



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 05:03 AM GMT

PDB ID : 2P9Q
Title : Crystal Structure of Phosphoglycerate Kinase-2
Authors : Sawyer, G.M.; Monzingo, A.F.; Poteet, E.C.; Robertus, J.D.
Deposited on : 2007-03-26
Resolution : 2.70 Å(reported)

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

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

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

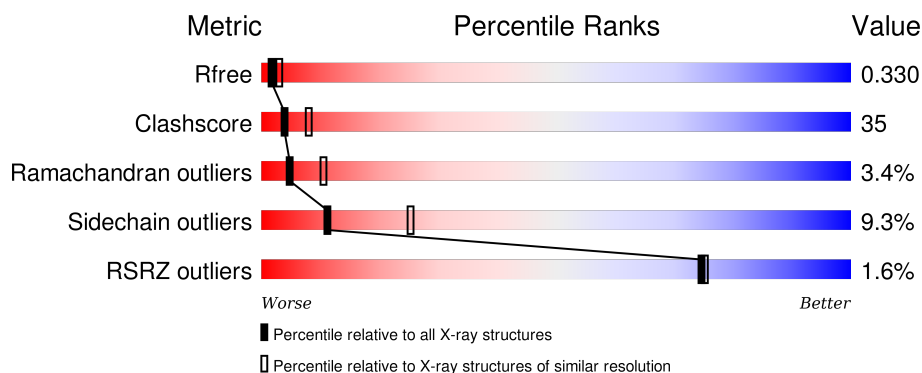
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	2103 (2.70-2.70)
Clashscore	102246	2422 (2.70-2.70)
Ramachandran outliers	100387	2382 (2.70-2.70)
Sidechain outliers	100360	2382 (2.70-2.70)
RSRZ outliers	91569	2107 (2.70-2.70)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	416	<div> <div>2%</div> <div>45%</div> <div>44%</div> <div>8%</div> <div>•</div> </div>
1	B	416	<div> <div>%</div> <div>47%</div> <div>43%</div> <div>7%</div> <div>•</div> </div>

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 6125 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 Phosphoglycerate kinase, testis specific.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	404	Total	C	N	O	S	0	0	0
			3043	1933	514	577	19			
1	B	403	Total	C	N	O	S	0	0	0
			3004	1907	506	572	19			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	150	ARG	GLN	SEE REMARK 999	UNP P09041
B	150	ARG	GLN	SEE REMARK 999	UNP P09041

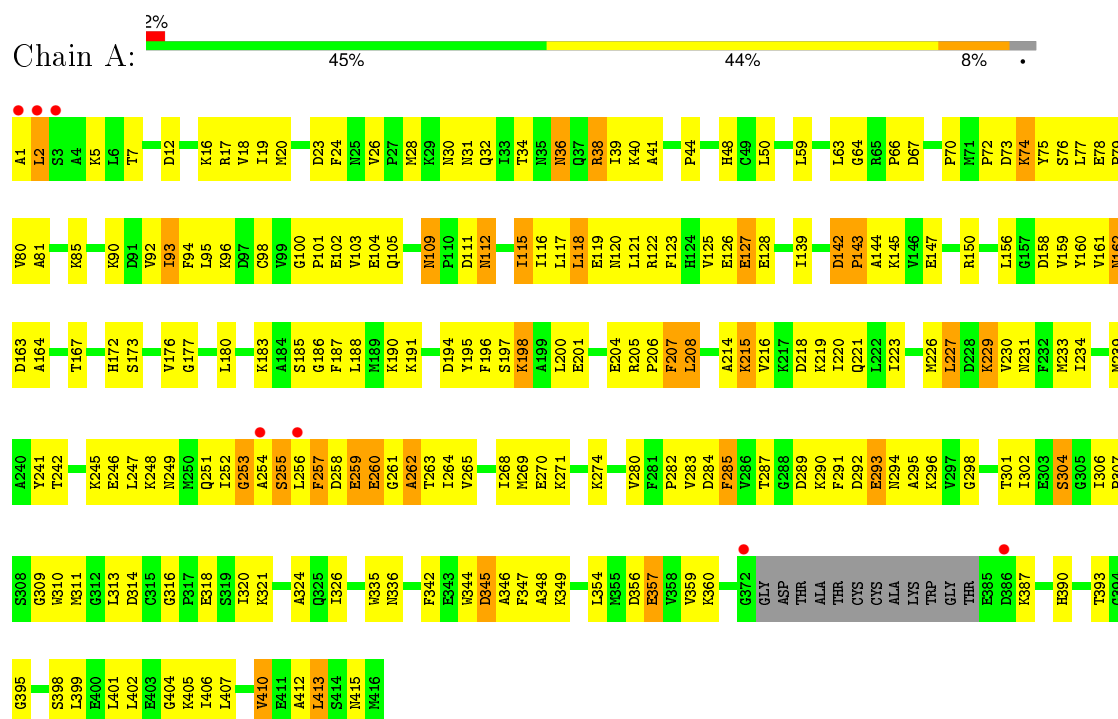
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	48	Total	O	0	0
			48	48		
2	B	30	Total	O	0	0
			30	30		

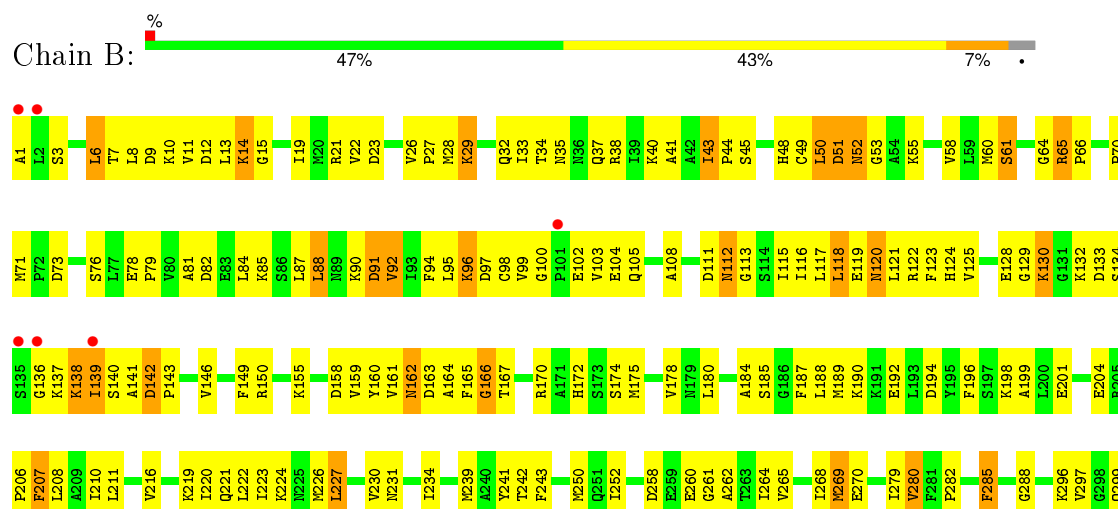
3 Residue-property plots

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: Phosphoglycerate kinase, testis specific



- Molecule 1: Phosphoglycerate kinase, testis specific





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	52.04Å 80.85Å 92.90Å 90.00° 94.63° 90.00°	Depositor
Resolution (Å)	20.00 – 2.70 29.70 – 2.80	Depositor EDS
% Data completeness (in resolution range)	82.3 (20.00-2.70) 93.7 (29.70-2.80)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.98 (at 2.80Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.217 , 0.328 0.222 , 0.330	Depositor DCC
R_{free} test set	873 reflections (4.89%)	DCC
Wilson B-factor (Å ²)	35.7	Xtriage
Anisotropy	0.217	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 44.8	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Outliers	0 of 18266 reflections	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	6125	wwPDB-VP
Average B, all atoms (Å ²)	25.0	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 38.79 % 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 3.4985e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

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	0.43	0/3090	0.65	0/4158
1	B	0.41	0/3051	0.67	0/4115
All	All	0.42	0/6141	0.66	0/8273

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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	3043	0	3118	195	0
1	B	3004	0	3029	229	0
2	A	48	0	0	3	0
2	B	30	0	0	3	0
All	All	6125	0	6147	421	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 35.

All (421) 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:215:LYS:H	1:A:215:LYS:HD2	1.05	1.08

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:6:LEU:HD13	1:B:184:ALA:HB2	1.46	0.97
1:B:139:ILE:HG22	1:B:140:SER:H	1.28	0.96
1:A:207:PHE:H	1:A:231:ASN:HD22	1.06	0.95
1:B:88:LEU:HD13	1:B:90:LYS:HB3	1.54	0.89
1:B:13:LEU:HD13	1:B:49:CYS:HA	1.55	0.89
1:A:215:LYS:H	1:A:215:LYS:CD	1.77	0.88
1:A:215:LYS:HD2	1:A:215:LYS:N	1.88	0.88
1:A:41:ALA:HB1	1:A:188:LEU:HD21	1.56	0.87
1:B:6:LEU:CD1	1:B:184:ALA:HB2	2.05	0.86
1:A:85:LYS:HB3	1:A:92:VAL:HG12	1.59	0.84
1:A:36:ASN:ND2	1:A:40:LYS:HE3	1.93	0.83
1:B:13:LEU:HD12	1:B:52:ASN:HB3	1.62	0.82
1:B:95:LEU:HD23	1:B:103:VAL:HG13	1.62	0.81
1:B:223:ILE:HD11	1:B:239:MET:HE1	1.63	0.80
1:B:407:LEU:HB2	1:B:410:VAL:HG13	1.65	0.79
1:A:100:GLY:O	1:A:104:GLU:HG3	1.83	0.79
1:B:94:PHE:O	1:B:95:LEU:HD12	1.82	0.79
1:A:7:THR:HG21	1:A:190:LYS:HD3	1.66	0.77
1:B:12:ASP:OD1	1:B:14:LYS:HB2	1.84	0.77
1:B:206:PRO:HA	1:B:231:ASN:HD22	1.48	0.77
1:A:220:ILE:HG13	1:A:268:ILE:HD11	1.67	0.77
1:B:280:VAL:HG11	1:B:326:ILE:CD1	2.15	0.76
1:B:219:LYS:O	1:B:223:ILE:HG13	1.86	0.75
1:B:27:PRO:HD2	1:B:35:ASN:HB3	1.68	0.74
1:B:341:VAL:HG23	1:B:341:VAL:O	1.88	0.74
1:B:279:ILE:HG22	1:B:280:VAL:H	1.52	0.73
1:B:27:PRO:HB2	1:B:34:THR:HB	1.70	0.73
1:A:191:LYS:HE3	1:A:390:HIS:ND1	2.03	0.73
1:B:220:ILE:HD12	1:B:264:ILE:HG23	1.71	0.72
1:B:206:PRO:HA	1:B:231:ASN:ND2	2.03	0.72
1:B:279:ILE:HG22	1:B:280:VAL:N	2.03	0.72
1:B:99:VAL:HG11	1:B:149:PHE:CD1	2.24	0.72
1:B:1:ALA:HA	1:B:201:GLU:OE2	1.90	0.72
1:B:301:THR:HG23	1:B:303:GLU:N	2.05	0.72
1:A:195:TYR:O	1:A:198:LYS:HG2	1.90	0.72
1:B:120:ASN:HD22	1:B:121:LEU:N	1.89	0.71
1:A:95:LEU:HD23	1:A:103:VAL:HG22	1.73	0.71
1:B:98:CYS:HA	1:B:118:LEU:HB3	1.73	0.71
1:B:143:PRO:HA	1:B:146:VAL:HG22	1.71	0.71
1:A:324:ALA:HA	1:A:357:GLU:HG2	1.72	0.70
1:B:41:ALA:O	1:B:44:PRO:HD2	1.91	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:160:TYR:HB2	1:B:178:VAL:HG11	1.74	0.70
1:B:241:TYR:HB3	1:B:252:ILE:HG21	1.73	0.69
1:A:207:PHE:N	1:A:231:ASN:HD22	1.86	0.69
1:A:98:CYS:HA	1:A:118:LEU:HG	1.75	0.68
1:B:6:LEU:HD13	1:B:184:ALA:CB	2.23	0.68
1:A:2:LEU:H	1:A:2:LEU:HD23	1.57	0.68
1:B:22:VAL:HG22	1:B:23:ASP:H	1.58	0.67
1:A:344:TRP:O	1:A:346:ALA:N	2.27	0.67
1:B:133:ASP:HB3	1:B:139:ILE:HD11	1.77	0.67
1:A:207:PHE:H	1:A:231:ASN:ND2	1.86	0.67
1:B:288:GLY:HA2	1:B:296:LYS:O	1.95	0.67
1:B:22:VAL:O	1:B:61:SER:HB2	1.96	0.66
1:B:162:ASN:ND2	1:B:164:ALA:H	1.93	0.66
1:A:216:VAL:HG23	1:A:258:ASP:OD2	1.95	0.66
1:B:207:PHE:H	1:B:231:ASN:ND2	1.94	0.66
1:B:207:PHE:H	1:B:231:ASN:HD22	1.44	0.66
1:A:176:VAL:HG12	1:A:412:ALA:HB2	1.76	0.66
1:B:40:LYS:HG2	1:B:87:LEU:HD13	1.78	0.65
1:B:45:SER:OG	1:B:187:PHE:HB2	1.95	0.65
1:A:289:ASP:OD2	1:A:295:ALA:HB1	1.96	0.65
1:A:93:ILE:HD12	1:A:94:PHE:N	2.12	0.65
1:A:162:ASN:ND2	1:A:164:ALA:H	1.95	0.65
1:A:101:PRO:O	1:A:105:GLN:HG3	1.96	0.65
1:A:257:PHE:HD1	1:A:258:ASP:N	1.94	0.64
1:B:226:MET:O	1:B:230:VAL:HG22	1.97	0.64
1:A:247:LEU:HD21	1:A:269:MET:HG3	1.78	0.64
1:B:139:ILE:HG22	1:B:140:SER:N	2.08	0.64
1:A:116:ILE:HD12	1:A:116:ILE:N	2.11	0.64
1:B:164:ALA:HB3	1:B:175:MET:HE3	1.78	0.64
1:B:92:VAL:HB	1:B:115:ILE:HG22	1.80	0.63
1:B:301:THR:HG23	1:B:303:GLU:H	1.62	0.63
1:A:162:ASN:HD22	1:A:163:ASP:N	1.97	0.63
1:A:205:ARG:NH2	1:A:229:LYS:O	2.32	0.63
1:B:27:PRO:CD	1:B:35:ASN:HB3	2.28	0.63
1:A:410:VAL:O	1:A:413:LEU:HB2	1.98	0.63
1:B:167:THR:HG22	1:B:175:MET:HG3	1.81	0.63
1:B:23:ASP:OD1	1:B:38:ARG:HD3	1.99	0.62
1:A:324:ALA:HA	1:A:357:GLU:CG	2.28	0.62
1:B:85:LYS:HE2	1:B:91:ASP:HA	1.82	0.62
1:A:109:ASN:C	1:A:109:ASN:HD22	2.02	0.62
1:B:60:MET:HB2	1:B:121:LEU:HD21	1.81	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:8:LEU:C	1:B:8:LEU:HD23	2.20	0.62
1:B:269:MET:CE	1:B:279:ILE:HD12	2.30	0.62
1:B:81:ALA:HB2	1:B:117:LEU:HD23	1.81	0.62
1:B:48:HIS:O	1:B:52:ASN:HB2	1.99	0.61
1:A:220:ILE:HD12	1:A:264:ILE:HB	1.82	0.61
1:B:146:VAL:O	1:B:150:ARG:HG3	2.00	0.61
1:B:58:VAL:CG1	1:B:118:LEU:HD11	2.30	0.61
1:B:119:GLU:HG3	1:B:120:ASN:N	2.16	0.61
1:A:406:ILE:HD12	1:A:406:ILE:C	2.20	0.60
1:A:260:GLU:OE1	1:A:262:ALA:HB3	2.00	0.60
1:B:120:ASN:HD22	1:B:120:ASN:C	2.04	0.60
1:B:162:ASN:HD22	1:B:164:ALA:H	1.50	0.60
1:A:162:ASN:C	1:A:162:ASN:HD22	2.05	0.59
1:A:215:LYS:HB2	1:A:218:ASP:HB2	1.83	0.59
1:A:206:PRO:HA	1:A:231:ASN:ND2	2.17	0.59
1:B:158:ASP:C	1:B:180:LEU:HD13	2.23	0.59
1:A:36:ASN:HD21	1:A:40:LYS:HE3	1.63	0.59
1:B:1:ALA:C	1:B:3:SER:H	2.04	0.59
1:B:29:LYS:NZ	1:B:29:LYS:HB3	2.17	0.59
1:B:82:ASP:O	1:B:85:LYS:N	2.36	0.59
1:A:242:THR:HG22	1:A:265:VAL:HG21	1.84	0.59
1:A:64:GLY:HA3	1:A:75:TYR:CD1	2.37	0.59
1:B:22:VAL:HG22	1:B:23:ASP:N	2.19	0.58
1:A:36:ASN:CG	1:A:40:LYS:HE3	2.25	0.58
1:B:58:VAL:HG13	1:B:118:LEU:HD11	1.86	0.58
1:A:287:THR:HG22	1:A:306:ILE:HD12	1.85	0.58
1:A:293:GLU:HB3	1:A:344:TRP:CG	2.39	0.57
1:A:259:GLU:HB3	1:B:10:LYS:NZ	2.19	0.57
1:B:395:GLY:O	1:B:399:LEU:HD13	2.05	0.57
1:A:270:GLU:OE1	1:A:274:LYS:HE3	2.04	0.57
1:B:216:VAL:HG21	1:B:242:THR:HG21	1.86	0.57
1:A:301:THR:H	1:A:304:SER:HB3	1.70	0.57
1:B:269:MET:HE3	1:B:279:ILE:HD12	1.86	0.57
1:A:2:LEU:HD13	1:A:197:SER:O	2.03	0.57
1:A:196:PHE:O	1:A:200:LEU:HD12	2.05	0.57
1:A:254:ALA:HB3	1:A:310:TRP:O	2.03	0.57
1:B:8:LEU:HD21	1:B:48:HIS:CG	2.40	0.57
1:B:60:MET:HA	2:B:417:HOH:O	2.05	0.57
1:B:130:LYS:O	1:B:130:LYS:HD2	2.05	0.57
1:A:234:ILE:HA	1:A:280:VAL:HG22	1.87	0.57
1:B:401:LEU:HD13	1:B:407:LEU:HD11	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:7:THR:HB	2:A:445:HOH:O	2.03	0.56
1:A:219:LYS:HE3	2:A:427:HOH:O	2.05	0.56
1:A:81:ALA:O	1:A:92:VAL:HG11	2.05	0.56
1:B:399:LEU:O	1:B:403:GLU:HG3	2.04	0.56
1:A:227:LEU:HD23	1:A:271:LYS:HG2	1.87	0.56
1:A:257:PHE:HD1	1:A:258:ASP:H	1.52	0.56
1:A:301:THR:HG22	1:A:302:ILE:N	2.20	0.56
1:B:198:LYS:CG	1:B:199:ALA:N	2.69	0.56
1:B:105:GLN:HA	1:B:108:ALA:HB2	1.86	0.56
1:A:36:ASN:HD21	1:A:40:LYS:CE	2.18	0.55
1:B:65:ARG:N	1:B:65:ARG:HD3	2.21	0.55
1:A:30:ASN:O	1:A:32:GLN:HG3	2.06	0.55
1:A:284:ASP:OD2	1:A:318:GLU:HB2	2.07	0.55
1:A:252:ILE:HG13	1:A:252:ILE:O	2.06	0.55
1:A:218:ASP:O	1:A:219:LYS:HG2	2.06	0.55
1:B:13:LEU:CD1	1:B:49:CYS:HA	2.30	0.55
1:A:290:LYS:O	1:A:292:ASP:N	2.39	0.55
1:A:143:PRO:O	1:A:147:GLU:HG2	2.06	0.55
1:B:129:GLY:O	1:B:141:ALA:HB3	2.07	0.55
1:B:220:ILE:HG23	1:B:221:GLN:N	2.22	0.55
1:B:322:ILE:O	1:B:325:GLN:HB2	2.05	0.55
1:B:170:ARG:HD2	1:B:172:HIS:CE1	2.42	0.55
1:B:211:LEU:HD22	1:B:222:LEU:HD21	1.88	0.55
1:A:227:LEU:HD23	1:A:271:LYS:CG	2.37	0.55
1:B:50:LEU:O	1:B:52:ASN:N	2.39	0.55
1:A:306:ILE:HG21	1:A:311:MET:HA	1.89	0.55
1:B:400:GLU:HG3	1:B:405:LYS:HD2	1.89	0.55
1:A:282:PRO:HB2	1:A:285:PHE:CE2	2.41	0.55
1:B:50:LEU:C	1:B:52:ASN:H	2.10	0.55
1:B:120:ASN:ND2	1:B:122:ARG:H	2.05	0.55
1:B:102:GLU:O	1:B:105:GLN:HG2	2.07	0.55
1:B:55:LYS:O	1:B:113:GLY:N	2.37	0.55
1:A:214:ALA:HB3	1:A:215:LYS:HE3	1.88	0.54
1:B:220:ILE:HD11	1:B:224:LYS:NZ	2.21	0.54
1:B:139:ILE:CG2	1:B:140:SER:H	2.11	0.54
1:A:41:ALA:O	1:A:44:PRO:HD2	2.06	0.54
1:B:216:VAL:HA	1:B:239:MET:HE3	1.89	0.54
1:B:162:ASN:C	1:B:162:ASN:HD22	2.10	0.54
1:A:5:LYS:NZ	1:A:415:ASN:ND2	2.56	0.54
1:B:8:LEU:HD22	1:B:187:PHE:CE2	2.42	0.54
1:A:2:LEU:H	1:A:2:LEU:CD2	2.21	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:125:VAL:HG11	1:A:139:ILE:CD1	2.38	0.54
1:B:220:ILE:HG13	1:B:268:ILE:HD11	1.89	0.54
1:A:293:GLU:HB3	1:A:344:TRP:CD1	2.42	0.54
1:A:17:ARG:HD3	1:A:158:ASP:OD2	2.08	0.54
1:A:1:ALA:HB1	1:A:201:GLU:OE1	2.07	0.54
1:A:247:LEU:O	1:A:248:LYS:HD2	2.07	0.53
1:B:282:PRO:HB2	1:B:285:PHE:CE2	2.42	0.53
1:B:21:ARG:HG3	1:B:174:SER:HB2	1.89	0.53
1:A:128:GLU:HG2	1:A:172:HIS:CE1	2.43	0.53
1:A:18:VAL:HG22	1:A:159:VAL:CG2	2.38	0.53
1:A:245:LYS:HG2	1:A:245:LYS:O	2.08	0.53
1:B:95:LEU:O	1:B:97:ASP:N	2.41	0.53
1:B:280:VAL:HG11	1:B:326:ILE:HD11	1.89	0.53
1:A:2:LEU:HD22	1:A:201:GLU:OE1	2.09	0.53
1:B:29:LYS:O	1:B:32:GLN:HB2	2.08	0.53
1:B:166:GLY:HA2	1:B:394:GLY:HA3	1.91	0.53
1:A:39:ILE:CD1	1:A:80:VAL:HG13	2.39	0.52
1:B:162:ASN:HD22	1:B:163:ASP:N	2.08	0.52
1:B:95:LEU:C	1:B:97:ASP:H	2.13	0.52
1:A:252:ILE:O	1:A:253:GLY:C	2.47	0.52
1:B:90:LYS:HD2	1:B:91:ASP:H	1.75	0.52
1:A:227:LEU:HD23	1:A:271:LYS:HD3	1.92	0.52
1:A:321:LYS:O	1:A:324:ALA:HB3	2.10	0.52
1:A:163:ASP:CG	1:A:186:GLY:HA3	2.30	0.52
1:B:198:LYS:HE2	1:B:204:GLU:OE2	2.10	0.52
1:A:285:PHE:N	1:A:285:PHE:CD1	2.78	0.52
1:A:219:LYS:O	1:A:223:ILE:HG13	2.10	0.52
1:B:21:ARG:CG	1:B:174:SER:HB2	2.40	0.51
1:B:190:LYS:HZ3	1:B:194:ASP:CG	2.14	0.51
1:A:115:ILE:HD12	1:A:116:ILE:N	2.25	0.51
1:A:17:ARG:O	1:A:158:ASP:N	2.40	0.51
1:A:81:ALA:HB2	1:A:117:LEU:HD23	1.92	0.51
1:A:85:LYS:HB2	1:A:90:LYS:O	2.11	0.51
1:B:128:GLU:HG2	1:B:172:HIS:CE1	2.46	0.51
1:B:279:ILE:CG2	1:B:280:VAL:H	2.21	0.51
1:A:356:ASP:O	1:A:359:VAL:HG12	2.11	0.51
1:B:219:LYS:HB2	1:B:239:MET:CE	2.41	0.51
1:B:28:MET:HA	1:B:32:GLN:O	2.11	0.50
1:A:119:GLU:HG3	1:A:120:ASN:N	2.26	0.50
1:B:279:ILE:CG2	1:B:280:VAL:N	2.73	0.50
1:B:219:LYS:HB2	1:B:239:MET:HE1	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:207:PHE:N	1:B:231:ASN:HD22	2.07	0.50
1:B:43:ILE:HG13	1:B:44:PRO:HD3	1.93	0.50
1:A:289:ASP:OD1	1:A:290:LYS:NZ	2.45	0.50
1:B:76:SER:O	1:B:79:PRO:HD2	2.10	0.50
1:B:260:GLU:O	1:B:264:ILE:HG13	2.11	0.50
1:B:132:LYS:HA	1:B:138:LYS:HA	1.94	0.50
1:B:243:PHE:CD2	1:B:265:VAL:HG13	2.47	0.50
1:B:120:ASN:HB3	1:B:123:PHE:CD1	2.46	0.50
1:A:401:LEU:O	1:A:404:GLY:N	2.36	0.50
1:B:37:GLN:HG3	1:B:38:ARG:N	2.26	0.50
1:B:163:ASP:OD1	1:B:188:LEU:HB3	2.11	0.50
1:A:142:ASP:O	1:A:144:ALA:N	2.45	0.50
1:B:406:ILE:HG22	1:B:406:ILE:O	2.12	0.50
1:B:234:ILE:HG12	1:B:280:VAL:CG2	2.42	0.49
1:A:287:THR:N	1:A:298:GLY:O	2.44	0.49
1:A:28:MET:HE1	1:A:31:ASN:HA	1.93	0.49
1:A:260:GLU:O	1:A:260:GLU:CD	2.51	0.49
1:A:234:ILE:HG12	1:A:280:VAL:CG2	2.42	0.49
1:B:90:LYS:HD2	1:B:91:ASP:N	2.27	0.49
1:B:207:PHE:HD1	1:B:208:LEU:N	2.10	0.49
1:B:210:ILE:HD13	1:B:354:LEU:HD21	1.93	0.49
1:A:313:LEU:HD12	1:A:347:PHE:CE2	2.47	0.49
1:B:7:THR:HG22	1:B:8:LEU:N	2.28	0.49
1:A:12:ASP:O	1:A:16:LYS:HD2	2.12	0.49
1:A:287:THR:OG1	1:A:298:GLY:C	2.50	0.49
1:A:167:THR:O	1:A:167:THR:HG22	2.13	0.49
1:A:24:PHE:O	1:A:26:VAL:HG13	2.12	0.49
1:B:196:PHE:HB3	1:B:401:LEU:HD23	1.93	0.49
1:B:43:ILE:HG13	1:B:44:PRO:CD	2.42	0.49
1:B:185:SER:HB3	1:B:413:LEU:HD21	1.95	0.49
1:A:150:ARG:HD3	1:A:177:GLY:HA3	1.95	0.49
1:B:250:MET:CE	1:B:252:ILE:HG22	2.42	0.49
1:A:162:ASN:C	1:A:162:ASN:ND2	2.67	0.49
1:B:60:MET:O	1:B:61:SER:HB3	2.13	0.48
1:A:23:ASP:OD1	1:A:38:ARG:HG2	2.13	0.48
1:A:104:GLU:HA	1:A:156:LEU:CD2	2.43	0.48
1:A:63:LEU:HB2	1:A:77:LEU:HD21	1.94	0.48
1:B:23:ASP:CG	1:B:38:ARG:HD3	2.33	0.48
1:B:6:LEU:HD11	1:B:11:VAL:HG22	1.94	0.48
1:A:125:VAL:HG11	1:A:139:ILE:HD11	1.95	0.48
1:A:81:ALA:O	1:A:92:VAL:CG1	2.62	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:234:ILE:HG12	1:A:280:VAL:HG21	1.95	0.48
1:A:241:TYR:HB3	1:A:252:ILE:HG21	1.95	0.48
1:B:6:LEU:HD22	1:B:7:THR:H	1.79	0.48
1:A:220:ILE:HG13	1:A:268:ILE:CD1	2.42	0.48
1:A:20:MET:HG3	1:A:161:VAL:HB	1.96	0.48
1:B:6:LEU:HD22	1:B:7:THR:N	2.29	0.48
1:A:95:LEU:HD13	1:A:116:ILE:HG23	1.95	0.48
1:A:19:ILE:HG23	1:A:19:ILE:O	2.13	0.48
1:A:335:TRP:CD1	1:A:335:TRP:C	2.87	0.48
1:A:335:TRP:HD1	1:A:336:ASN:N	2.12	0.48
1:B:95:LEU:HD13	1:B:116:ILE:HG23	1.96	0.48
1:A:257:PHE:CD1	1:A:258:ASP:N	2.79	0.48
1:A:115:ILE:C	1:A:116:ILE:HD12	2.34	0.47
1:A:39:ILE:HD11	1:A:80:VAL:HG13	1.96	0.47
1:B:356:ASP:HA	1:B:359:VAL:HG12	1.96	0.47
1:B:165:PHE:HA	1:B:189:MET:HE2	1.96	0.47
1:B:207:PHE:C	1:B:207:PHE:CD1	2.87	0.47
1:B:303:GLU:O	1:B:304:SER:HB3	2.14	0.47
1:A:92:VAL:HG23	1:A:115:ILE:HD11	1.97	0.47
1:A:128:GLU:HB2	2:A:440:HOH:O	2.15	0.47
1:B:96:LYS:HE3	1:B:96:LYS:O	2.14	0.47
1:B:261:GLY:O	1:B:262:ALA:C	2.51	0.47
1:A:176:VAL:HG12	1:A:412:ALA:CB	2.45	0.47
1:B:136:GLY:O	1:B:138:LYS:N	2.48	0.47
1:A:127:GLU:OE1	1:A:173:SER:HB2	2.14	0.47
1:B:84:LEU:O	1:B:88:LEU:HG	2.14	0.47
1:A:122:ARG:HD3	1:A:128:GLU:OE1	2.15	0.47
1:A:18:VAL:HG22	1:A:159:VAL:HG23	1.96	0.47
1:B:317:PRO:O	1:B:321:LYS:HG3	2.15	0.47
1:B:285:PHE:O	1:B:299:GLN:NE2	2.48	0.47
1:A:190:LYS:HE3	1:A:194:ASP:OD1	2.15	0.47
1:B:341:VAL:HG21	1:B:344:TRP:CE3	2.50	0.47
1:B:206:PRO:CA	1:B:231:ASN:HD22	2.21	0.46
1:B:118:LEU:N	1:B:118:LEU:CD1	2.78	0.46
1:A:216:VAL:HG22	1:A:239:MET:HB2	1.97	0.46
1:B:199:ALA:CB	1:B:332:LEU:HD21	2.45	0.46
1:A:359:VAL:HG23	1:A:387:LYS:HB3	1.97	0.46
1:B:94:PHE:C	1:B:95:LEU:HD12	2.36	0.46
1:B:301:THR:HG22	1:B:304:SER:OG	2.15	0.46
1:B:43:ILE:HG13	1:B:44:PRO:N	2.30	0.46
1:B:130:LYS:C	1:B:130:LYS:HD2	2.36	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:208:LEU:O	1:B:333:ILE:HA	2.15	0.46
1:B:22:VAL:O	1:B:61:SER:CB	2.63	0.46
1:A:109:ASN:ND2	1:A:109:ASN:C	2.68	0.46
1:A:73:ASP:O	1:A:74:LYS:HB2	2.14	0.46
1:A:254:ALA:O	1:A:255:SER:C	2.54	0.46
1:B:400:GLU:HG3	1:B:405:LYS:CD	2.46	0.46
1:A:142:ASP:OD1	1:A:144:ALA:HB3	2.15	0.46
1:A:316:GLY:O	1:A:320:ILE:HG13	2.15	0.46
1:A:407:LEU:HB2	1:A:410:VAL:HG13	1.97	0.46
1:B:128:GLU:HB3	1:B:130:LYS:NZ	2.31	0.46
1:A:249:ASN:O	1:A:251:GLN:NE2	2.48	0.46
1:A:223:ILE:HG23	1:A:233:MET:SD	2.55	0.46
1:A:301:THR:O	1:A:304:SER:HB3	2.16	0.46
1:B:6:LEU:HD12	1:B:184:ALA:HB2	1.93	0.46
1:A:198:LYS:NZ	1:A:204:GLU:OE2	2.45	0.46
1:B:100:GLY:O	1:B:104:GLU:HG3	2.17	0.45
1:A:96:LYS:NZ	1:A:96:LYS:HB2	2.31	0.45
1:B:111:ASP:O	1:B:112:ASN:O	2.33	0.45
1:B:29:LYS:HB3	1:B:29:LYS:HZ3	1.79	0.45
1:B:29:LYS:HD2	1:B:29:LYS:O	2.16	0.45
1:A:283:VAL:O	1:A:302:ILE:HG13	2.16	0.45
1:A:150:ARG:HD3	1:A:177:GLY:CA	2.47	0.45
1:B:159:VAL:HG23	1:B:159:VAL:O	2.16	0.45
1:B:26:VAL:HB	1:B:35:ASN:O	2.17	0.45
1:A:125:VAL:CG1	1:A:139:ILE:HD11	2.47	0.45
1:A:59:LEU:HD11	1:A:115:ILE:HD13	1.99	0.45
1:A:103:VAL:HG12	1:A:156:LEU:HD21	1.98	0.45
1:B:61:SER:O	1:B:121:LEU:HG	2.17	0.45
1:B:78:GLU:N	1:B:79:PRO:CD	2.80	0.45
1:A:36:ASN:HD21	1:A:40:LYS:NZ	2.14	0.45
1:B:166:GLY:HA2	1:B:394:GLY:CA	2.47	0.45
1:B:82:ASP:O	1:B:85:LYS:HB3	2.17	0.45
1:B:234:ILE:HA	1:B:280:VAL:HG22	1.97	0.45
1:B:250:MET:HE1	1:B:252:ILE:HG22	1.97	0.45
1:A:126:GLU:HG2	1:A:145:LYS:O	2.17	0.45
1:B:120:ASN:ND2	1:B:120:ASN:C	2.69	0.45
1:B:60:MET:HG3	1:B:121:LEU:HD11	1.97	0.45
1:A:254:ALA:HB2	1:A:309:GLY:C	2.37	0.45
1:B:167:THR:HG22	1:B:175:MET:CG	2.45	0.44
1:A:406:ILE:C	1:A:406:ILE:CD1	2.85	0.44
1:B:332:LEU:HA	1:B:367:VAL:O	2.16	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:8:LEU:HD21	1:B:48:HIS:ND1	2.31	0.44
1:B:407:LEU:O	1:B:411:GLU:HG2	2.16	0.44
1:A:96:LYS:HB2	1:A:96:LYS:HZ2	1.82	0.44
1:A:7:THR:HG22	1:A:185:SER:OG	2.17	0.44
1:B:92:VAL:CG2	1:B:92:VAL:O	2.65	0.44
1:B:196:PHE:CB	1:B:401:LEU:HD23	2.47	0.44
1:A:398:SER:O	1:A:401:LEU:HB2	2.17	0.44
1:B:70:PRO:O	1:B:71:MET:HG3	2.18	0.44
1:B:269:MET:HE1	1:B:279:ILE:HD12	1.98	0.44
1:A:74:LYS:HE2	1:A:75:TYR:CZ	2.52	0.44
1:A:227:LEU:HD23	1:A:271:LYS:CD	2.47	0.44
1:A:344:TRP:O	1:A:345:ASP:C	2.56	0.44
1:B:15:GLY:N	1:B:53:GLY:O	2.48	0.44
1:A:344:TRP:C	1:A:346:ALA:N	2.71	0.43
1:A:115:ILE:HD12	1:A:115:ILE:C	2.39	0.43
1:A:92:VAL:HG23	1:A:115:ILE:CD1	2.48	0.43
1:B:142:ASP:HA	1:B:143:PRO:HD3	1.88	0.43
1:A:95:LEU:HD13	1:A:116:ILE:CG2	2.49	0.43
1:B:6:LEU:HD23	1:B:416:MET:SD	2.59	0.43
1:B:19:ILE:HG23	1:B:160:TYR:HA	2.01	0.43
1:B:95:LEU:CD2	1:B:103:VAL:HG13	2.41	0.43
1:B:219:LYS:HA	1:B:219:LYS:HE2	2.00	0.43
1:A:63:LEU:HD22	1:A:77:LEU:HD23	2.00	0.43
1:A:66:PRO:O	1:A:67:ASP:HB2	2.19	0.43
1:A:70:PRO:HA	1:A:123:PHE:CG	2.53	0.43
1:A:116:ILE:CD1	1:A:116:ILE:N	2.81	0.43
1:B:158:ASP:O	1:B:180:LEU:HB3	2.19	0.43
1:B:394:GLY:O	1:B:395:GLY:C	2.57	0.43
1:B:81:ALA:CB	1:B:117:LEU:HD23	2.47	0.43
1:B:136:GLY:C	1:B:138:LYS:H	2.21	0.43
1:B:282:PRO:HB2	1:B:285:PHE:HE2	1.83	0.43
1:B:118:LEU:N	1:B:118:LEU:HD12	2.34	0.43
1:B:98:CYS:SG	1:B:124:HIS:CE1	3.12	0.43
1:B:104:GLU:OE1	1:B:155:LYS:HD2	2.19	0.43
1:B:227:LEU:HD12	1:B:227:LEU:HA	1.86	0.43
1:B:28:MET:HE2	1:B:33:ILE:HA	2.01	0.42
1:A:111:ASP:O	1:A:112:ASN:C	2.57	0.42
1:B:7:THR:O	1:B:11:VAL:HG23	2.19	0.42
1:B:66:PRO:HG3	1:B:120:ASN:OD1	2.19	0.42
1:A:5:LYS:HZ2	1:A:415:ASN:ND2	2.18	0.42
1:B:64:GLY:C	1:B:65:ARG:HD3	2.40	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:72:PRO:O	1:A:76:SER:HB2	2.20	0.42
1:B:331:LYS:NZ	2:B:430:HOH:O	2.52	0.42
1:B:160:TYR:HB2	1:B:178:VAL:CG1	2.46	0.42
1:B:6:LEU:HA	1:B:416:MET:SD	2.59	0.42
1:B:1:ALA:HA	1:B:201:GLU:CD	2.39	0.42
1:A:229:LYS:HB3	1:A:229:LYS:NZ	2.35	0.42
1:B:125:VAL:HG22	1:B:141:ALA:HB2	2.01	0.42
1:B:285:PHE:N	1:B:285:PHE:CD1	2.88	0.42
1:B:111:ASP:O	1:B:112:ASN:C	2.56	0.42
1:B:104:GLU:O	1:B:108:ALA:N	2.52	0.42
1:A:48:HIS:CD2	1:A:187:PHE:HZ	2.37	0.42
1:A:96:LYS:NZ	1:A:96:LYS:CB	2.82	0.42
1:B:335:TRP:CD1	1:B:335:TRP:C	2.94	0.42
1:B:161:VAL:HA	1:B:184:ALA:O	2.20	0.41
1:B:407:LEU:N	2:B:439:HOH:O	2.51	0.41
1:A:301:THR:CG2	1:A:302:ILE:N	2.83	0.41
1:A:259:GLU:HB3	1:B:10:LYS:HZ1	1.85	0.41
1:B:65:ARG:N	1:B:65:ARG:CD	2.83	0.41
1:A:242:THR:HG23	1:A:261:GLY:HA3	2.02	0.41
1:A:342:PHE:HA	1:A:348:ALA:HB2	2.02	0.41
1:B:13:LEU:HD12	1:B:52:ASN:CB	2.40	0.41
1:B:342:PHE:HA	1:B:348:ALA:HB2	2.02	0.41
1:A:160:TYR:HB2	1:A:180:LEU:HD12	2.03	0.41
1:A:226:MET:O	1:A:230:VAL:HG22	2.20	0.41
1:B:210:ILE:HG12	1:B:234:ILE:HD12	2.03	0.41
1:B:268:ILE:HG12	1:B:268:ILE:H	1.74	0.41
1:A:292:ASP:O	1:A:294:ASN:N	2.54	0.41
1:A:359:VAL:HG13	1:A:360:LYS:N	2.36	0.41
1:A:121:LEU:HB3	1:A:127:GLU:HG3	2.01	0.41
1:A:207:PHE:CD1	1:A:207:PHE:C	2.91	0.41
1:B:401:LEU:HD13	1:B:407:LEU:CD1	2.50	0.41
1:B:234:ILE:HG12	1:B:280:VAL:HG21	2.02	0.41
1:B:279:ILE:O	1:B:280:VAL:HG12	2.21	0.41
1:B:1:ALA:C	1:B:3:SER:N	2.70	0.41
1:A:335:TRP:CD1	1:A:336:ASN:N	2.89	0.41
1:A:208:LEU:HD13	1:A:326:ILE:CG2	2.51	0.41
1:A:78:GLU:N	1:A:79:PRO:CD	2.83	0.41
1:A:36:ASN:HD22	1:A:36:ASN:H	1.67	0.41
1:A:314:ASP:OD2	1:A:349:LYS:HB3	2.21	0.41
1:A:259:GLU:HB3	1:B:10:LYS:HZ2	1.84	0.40
1:A:17:ARG:NH1	1:A:158:ASP:OD1	2.52	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:221:GLN:HE22	1:A:405:LYS:HD3	1.85	0.40
1:B:95:LEU:HD13	1:B:116:ILE:CG2	2.50	0.40
1:B:216:VAL:HG23	1:B:258:ASP:OD2	2.21	0.40
1:A:116:ILE:HG22	1:A:117:LEU:N	2.36	0.40
1:A:150:ARG:HB3	1:A:177:GLY:O	2.22	0.40
1:B:70:PRO:O	1:B:71:MET:CG	2.70	0.40
1:B:192:GLU:OE1	1:B:390:HIS:NE2	2.46	0.40
1:B:234:ILE:HG12	1:B:280:VAL:HG22	2.04	0.40
1:A:260:GLU:O	1:A:261:GLY:C	2.60	0.40
1:A:119:GLU:CG	1:A:120:ASN:N	2.84	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	400/416 (96%)	337 (84%)	49 (12%)	14 (4%)	4	10
1	B	399/416 (96%)	344 (86%)	42 (10%)	13 (3%)	5	11
All	All	799/832 (96%)	681 (85%)	91 (11%)	27 (3%)	5	10

All (27) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	262	ALA
1	A	345	ASP
1	B	14	LYS
1	B	73	ASP
1	B	112	ASN
1	B	138	LYS
1	B	304	SER
1	A	74	LYS

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Mol	Chain	Res	Type
1	A	112	ASN
1	A	253	GLY
1	A	255	SER
1	A	293	GLU
1	A	395	GLY
1	B	51	ASP
1	B	61	SER
1	B	96	LYS
1	B	137	LYS
1	B	139	ILE
1	B	395	GLY
1	A	304	SER
1	B	134	SER
1	A	198	LYS
1	A	291	PHE
1	A	402	LEU
1	A	143	PRO
1	B	166	GLY
1	A	307	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	A	329/340 (97%)	296 (90%)	33 (10%)	9	22
1	B	319/340 (94%)	292 (92%)	27 (8%)	13	30
All	All	648/680 (95%)	588 (91%)	60 (9%)	11	25

All (60) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	LEU
1	A	34	THR
1	A	36	ASN
1	A	38	ARG

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Mol	Chain	Res	Type
1	A	50	LEU
1	A	93	ILE
1	A	102	GLU
1	A	109	ASN
1	A	115	ILE
1	A	118	LEU
1	A	127	GLU
1	A	142	ASP
1	A	162	ASN
1	A	183	LYS
1	A	207	PHE
1	A	208	LEU
1	A	215	LYS
1	A	227	LEU
1	A	229	LYS
1	A	246	GLU
1	A	256	LEU
1	A	257	PHE
1	A	259	GLU
1	A	260	GLU
1	A	263	THR
1	A	285	PHE
1	A	296	LYS
1	A	354	LEU
1	A	357	GLU
1	A	393	THR
1	A	399	LEU
1	A	410	VAL
1	A	413	LEU
1	B	6	LEU
1	B	9	ASP
1	B	29	LYS
1	B	43	ILE
1	B	50	LEU
1	B	51	ASP
1	B	52	ASN
1	B	65	ARG
1	B	88	LEU
1	B	91	ASP
1	B	92	VAL
1	B	118	LEU
1	B	120	ASN

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Mol	Chain	Res	Type
1	B	130	LYS
1	B	142	ASP
1	B	162	ASN
1	B	207	PHE
1	B	227	LEU
1	B	269	MET
1	B	270	GLU
1	B	280	VAL
1	B	285	PHE
1	B	297	VAL
1	B	351	THR
1	B	386	ASP
1	B	400	GLU
1	B	402	LEU

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

Mol	Chain	Res	Type
1	A	36	ASN
1	A	37	GLN
1	A	105	GLN
1	A	109	ASN
1	A	124	HIS
1	A	162	ASN
1	A	179	ASN
1	A	221	GLN
1	A	231	ASN
1	A	251	GLN
1	A	323	ASN
1	A	336	ASN
1	A	364	ASN
1	A	415	ASN
1	B	30	ASN
1	B	105	GLN
1	B	109	ASN
1	B	120	ASN
1	B	162	ASN
1	B	172	HIS
1	B	182	GLN
1	B	231	ASN
1	B	323	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	404/416 (97%)	-0.04	7 (1%) 73 74	4, 24, 38, 48	0
1	B	403/416 (96%)	-0.04	6 (1%) 76 76	11, 27, 39, 45	0
All	All	807/832 (96%)	-0.04	13 (1%) 74 75	4, 25, 38, 48	0

All (13) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	3	SER	4.3
1	B	1	ALA	4.2
1	A	1	ALA	3.5
1	B	135	SER	3.2
1	A	372	GLY	3.2
1	B	136	GLY	3.0
1	B	2	LEU	2.9
1	B	139	ILE	2.8
1	A	254	ALA	2.8
1	B	101	PRO	2.5
1	A	256	LEU	2.2
1	A	386	ASP	2.2
1	A	2	LEU	2.2

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

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

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.