.96	101.46	106.59
4	S	367	NDP	O4B-C1B-C2B	-2.94	101.48	106.59
4	T	368	NDP	O3D-C3D-C2D	-2.22	104.63	111.82
4	Q	365	NDP	O3D-C3D-C2D	-2.21	104.68	111.82
4	O	363	NDP	O3D-C3D-C2D	-2.21	104.69	111.82
4	S	367	NDP	O3D-C3D-C2D	-2.18	104.76	111.82
4	S	367	NDP	C1B-N9A-C4A	-2.18	122.81	126.64
4	P	364	NDP	O3D-C3D-C2D	-2.18	104.78	111.82
4	R	366	NDP	C1B-N9A-C4A	-2.16	122.84	126.64
4	R	366	NDP	O3D-C3D-C2D	-2.16	104.84	111.82
4	T	368	NDP	C1B-N9A-C4A	-2.15	122.86	126.64
4	O	363	NDP	C1B-N9A-C4A	-2.15	122.86	126.64

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Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
4	P	364	NDP	C1B-N9A-C4A	-2.14	122.88	126.64
4	Q	365	NDP	C1B-N9A-C4A	-2.13	122.90	126.64
4	S	367	NDP	N6A-C6A-N1A	2.02	122.78	118.57

There are no chirality outliers.

All (43) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	P	364	NDP	C2D-C1D-N1N-C6N
4	S	367	NDP	C2D-C1D-N1N-C6N
4	T	368	NDP	C2D-C1D-N1N-C6N
4	O	363	NDP	C2D-C1D-N1N-C6N
4	R	366	NDP	C2D-C1D-N1N-C6N
4	Q	365	NDP	C2D-C1D-N1N-C6N
4	T	368	NDP	PN-O3-PA-O1A
4	O	363	NDP	PN-O3-PA-O1A
4	Q	365	NDP	PN-O3-PA-O1A
4	P	364	NDP	O4D-C1D-N1N-C6N
4	S	367	NDP	O4D-C1D-N1N-C6N
4	T	368	NDP	O4D-C1D-N1N-C6N
4	O	363	NDP	O4D-C1D-N1N-C6N
4	R	366	NDP	O4D-C1D-N1N-C6N
4	Q	365	NDP	O4D-C1D-N1N-C6N
4	P	364	NDP	C2D-C1D-N1N-C2N
4	S	367	NDP	C2D-C1D-N1N-C2N
4	T	368	NDP	C2D-C1D-N1N-C2N
4	O	363	NDP	C2D-C1D-N1N-C2N
4	R	366	NDP	C2D-C1D-N1N-C2N
4	Q	365	NDP	C2D-C1D-N1N-C2N
4	P	364	NDP	O4D-C1D-N1N-C2N
4	S	367	NDP	O4D-C1D-N1N-C2N
4	T	368	NDP	O4D-C1D-N1N-C2N
4	O	363	NDP	O4D-C1D-N1N-C2N
4	R	366	NDP	O4D-C1D-N1N-C2N
4	Q	365	NDP	O4D-C1D-N1N-C2N
4	T	368	NDP	PN-O3-PA-O2A
4	O	363	NDP	PN-O3-PA-O2A
4	Q	365	NDP	PN-O3-PA-O2A
4	R	366	NDP	C4B-C5B-O5B-PA
4	P	364	NDP	C2N-C3N-C7N-N7N
4	S	367	NDP	C2N-C3N-C7N-N7N
4	T	368	NDP	C2N-C3N-C7N-N7N

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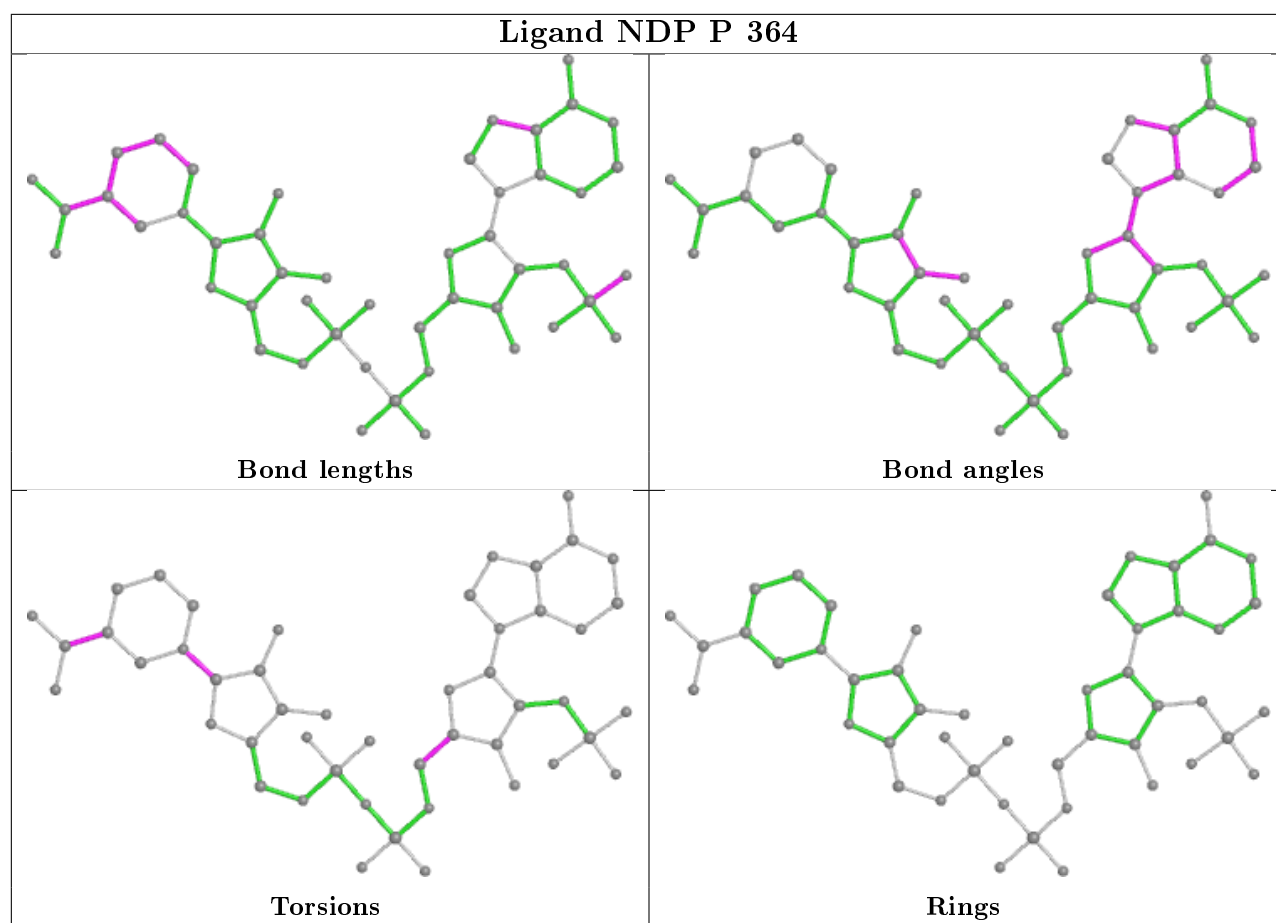
Mol	Chain	Res	Type	Atoms
4	O	363	NDP	C2N-C3N-C7N-N7N
4	R	366	NDP	C2N-C3N-C7N-N7N
4	Q	365	NDP	C2N-C3N-C7N-N7N
4	P	364	NDP	O4B-C4B-C5B-O5B
4	S	367	NDP	O4B-C4B-C5B-O5B
4	T	368	NDP	O4B-C4B-C5B-O5B
4	O	363	NDP	O4B-C4B-C5B-O5B
4	R	366	NDP	O4B-C4B-C5B-O5B
4	Q	365	NDP	O4B-C4B-C5B-O5B

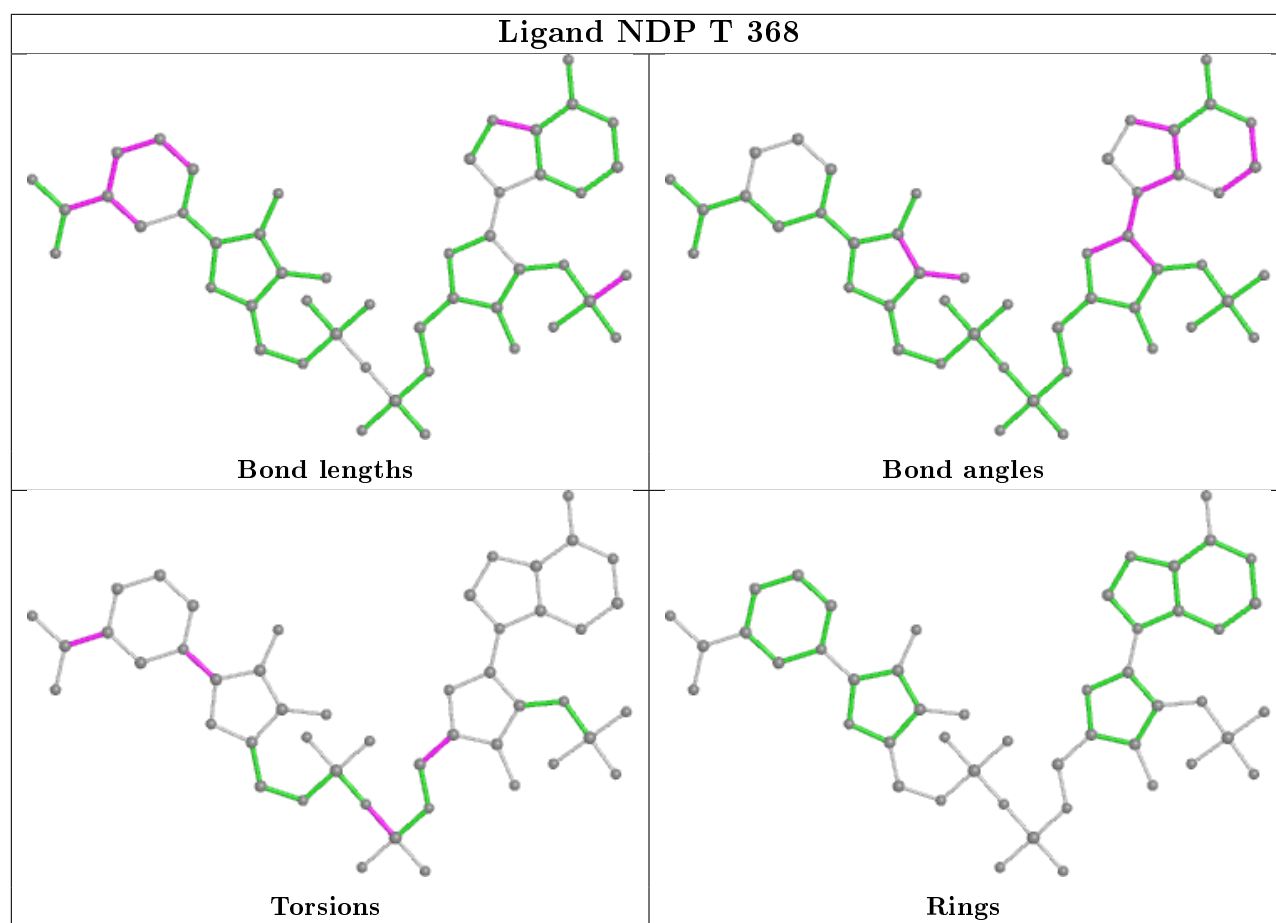
There are no ring outliers.

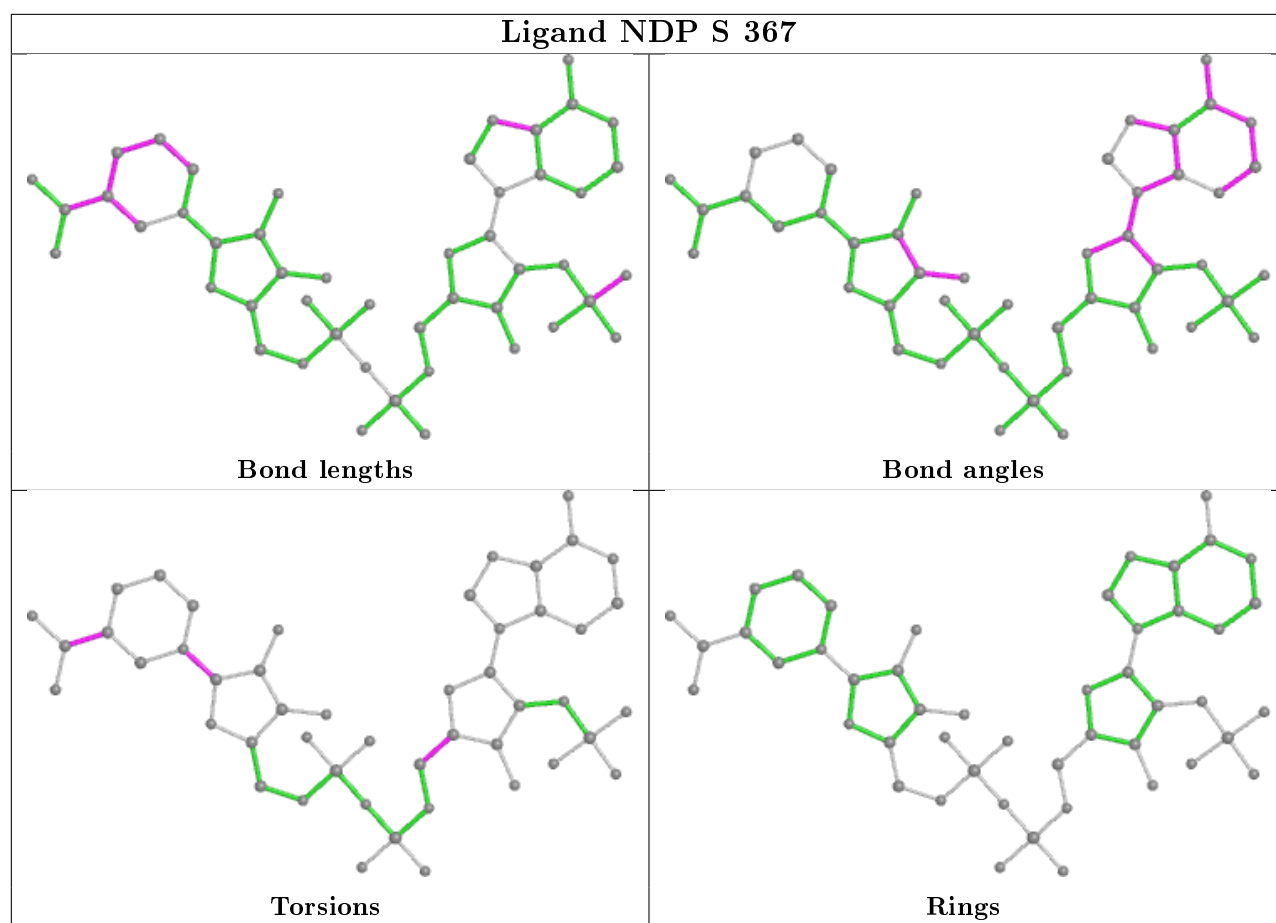
8 monomers are involved in 17 short contacts:

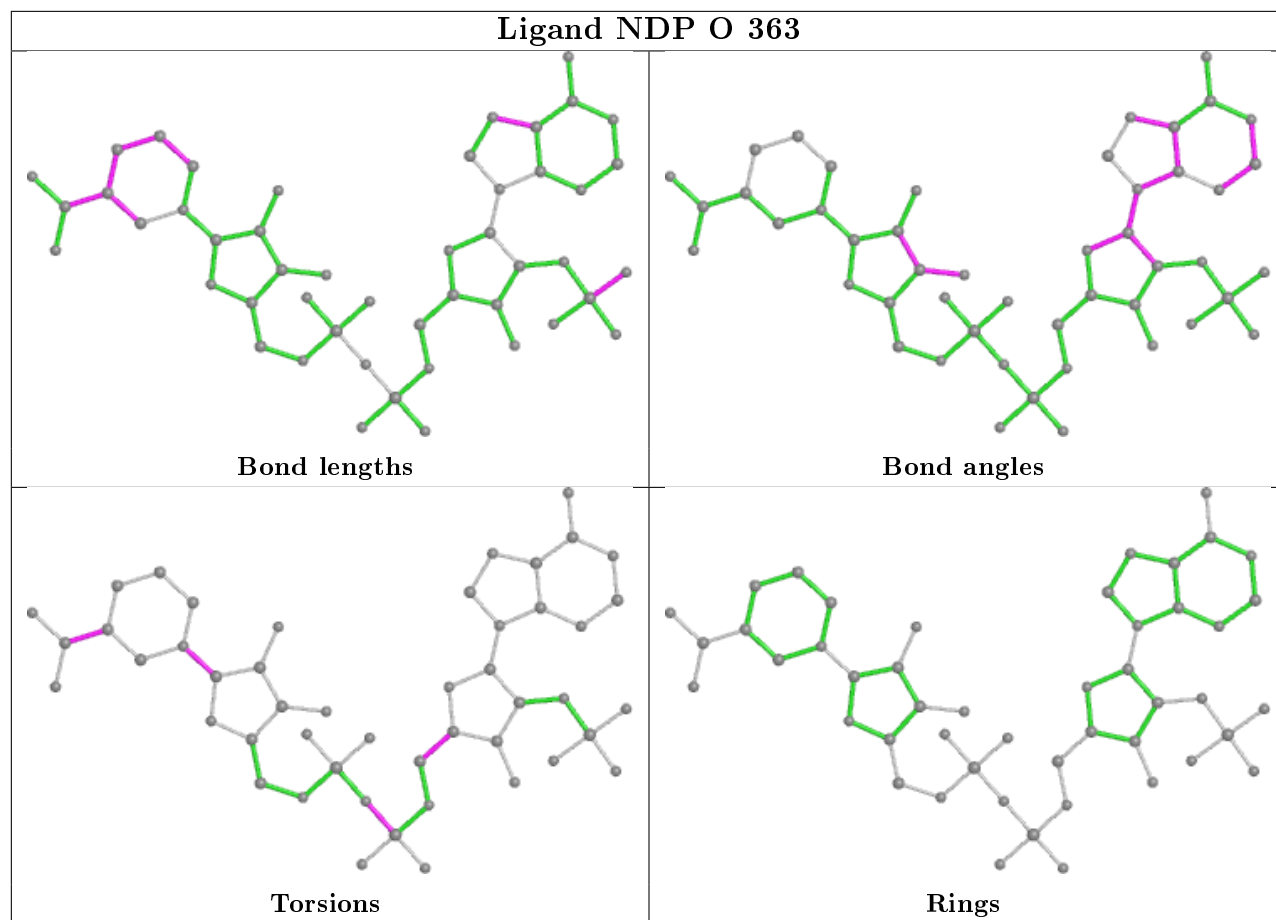
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	P	364	NDP	2	0
3	S	380	SO4	1	0
4	T	368	NDP	8	0
4	S	367	NDP	2	0
3	T	383	SO4	1	0
4	O	363	NDP	1	0
4	R	366	NDP	1	0
4	Q	365	NDP	1	0

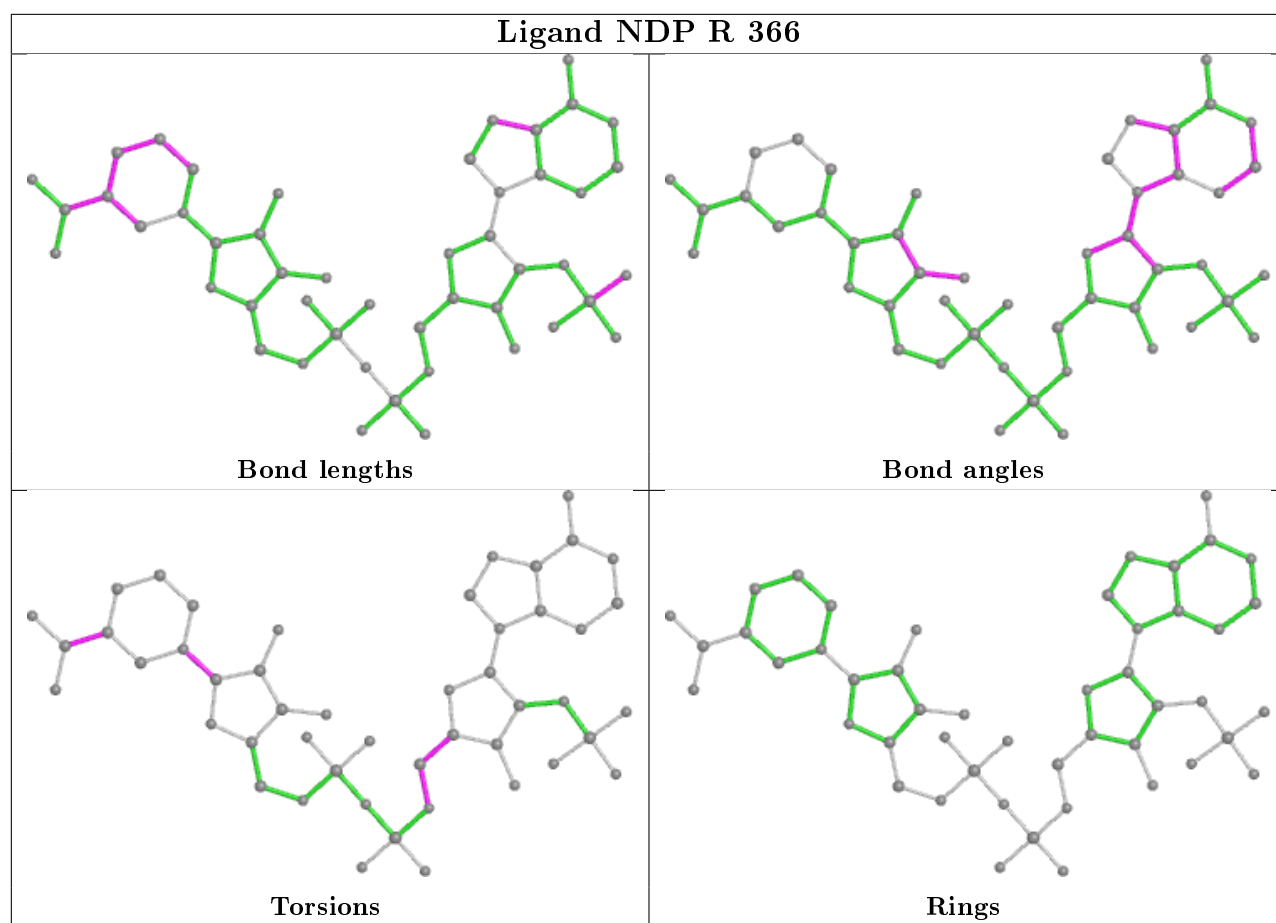
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

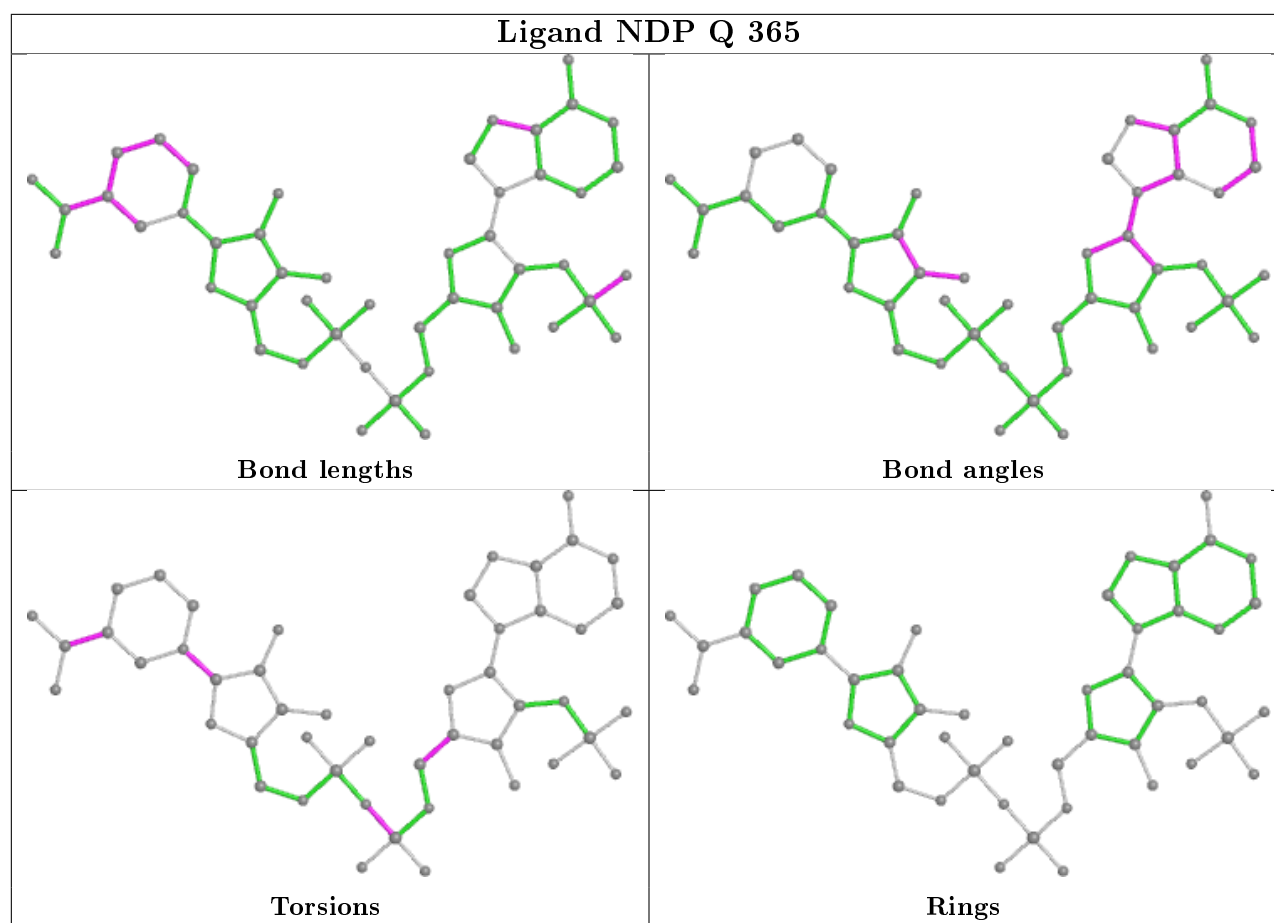












5.7 Other polymers [i](#)

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	O	346/368 (94%)	-0.05	0 100 100	5, 32, 53, 69	0
1	Q	347/368 (94%)	-0.23	0 100 100	3, 34, 55, 70	0
1	T	349/368 (94%)	-0.20	4 (1%) 80 68	2, 33, 54, 90	0
2	P	337/337 (100%)	-0.27	0 100 100	1, 23, 47, 74	0
2	R	337/337 (100%)	0.20	6 (1%) 68 53	1, 26, 49, 76	0
2	S	336/337 (99%)	-0.34	0 100 100	1, 23, 47, 70	0
All	All	2052/2115 (97%)	-0.15	10 (0%) 91 83	1, 29, 53, 90	0

All (10) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	T	335	LEU	4.5
1	T	336	GLU	2.8
2	R	333	GLN	2.7
2	R	289	SER	2.6
1	T	337	GLY	2.6
2	R	334	ALA	2.6
1	T	349	CYS	2.2
2	R	114	LYS	2.2
2	R	3	VAL	2.1
2	R	1	LEU	2.0

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

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

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

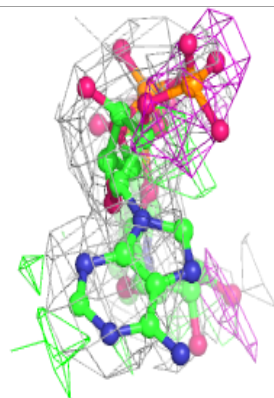
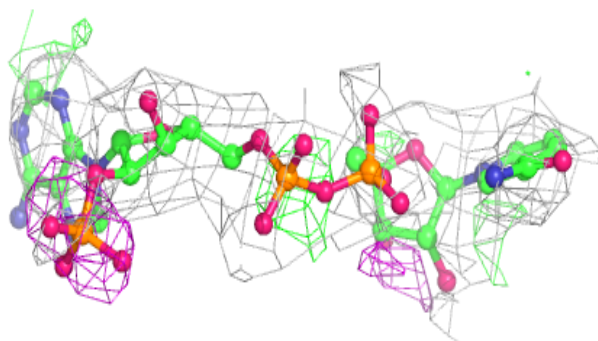
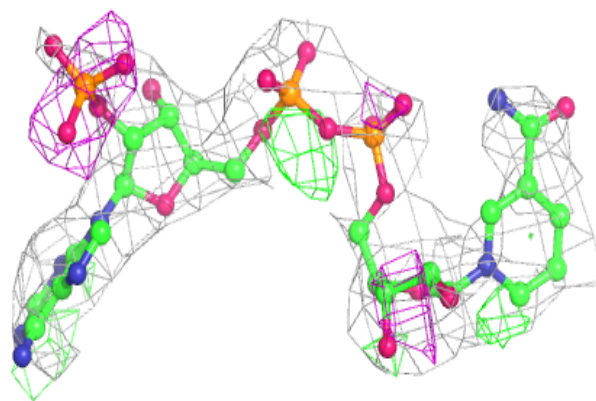
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	SO4	Q	382	5/5	0.67	0.40	38,38,38,38	5
3	SO4	O	370	5/5	0.77	0.38	59,59,59,59	5
3	SO4	T	379	5/5	0.78	0.41	51,51,51,51	5
4	NDP	Q	365	48/48	0.80	0.32	66,70,94,95	0
3	SO4	T	378	5/5	0.82	0.42	64,64,65,65	5
4	NDP	R	366	48/48	0.84	0.33	46,60,96,97	0
3	SO4	Q	384	5/5	0.84	0.64	55,55,55,55	5
4	NDP	T	368	48/48	0.85	0.33	60,70,103,104	0
3	SO4	R	381	5/5	0.86	0.20	44,44,45,46	5
4	NDP	S	367	48/48	0.86	0.33	21,32,75,76	0
3	SO4	T	383	5/5	0.88	0.31	52,52,53,53	5
3	SO4	S	380	5/5	0.89	0.38	47,47,48,48	5
4	NDP	O	363	48/48	0.89	0.30	32,45,75,76	0
4	NDP	P	364	48/48	0.90	0.31	17,24,76,77	0
3	SO4	P	372	5/5	0.92	0.28	44,44,45,45	5
3	SO4	P	371	5/5	0.92	0.17	39,39,40,41	5
3	SO4	Q	373	5/5	0.92	0.16	30,31,31,32	5
3	SO4	S	377	5/5	0.93	0.44	63,63,64,64	5
3	SO4	R	375	5/5	0.93	0.13	42,42,43,43	5
3	SO4	R	374	5/5	0.94	0.20	47,48,48,48	5
3	SO4	S	376	5/5	0.98	0.13	17,18,18,19	0

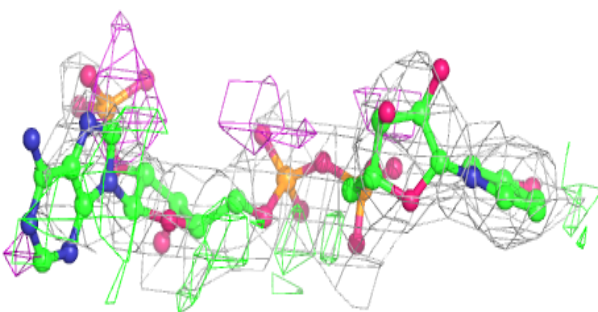
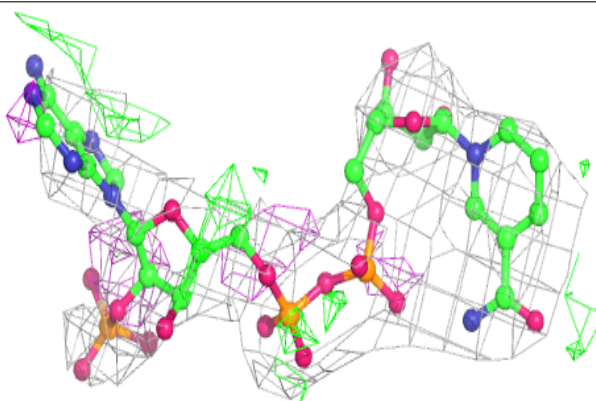
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around NDP Q 365:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

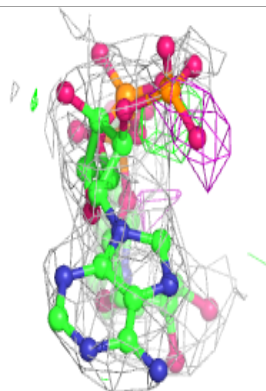
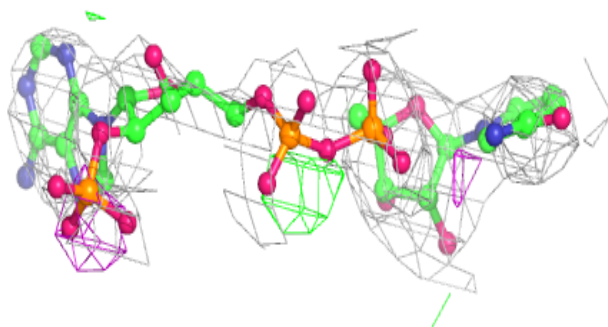
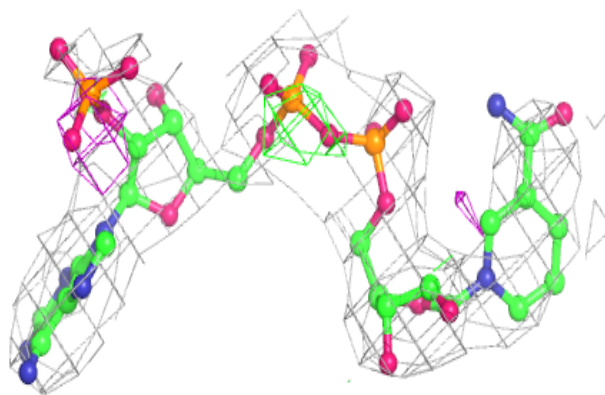
**Electron density around NDP R 366:**

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

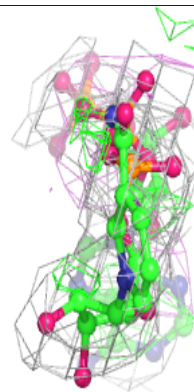
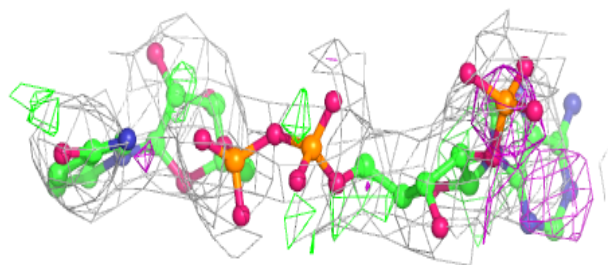
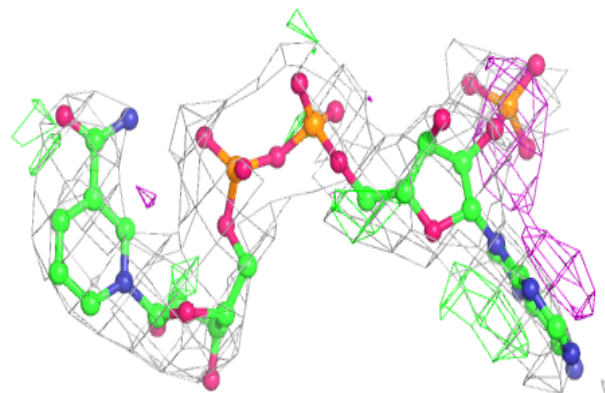


Electron density around NDP T 368:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

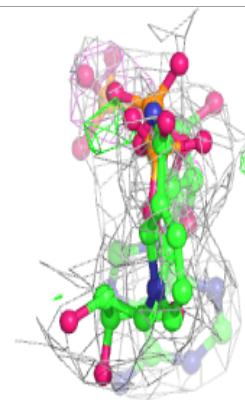
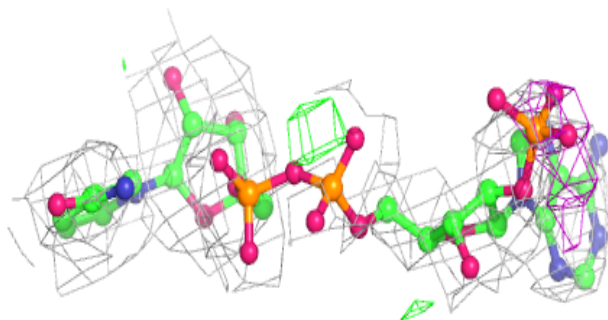
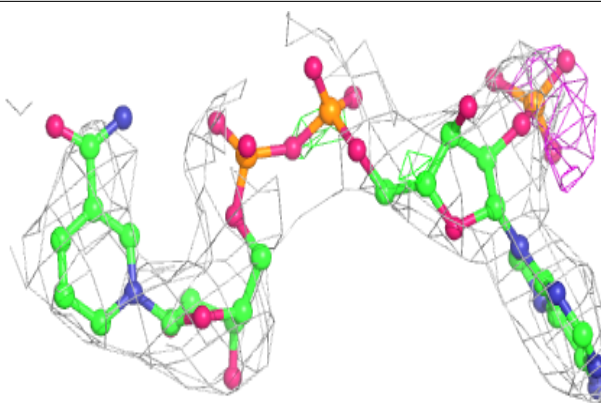
**Electron density around NDP S 367:**

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

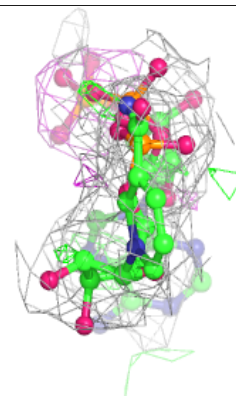
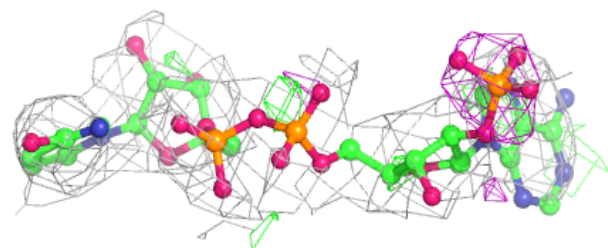
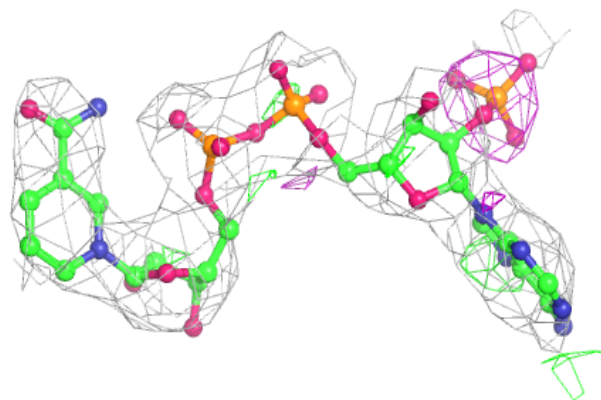


Electron density around NDP O 363:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

**Electron density around NDP P 364:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers [i](#)

There are no such residues in this entry.