



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 07:43 AM GMT

PDB ID : 3BWE  
Title : Crystal structure of aggregated form of DJ1  
Authors : Cha, S.S.  
Deposited on : 2008-01-09  
Resolution : 2.40 Å(reported)

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

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

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

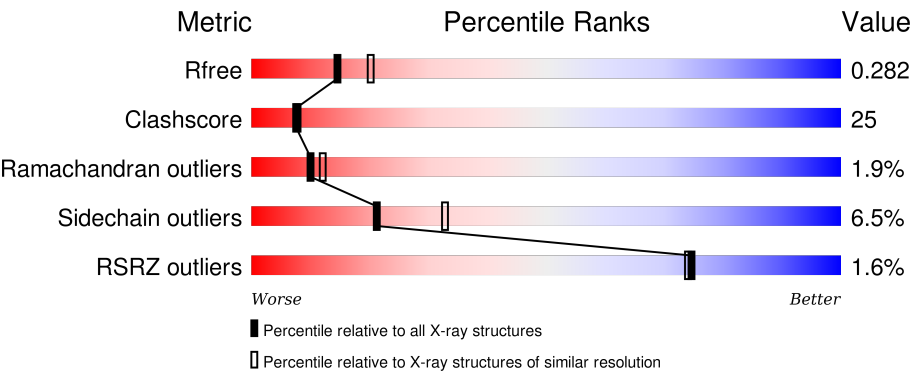
# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.40 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R <sub>free</sub>	91344	2919 (2.40-2.40)
Clashscore	102246	3407 (2.40-2.40)
Ramachandran outliers	100387	3351 (2.40-2.40)
Sidechain outliers	100360	3352 (2.40-2.40)
RSRZ outliers	91569	2928 (2.40-2.40)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=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	189	<div><div>%</div><div><div></div><div>62%</div><div>33%</div><div>• •</div></div></div>
1	B	189	<div><div></div><div>62%</div><div>33%</div><div>• •</div></div>
1	C	189	<div><div>%</div><div><div></div><div>56%</div><div>37%</div><div>7%</div><div>•</div></div></div>
1	D	189	<div><div></div><div>59%</div><div>34%</div><div>5%</div><div>•</div></div>
1	E	189	<div><div>4%</div><div><div></div><div>46%</div><div>48%</div><div>6%</div><div>•</div></div></div>

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Mol	Chain	Length	Quality of chain
1	F	189	<div> <div>%</div> <div> <div></div> <div>60%</div> <div>35%</div> <div>• •</div> </div> </div>
1	G	189	<div> <div>4%</div> <div> <div></div> <div>49%</div> <div>45%</div> <div>• •</div> </div> </div>

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	PO4	A	191	-	-	-	X
2	PO4	C	3	-	-	-	X

## 2 Entry composition [i](#)

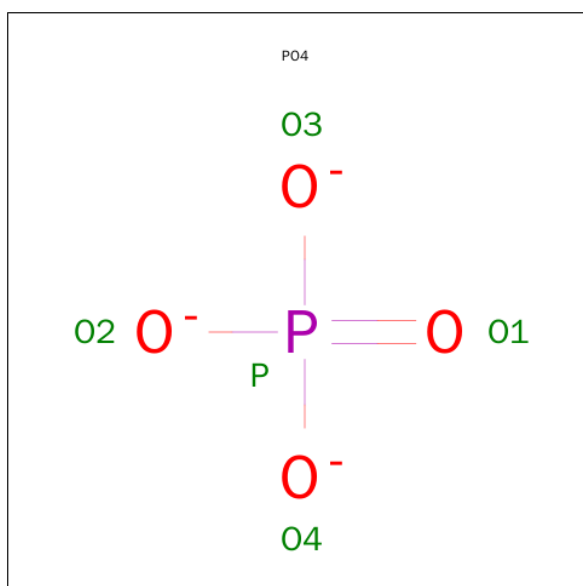
There are 3 unique types of molecules in this entry. The entry contains 9808 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Protein DJ-1.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	188	Total	C	N	O	S	Se	0	0	0
			1368	859	238	264	3	4			
1	B	187	Total	C	N	O	S	Se	0	0	0
			1363	857	238	261	3	4			
1	C	188	Total	C	N	O	S	Se	0	0	0
			1368	859	238	264	3	4			
1	D	186	Total	C	N	O	S	Se	0	0	0
			1358	854	237	260	3	4			
1	E	188	Total	C	N	O	S	Se	0	0	0
			1351	849	238	257	3	4			
1	F	186	Total	C	N	O	S	Se	0	0	0
			1350	849	236	258	3	4			
1	G	186	Total	C	N	O	S	Se	0	0	0
			1332	838	231	256	3	4			

- Molecule 2 is PHOSPHATE ION (three-letter code: PO4) (formula: O<sub>4</sub>P).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	P	0	0
			5	4	1		
2	A	1	Total	O	P	0	0
			5	4	1		
2	C	1	Total	O	P	0	0
			5	4	1		
2	D	1	Total	O	P	0	0
			5	4	1		
2	E	1	Total	O	P	0	0
			5	4	1		
2	F	1	Total	O	P	0	0
			5	4	1		
2	F	1	Total	O	P	0	0
			5	4	1		

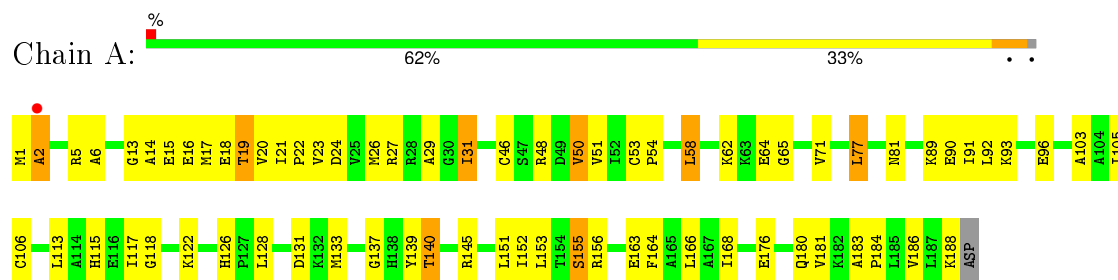
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	37	Total	O	0	0
			37	37		
3	B	60	Total	O	0	0
			60	60		
3	C	56	Total	O	0	0
			56	56		
3	D	54	Total	O	0	0
			54	54		
3	E	42	Total	O	0	0
			42	42		
3	F	22	Total	O	0	0
			22	22		
3	G	12	Total	O	0	0
			12	12		

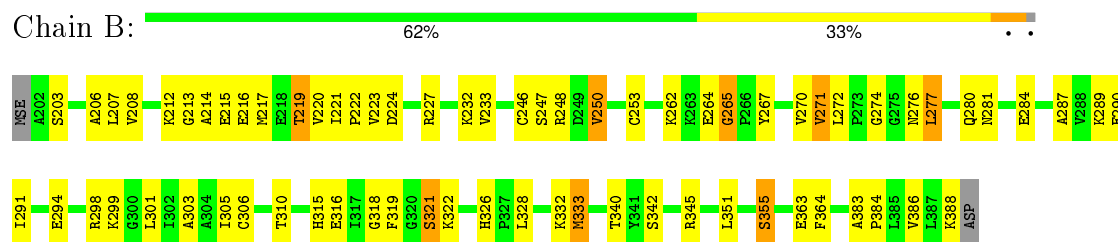
### 3 Residue-property plots

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.

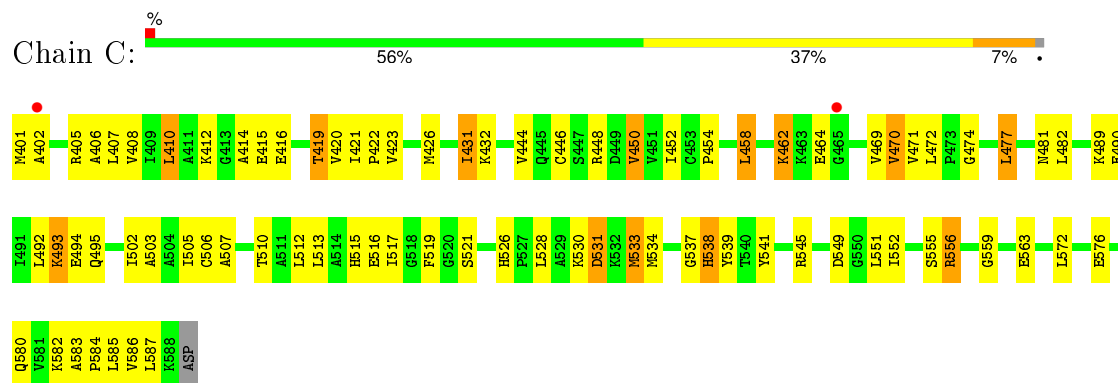
#### • Molecule 1: Protein DJ-1



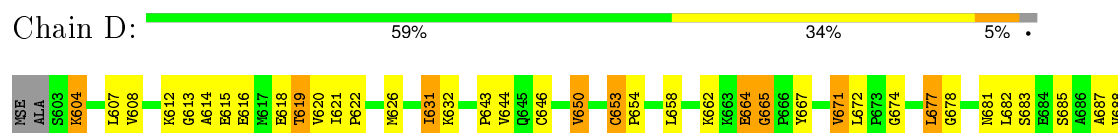
#### • Molecule 1: Protein DJ-1



#### • Molecule 1: Protein DJ-1

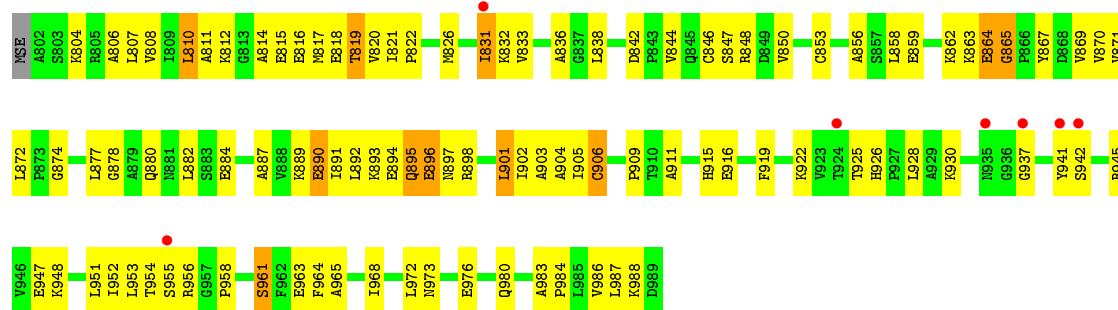


#### • Molecule 1: Protein DJ-1

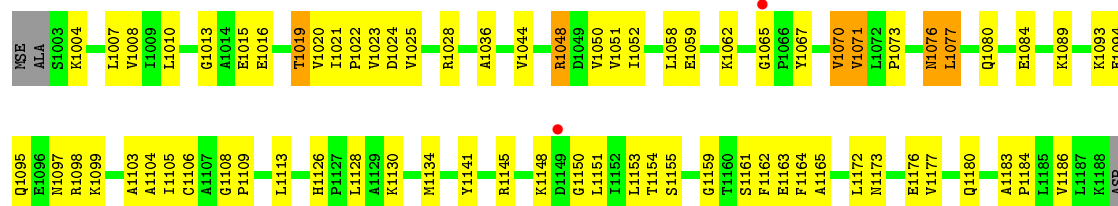




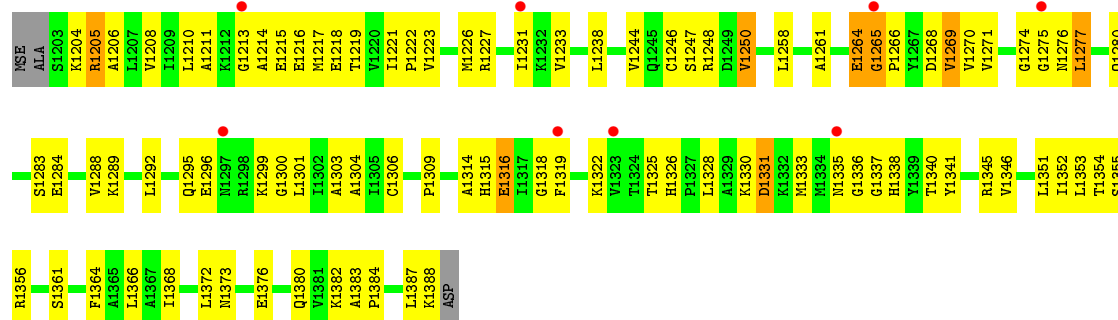
• Molecule 1: Protein DJ-1



• Molecule 1: Protein DJ-1



• Molecule 1: Protein DJ-1



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	193.62Å 102.58Å 85.53Å 90.00° 113.69° 90.00°	Depositor
Resolution (Å)	19.99 – 2.40 53.63 – 2.40	Depositor EDS
% Data completeness (in resolution range)	94.5 (19.99-2.40) 94.6 (53.63-2.40)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.05 (at 2.39Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, $R_{free}$	0.232 , 0.282 0.232 , 0.282	Depositor DCC
$R_{free}$ test set	5760 reflections (10.17%)	DCC
Wilson B-factor (Å <sup>2</sup> )	27.8	Xtriage
Anisotropy	0.396	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 45.1	EDS
Estimated twinning fraction	0.023 for -h-2*k,l	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	1 of 56720 reflections (0.002%)	Xtriage
$F_o, F_c$ correlation	0.91	EDS
Total number of atoms	9808	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.36% of the height of the origin peak. No significant pseudotranslation is detected.*

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

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



## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: PO4

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	0.38	0/1381	0.65	0/1863
1	B	0.39	0/1376	0.65	0/1855
1	C	0.40	0/1381	0.67	1/1863 (0.1%)
1	D	0.40	0/1371	0.69	0/1848
1	E	0.38	0/1364	0.66	0/1840
1	F	0.38	0/1363	0.65	0/1839
1	G	0.39	0/1345	0.65	0/1819
All	All	0.39	0/9581	0.66	1/12927 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	556	ARG	N-CA-C	5.06	124.66	111.00

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	1368	0	1403	70	0
1	B	1363	0	1405	66	0
1	C	1368	0	1399	80	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	D	1358	0	1399	64	0
1	E	1351	0	1377	83	0
1	F	1350	0	1385	52	0
1	G	1332	0	1348	97	0
2	A	10	0	0	0	0
2	C	5	0	0	0	0
2	D	5	0	0	0	0
2	E	5	0	0	0	0
2	F	10	0	0	0	0
3	A	37	0	0	1	0
3	B	60	0	0	4	0
3	C	56	0	0	2	0
3	D	54	0	0	1	0
3	E	42	0	0	2	0
3	F	22	0	0	1	0
3	G	12	0	0	1	0
All	All	9808	0	9716	487	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 25.

All (487) 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:113:LEU:HB2	1:A:133:MSE:HE1	1.23	1.15
1:B:203:SER:HB2	1:B:232:LYS:HE2	1.38	1.05
1:G:1205:ARG:HH11	1:G:1205:ARG:HB3	0.90	1.04
1:G:1205:ARG:NH1	1:G:1205:ARG:HB3	1.73	1.03
1:G:1205:ARG:CB	1:G:1205:ARG:HH11	1.75	0.98
1:A:16:GLU:HG2	1:A:50:VAL:HG22	1.45	0.95
1:A:6:ALA:HB2	1:A:31:ILE:HD11	1.47	0.94
1:D:705:ILE:HG13	1:D:755:SER:HB3	1.50	0.94
1:F:1070:VAL:HG12	1:F:1095:GLN:HE21	1.34	0.91
1:E:831:ILE:HD11	1:E:833:VAL:HG22	1.52	0.91
1:G:1221:ILE:HB	1:G:1222:PRO:HD3	1.51	0.91
1:E:948:LYS:HD3	1:E:953:LEU:HD12	1.53	0.90
1:F:1134:MSE:HE2	1:F:1141:TYR:HB2	1.55	0.89
1:B:383:ALA:HB3	1:B:384:PRO:HD3	1.54	0.88
1:B:310:THR:HA	1:B:333:MSE:HE1	1.56	0.88
1:A:113:LEU:HB2	1:A:133:MSE:CE	2.03	0.88
1:A:92:LEU:HB3	1:A:117:ILE:CD1	2.05	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:333:MSE:HA	1:B:333:MSE:CE	2.06	0.84
1:C:416:GLU:OE2	1:C:450:VAL:HG13	1.77	0.83
1:B:290:GLU:O	1:B:294:GLU:HG3	1.78	0.83
1:G:1383:ALA:HB3	1:G:1384:PRO:HD3	1.59	0.82
1:C:583:ALA:HB3	1:C:584:PRO:HD3	1.61	0.82
1:A:62:LYS:HE2	1:A:91:ILE:HG13	1.62	0.82
1:A:183:ALA:HB3	1:A:184:PRO:HD3	1.59	0.82
1:A:156:ARG:HG2	1:A:156:ARG:HH11	1.44	0.81
1:B:280:GLN:O	1:B:284:GLU:HG3	1.79	0.81
1:E:816:GLU:HG2	1:E:850:VAL:HG13	1.62	0.80
1:G:1210:LEU:HD12	1:G:1244:VAL:HG21	1.63	0.80
1:E:815:GLU:O	1:E:819:THR:HG22	1.82	0.80
1:B:305:ILE:HG13	1:B:355:SER:HB3	1.62	0.80
1:D:615:GLU:O	1:D:619:THR:HG22	1.82	0.80
1:A:16:GLU:HG2	1:A:50:VAL:CG2	2.13	0.79
1:C:526:HIS:HD2	1:C:528:LEU:H	1.30	0.78
1:C:410:LEU:HD22	1:C:444:VAL:HG11	1.66	0.76
1:C:406:ALA:HB2	1:C:431:ILE:HD11	1.67	0.75
1:B:318:GLY:O	1:B:321:SER:HB2	1.86	0.75
1:F:1148:LYS:HE2	1:F:1150:GLY:O	1.86	0.75
1:F:1016:GLU:HG2	1:F:1050:VAL:HG13	1.68	0.75
1:C:492:LEU:HB3	1:C:517:ILE:HD13	1.68	0.74
1:G:1295:GLN:NE2	1:G:1300:GLY:HA3	2.03	0.74
1:A:133:MSE:HA	1:A:133:MSE:HE3	1.68	0.74
1:A:13:GLY:HA3	1:A:77:LEU:HB3	1.70	0.74
1:B:333:MSE:HA	1:B:333:MSE:HE3	1.69	0.73
1:G:1213:GLY:HA2	1:G:1277:LEU:HD12	1.70	0.73
1:B:310:THR:HA	1:B:333:MSE:CE	2.17	0.73
1:D:621:ILE:HB	1:D:622:PRO:HD3	1.70	0.73
1:G:1264:GLU:O	1:G:1265:GLY:O	2.06	0.73
1:A:16:GLU:OE2	1:A:50:VAL:HG13	1.89	0.73
1:E:816:GLU:HG2	1:E:850:VAL:CG1	2.20	0.72
1:G:1210:LEU:CD1	1:G:1244:VAL:HG11	2.18	0.72
1:A:6:ALA:CB	1:A:31:ILE:HD11	2.19	0.72
1:F:1105:ILE:HG13	1:F:1155:SER:HB3	1.72	0.72
1:C:416:GLU:HG3	1:C:446:CYS:CB	2.20	0.72
1:A:16:GLU:HG3	1:A:46:CYS:CB	2.20	0.71
1:C:516:GLU:HA	1:C:519:PHE:CE1	2.26	0.71
1:G:1210:LEU:C	1:G:1210:LEU:HD13	2.10	0.71
1:E:863:LYS:O	1:E:865:GLY:N	2.23	0.70
1:G:1213:GLY:HA3	1:G:1277:LEU:HB2	1.71	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:905:ILE:HG13	1:E:955:SER:HB3	1.73	0.70
1:F:1013:GLY:HA3	1:F:1077:LEU:HB3	1.71	0.70
1:D:616:GLU:HG2	1:D:650:VAL:HG22	1.73	0.70
1:G:1214:ALA:O	1:G:1246:CYS:HB3	1.91	0.70
1:G:1213:GLY:CA	1:G:1277:LEU:HD12	2.23	0.69
1:G:1216:GLU:OE2	1:G:1216:GLU:N	2.23	0.69
1:B:232:LYS:HD2	1:C:401:MSE:O	1.91	0.69
1:A:16:GLU:HG3	1:A:46:CYS:HB2	1.73	0.69
1:B:208:VAL:HG22	1:B:271:VAL:HG22	1.73	0.69
1:D:722:LYS:HE2	1:D:742:SER:HB2	1.76	0.68
1:E:821:ILE:HB	1:E:822:PRO:HD3	1.75	0.68
1:B:216:GLU:HG2	1:B:250:VAL:HG22	1.76	0.67
1:D:674:GLY:HA3	1:D:706:CYS:HB3	1.76	0.67
1:G:1219:THR:O	1:G:1223:VAL:HG23	1.94	0.67
1:F:1183:ALA:HB3	1:F:1184:PRO:HD3	1.76	0.67
1:G:1210:LEU:HD11	1:G:1244:VAL:HG11	1.75	0.67
1:C:526:HIS:CD2	1:C:528:LEU:H	2.13	0.67
1:G:1216:GLU:HG2	1:G:1250:VAL:HG22	1.77	0.66
1:E:859:GLU:HA	1:E:862:LYS:NZ	2.10	0.66
1:G:1204:LYS:O	1:G:1231:ILE:HG13	1.95	0.66
1:G:1275:GLY:O	1:G:1277:LEU:HG	1.95	0.66
1:G:1316:GLU:HB3	1:G:1319:PHE:CE2	2.31	0.66
1:A:21:ILE:HB	1:A:22:PRO:HD3	1.76	0.66
1:C:416:GLU:HG3	1:C:446:CYS:HB2	1.78	0.66
1:F:1016:GLU:HG3	1:F:1050:VAL:HG22	1.78	0.66
1:E:810:LEU:HD22	1:E:844:VAL:HG11	1.78	0.66
1:G:1210:LEU:HD13	1:G:1211:ALA:N	2.10	0.65
1:A:122:LYS:HG3	1:A:140:THR:HG22	1.77	0.65
1:D:783:ALA:HB3	1:D:784:PRO:HD3	1.79	0.65
1:E:877:LEU:HB2	1:G:1376:GLU:HG3	1.79	0.65
1:E:906:CYS:HA	1:E:956:ARG:O	1.97	0.65
1:B:213:GLY:HA3	1:B:277:LEU:HB3	1.79	0.65
1:E:804:LYS:HG2	1:E:973:ASN:HD21	1.61	0.64
1:A:26:MSE:O	1:A:31:ILE:HG23	1.97	0.64
1:B:345:ARG:HD3	1:B:363:GLU:OE1	1.97	0.64
1:D:687:ALA:O	1:D:691:ILE:HG12	1.98	0.64
1:F:1108:GLY:N	1:F:1109:PRO:HD2	2.13	0.63
1:C:533:MSE:CE	1:C:533:MSE:HA	2.28	0.63
1:B:333:MSE:HA	1:B:333:MSE:HE2	1.80	0.63
1:B:345:ARG:NH2	1:B:363:GLU:OE2	2.31	0.63
1:F:1019:THR:HG22	1:F:1073:PRO:HB3	1.80	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:662:LYS:HD3	1:D:691:ILE:HD11	1.79	0.63
1:C:551:LEU:C	1:C:552:ILE:HD12	2.19	0.63
1:A:113:LEU:CB	1:A:133:MSE:HE1	2.15	0.63
1:D:631:ILE:HD12	1:D:632:LYS:N	2.13	0.63
1:A:156:ARG:NH1	1:A:156:ARG:HG2	2.09	0.63
1:D:745:ARG:HA	1:D:756:ARG:HG3	1.79	0.63
1:G:1217:MSE:O	1:G:1221:ILE:HG12	1.99	0.62
1:C:510:THR:HA	1:C:533:MSE:HE1	1.80	0.62
1:E:826:MSE:HE2	1:E:831:ILE:HG12	1.80	0.62
1:C:582:LYS:HA	1:C:585:LEU:HD12	1.80	0.62
1:G:1275:GLY:O	1:G:1276:ASN:HB3	1.98	0.62
1:B:316:GLU:HA	1:B:319:PHE:CE1	2.34	0.62
1:E:814:ALA:O	1:E:846:CYS:HB3	1.99	0.62
1:E:880:GLN:O	1:E:884:GLU:HG3	1.99	0.62
1:E:808:VAL:HG22	1:E:871:VAL:CG1	2.29	0.62
1:F:1016:GLU:HG2	1:F:1050:VAL:CG1	2.29	0.61
1:D:786:VAL:HG12	1:D:786:VAL:O	2.00	0.61
1:E:986:VAL:HG12	1:E:986:VAL:O	2.00	0.61
1:A:58:LEU:O	1:A:62:LYS:HB2	2.01	0.61
1:E:816:GLU:OE1	1:E:850:VAL:HG13	2.01	0.61
1:G:1330:LYS:HE3	1:G:1341:TYR:CD2	2.36	0.61
1:F:1080:GLN:O	1:F:1084:GLU:HG3	2.01	0.61
1:D:705:ILE:CG1	1:D:755:SER:HB3	2.29	0.61
1:A:1:MSE:O	1:A:2:ALA:HB3	2.00	0.61
1:E:976:GLU:O	1:E:980:GLN:HG3	2.01	0.61
1:G:1216:GLU:HG3	1:G:1246:CYS:HB2	1.81	0.60
1:F:1089:LYS:O	1:F:1093:LYS:HG2	2.01	0.60
1:E:831:ILE:HD11	1:E:833:VAL:CG2	2.27	0.60
1:D:616:GLU:HG2	1:D:650:VAL:CG2	2.31	0.60
1:C:408:VAL:HG22	1:C:471:VAL:CG2	2.32	0.60
1:C:408:VAL:HG22	1:C:471:VAL:HG22	1.84	0.60
1:C:416:GLU:HG2	1:C:450:VAL:HG13	1.84	0.60
1:B:208:VAL:HG22	1:B:271:VAL:CG2	2.30	0.60
1:A:126:HIS:CD2	1:A:128:LEU:H	2.20	0.60
1:A:145:ARG:HD3	1:A:163:GLU:OE1	2.01	0.60
1:F:1059:GLU:HA	1:F:1062:LYS:HE3	1.82	0.60
1:G:1216:GLU:HG3	1:G:1246:CYS:CB	2.31	0.59
1:E:901:LEU:HD12	1:E:972:LEU:HD11	1.84	0.59
1:G:1216:GLU:HG2	1:G:1250:VAL:CG2	2.31	0.59
1:A:53:CYS:SG	1:B:253:CYS:SG	3.00	0.59
1:D:626:MSE:HB3	1:D:631:ILE:HG12	1.85	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:847:SER:OG	1:E:848:ARG:NH1	2.31	0.59
1:G:1325:THR:HG21	1:G:1333:MSE:HB2	1.83	0.59
1:A:105:ILE:HG13	1:A:155:SER:HB3	1.83	0.59
1:E:887:ALA:O	1:E:890:GLU:HB2	2.03	0.59
1:B:332:LYS:HE2	3:B:439:HOH:O	2.03	0.59
1:A:133:MSE:HE2	1:A:139:TYR:CE1	2.38	0.59
1:B:262:LYS:HD2	3:B:435:HOH:O	2.02	0.59
1:C:420:VAL:HG21	1:D:620:VAL:HG21	1.85	0.58
1:E:826:MSE:HE2	1:E:831:ILE:CD1	2.33	0.58
1:E:922:LYS:HG2	1:E:947:GLU:HG2	1.85	0.58
1:A:14:ALA:O	1:A:46:CYS:HB3	2.04	0.58
1:E:838:LEU:HD12	1:E:858:LEU:HD22	1.86	0.58
1:G:1376:GLU:O	1:G:1380:GLN:HG3	2.03	0.58
1:C:415:GLU:O	1:C:419:THR:HG22	2.04	0.58
1:E:831:ILE:HD12	1:E:831:ILE:C	2.24	0.58
1:A:96:GLU:CD	1:A:117:ILE:HG23	2.25	0.58
1:E:889:LYS:HB2	1:E:915:HIS:ND1	2.19	0.57
1:B:216:GLU:OE1	1:B:248:ARG:N	2.35	0.57
1:C:545:ARG:HD3	1:C:563:GLU:OE1	2.03	0.57
1:B:326:HIS:CD2	1:B:328:LEU:H	2.22	0.57
1:F:1104:ALA:O	1:F:1154:THR:HA	2.04	0.57
1:D:608:VAL:HG13	1:D:671:VAL:CG2	2.33	0.57
1:C:533:MSE:HE3	1:C:533:MSE:HA	1.86	0.57
1:F:1024:ASP:O	1:F:1028:ARG:HG3	2.05	0.57
1:G:1216:GLU:CG	1:G:1250:VAL:HG22	2.34	0.57
1:E:902:ILE:HD12	1:E:902:ILE:C	2.25	0.57
1:G:1351:LEU:O	1:G:1352:ILE:HD12	2.05	0.57
1:F:1015:GLU:O	1:F:1019:THR:HG23	2.04	0.57
1:E:826:MSE:HB3	1:E:831:ILE:CG1	2.35	0.56
1:G:1218:GLU:OE1	1:G:1306:CYS:HB2	2.05	0.56
1:E:983:ALA:HB3	1:E:984:PRO:HD3	1.87	0.56
1:G:1216:GLU:HG2	1:G:1250:VAL:HG13	1.87	0.56
1:G:1303:ALA:HA	1:G:1353:LEU:O	2.06	0.56
1:A:145:ARG:NH2	1:A:163:GLU:OE2	2.39	0.56
1:F:1021:ILE:O	1:F:1025:VAL:HG23	2.06	0.56
1:B:384:PRO:O	1:B:386:VAL:HG23	2.06	0.56
1:E:859:GLU:HA	1:E:862:LYS:HZ2	1.70	0.56
1:G:1238:LEU:HD12	1:G:1258:LEU:HD12	1.86	0.56
1:A:16:GLU:CG	1:A:50:VAL:HG22	2.29	0.56
1:D:616:GLU:CG	1:D:650:VAL:HG22	2.35	0.55
1:C:521:SER:HA	1:C:549:ASP:OD2	2.06	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:1289:LYS:HG3	1:G:1315:HIS:CG	2.41	0.55
1:B:216:GLU:CG	1:B:250:VAL:HG22	2.35	0.55
1:F:1008:VAL:HG22	1:F:1071:VAL:HG22	1.89	0.55
1:A:126:HIS:HD2	1:A:128:LEU:H	1.53	0.55
1:C:474:GLY:HA3	1:C:506:CYS:HB3	1.87	0.55
1:C:421:ILE:HB	1:C:422:PRO:HD3	1.89	0.54
1:B:287:ALA:O	1:B:291:ILE:HG12	2.07	0.54
1:G:1210:LEU:HD11	1:G:1244:VAL:CG1	2.37	0.54
1:D:723:VAL:HB	1:D:754:THR:HG21	1.89	0.54
1:C:416:GLU:HG2	1:C:450:VAL:HG22	1.90	0.54
1:E:821:ILE:HD12	1:E:961:SER:HB3	1.89	0.54
1:E:838:LEU:HD12	1:E:858:LEU:CD2	2.37	0.54
1:B:215:GLU:O	1:B:219:THR:HG22	2.07	0.54
1:C:414:ALA:O	1:C:446:CYS:HB3	2.08	0.54
1:A:24:ASP:CG	1:B:217:MSE:HE2	2.28	0.54
1:A:15:GLU:O	1:A:19:THR:HG22	2.07	0.54
1:A:20:VAL:HG21	1:B:220:VAL:HG21	1.90	0.53
1:F:1008:VAL:HG22	1:F:1071:VAL:CG2	2.39	0.53
1:B:322:LYS:HE2	1:B:342:SER:HB2	1.90	0.53
1:G:1280:GLN:HG2	1:G:1284:GLU:OE2	2.08	0.53
1:B:298:ARG:HG2	1:B:298:ARG:O	2.08	0.53
1:E:872:LEU:HD23	1:E:911:ALA:HB3	1.90	0.53
1:G:1216:GLU:HG2	1:G:1250:VAL:CG1	2.38	0.53
1:B:301:LEU:HD12	1:B:351:LEU:O	2.09	0.53
1:D:689:LYS:HB2	1:D:715:HIS:ND1	2.24	0.53
1:G:1345:ARG:HG2	1:G:1345:ARG:HH11	1.74	0.53
1:C:462:LYS:HD2	1:C:462:LYS:O	2.09	0.53
1:C:477:LEU:HD22	1:C:481:ASN:ND2	2.24	0.53
1:F:1021:ILE:HB	1:F:1022:PRO:HD3	1.90	0.53
1:A:92:LEU:HB3	1:A:117:ILE:HD12	1.89	0.53
1:E:816:GLU:CG	1:E:850:VAL:HG13	2.35	0.53
1:B:355:SER:HB2	1:B:364:PHE:CD1	2.43	0.53
1:B:216:GLU:HG2	1:B:250:VAL:CG2	2.38	0.53
1:A:155:SER:HB2	1:A:164:PHE:CD1	2.44	0.53
1:D:608:VAL:HG13	1:D:671:VAL:HG22	1.91	0.53
1:E:987:LEU:HD23	1:F:1159:GLY:CA	2.39	0.53
1:F:1022:PRO:HA	1:F:1165:ALA:HB2	1.91	0.52
1:A:151:LEU:C	1:A:152:ILE:HD12	2.30	0.52
1:F:1177:VAL:HG23	3:F:164:HOH:O	2.08	0.52
1:E:901:LEU:HD12	1:E:972:LEU:CD1	2.38	0.52
1:D:672:LEU:N	1:D:672:LEU:HD12	2.24	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:221:ILE:HB	1:B:222:PRO:HD3	1.92	0.52
1:A:16:GLU:O	1:A:20:VAL:HG23	2.10	0.52
1:E:818:GLU:OE2	1:E:874:GLY:HA3	2.10	0.52
1:D:745:ARG:HG3	3:D:123:HOH:O	2.08	0.52
1:G:1268:ASP:O	1:G:1269:VAL:HB	2.10	0.52
1:D:622:PRO:O	1:D:626:MSE:HG3	2.09	0.52
1:D:677:LEU:HD22	1:D:681:ASN:ND2	2.24	0.52
1:B:227:ARG:HD3	3:B:395:HOH:O	2.09	0.52
1:A:5:ARG:HH22	1:A:64:GLU:HG2	1.74	0.52
1:C:545:ARG:NH1	1:D:786:VAL:O	2.43	0.52
1:A:92:LEU:HB3	1:A:117:ILE:HD11	1.91	0.52
1:B:223:VAL:O	1:B:227:ARG:HG3	2.10	0.52
1:D:678:GLY:O	1:D:682:LEU:HD13	2.08	0.52
1:B:212:LYS:O	1:B:277:LEU:HD13	2.10	0.51
1:G:1322:LYS:HA	1:G:1340:THR:HB	1.90	0.51
1:G:1316:GLU:HA	1:G:1319:PHE:CZ	2.45	0.51
1:E:987:LEU:HD23	1:F:1159:GLY:HA2	1.91	0.51
1:A:188:LYS:N	1:B:345:ARG:NH1	2.58	0.51
1:C:510:THR:HA	1:C:533:MSE:CE	2.40	0.51
1:D:616:GLU:HG3	1:D:646:CYS:HB2	1.93	0.51
1:G:1213:GLY:O	1:G:1277:LEU:HD12	2.10	0.51
1:D:745:ARG:NH2	1:D:760:THR:HG22	2.26	0.51
1:E:807:LEU:HB2	1:E:867:TYR:CG	2.45	0.51
1:C:490:GLU:HG2	1:C:494:GLU:OE2	2.10	0.51
1:F:1094:GLU:O	1:F:1098:ARG:HB2	2.10	0.51
1:B:214:ALA:O	1:B:246:CYS:HB3	2.10	0.51
1:G:1223:VAL:O	1:G:1227:ARG:HG3	2.11	0.51
1:G:1366:LEU:HD11	1:G:1382:LYS:HG3	1.93	0.51
1:C:586:VAL:HG12	1:C:586:VAL:O	2.10	0.51
1:C:426:MSE:O	1:C:431:ILE:HG23	2.10	0.51
1:G:1326:HIS:CD2	1:G:1328:LEU:H	2.29	0.51
1:D:604:LYS:HB3	1:D:772:LEU:HD23	1.93	0.51
1:G:1208:VAL:HG22	1:G:1271:VAL:CG2	2.40	0.51
1:D:616:GLU:HG2	1:D:650:VAL:HG13	1.92	0.50
1:C:408:VAL:HA	1:C:471:VAL:HG22	1.93	0.50
1:D:643:PRO:HG3	1:D:653:CYS:HB3	1.93	0.50
1:D:734:MSE:HE1	1:D:739:TYR:O	2.10	0.50
1:B:271:VAL:HA	1:B:303:ALA:O	2.10	0.50
1:F:1036:ALA:HB1	1:F:1058:LEU:HA	1.92	0.50
1:C:416:GLU:CG	1:C:446:CYS:HB2	2.41	0.50
1:E:826:MSE:HE2	1:E:831:ILE:CG1	2.41	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:471:VAL:HA	1:C:503:ALA:O	2.10	0.50
1:G:1216:GLU:CG	1:G:1246:CYS:HB2	2.42	0.50
1:C:513:LEU:HB3	1:C:533:MSE:HE1	1.94	0.50
1:F:1176:GLU:O	1:F:1180:GLN:HG3	2.10	0.50
1:A:126:HIS:HE1	1:B:384:PRO:O	1.94	0.50
1:C:416:GLU:HG2	1:C:450:VAL:CG1	2.42	0.49
1:B:326:HIS:HD2	1:B:328:LEU:H	1.58	0.49
1:G:1215:GLU:HA	1:G:1247:SER:OG	2.12	0.49
1:D:723:VAL:HG21	1:D:733:MSE:CE	2.42	0.49
1:G:1345:ARG:HG2	1:G:1345:ARG:NH1	2.27	0.49
1:E:806:ALA:HB2	1:E:826:MSE:HE1	1.93	0.49
1:C:494:GLU:HA	3:C:237:HOH:O	2.11	0.49
1:A:89:LYS:HB2	1:A:115:HIS:CE1	2.47	0.49
1:F:1019:THR:O	1:F:1023:VAL:HG23	2.11	0.49
1:E:926:HIS:CD2	1:E:928:LEU:H	2.30	0.49
1:E:902:ILE:CG1	1:E:952:ILE:HD13	2.42	0.49
1:A:77:LEU:HD22	1:A:81:ASN:ND2	2.26	0.49
1:E:902:ILE:HD12	1:E:902:ILE:O	2.13	0.49
1:E:964:PHE:O	1:E:968:ILE:HG13	2.12	0.49
1:A:16:GLU:CG	1:A:46:CYS:HB2	2.41	0.49
1:E:816:GLU:HG3	1:E:846:CYS:CB	2.42	0.49
1:G:1210:LEU:C	1:G:1210:LEU:CD1	2.79	0.49
1:B:216:GLU:HG3	1:B:246:CYS:HB2	1.95	0.49
1:A:103:ALA:HA	1:A:153:LEU:O	2.12	0.49
1:D:616:GLU:HG3	1:D:646:CYS:CB	2.43	0.49
1:B:345:ARG:HH21	1:B:363:GLU:CD	2.17	0.49
1:C:405:ARG:NH2	1:C:464:GLU:O	2.46	0.49
1:E:916:GLU:HA	1:E:919:PHE:CE2	2.47	0.49
1:E:836:ALA:HA	1:E:856:ALA:O	2.13	0.49
1:B:274:GLY:HA3	1:B:306:CYS:HB3	1.95	0.48
1:C:472:LEU:HD11	1:C:492:LEU:HD11	1.95	0.48
1:E:878:GLY:O	1:E:882:LEU:HG	2.12	0.48
1:B:310:THR:HG22	1:B:333:MSE:HE3	1.94	0.48
1:C:431:ILE:HD12	1:C:572:LEU:HD23	1.95	0.48
1:C:492:LEU:HB3	1:C:517:ILE:CD1	2.40	0.48
1:E:945:ARG:HD3	1:E:963:GLU:OE1	2.14	0.48
1:G:1303:ALA:HB1	1:G:1364:PHE:CZ	2.49	0.48
1:D:607:LEU:HB2	1:D:667:TYR:CG	2.48	0.48
1:G:1277:LEU:N	1:G:1277:LEU:HD23	2.28	0.48
1:G:1216:GLU:OE1	1:G:1248:ARG:N	2.43	0.48
1:A:117:ILE:HG22	1:A:118:GLY:N	2.29	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:1335:ASN:O	1:G:1336:GLY:C	2.52	0.48
1:E:951:LEU:N	1:E:951:LEU:HD22	2.29	0.47
1:C:489:LYS:HG2	1:C:493:LYS:CE	2.44	0.47
1:E:831:ILE:HD12	1:E:832:LYS:N	2.29	0.47
1:G:1204:LYS:HG2	1:G:1373:ASN:HD21	1.79	0.47
1:E:894:GLU:O	1:E:897:ASN:HB3	2.14	0.47
1:G:1330:LYS:HG3	1:G:1341:TYR:CE1	2.50	0.47
1:G:1299:LYS:C	1:G:1351:LEU:HD13	2.35	0.47
1:D:683:SER:OG	1:D:711:ALA:HA	2.14	0.47
1:D:616:GLU:HG2	1:D:650:VAL:CG1	2.44	0.47
1:C:583:ALA:CB	1:C:584:PRO:HD3	2.40	0.47
1:B:305:ILE:CG1	1:B:355:SER:HB3	2.38	0.47
1:C:406:ALA:CB	1:C:431:ILE:HD11	2.40	0.47
1:C:519:PHE:CD2	1:C:538:HIS:HB3	2.49	0.47
1:G:1326:HIS:HD2	1:G:1328:LEU:H	1.63	0.47
1:C:505:ILE:HG13	1:C:555:SER:HB3	1.97	0.47
1:B:262:LYS:HE2	1:B:262:LYS:HB3	1.68	0.47
1:E:872:LEU:HD21	1:E:892:LEU:HD11	1.97	0.47
1:F:1145:ARG:NH2	1:F:1163:GLU:OE2	2.48	0.47
1:B:289:LYS:HG3	1:B:315:HIS:HB3	1.96	0.47
1:C:587:LEU:HD23	1:D:759:GLY:HA2	1.97	0.47
1:G:1206:ALA:HB2	1:G:1231:ILE:HD11	1.97	0.47
1:G:1206:ALA:HB3	1:G:1233:VAL:HG22	1.97	0.47
1:G:1296:GLU:OE2	1:G:1318:GLY:N	2.48	0.47
1:D:704:ALA:O	1:D:754:THR:HA	2.14	0.47
1:A:186:VAL:HG12	1:A:186:VAL:O	2.15	0.46
1:G:1330:LYS:O	1:G:1331:ASP:C	2.54	0.46
1:A:1:MSE:O	1:A:2:ALA:CB	2.63	0.46
1:C:469:VAL:HG22	1:C:470:VAL:N	2.29	0.46
1:F:1161:SER:O	1:F:1164:PHE:HB3	2.15	0.46
1:A:164:PHE:O	1:A:168:ILE:HG13	2.14	0.46
1:D:726:HIS:CD2	1:D:728:LEU:H	2.32	0.46
1:C:526:HIS:HA	1:C:556:ARG:O	2.15	0.46
1:D:608:VAL:HG22	1:D:671:VAL:HG22	1.98	0.46
1:D:708:GLY:N	1:D:709:PRO:HD2	2.29	0.46
1:A:51:VAL:HB	1:B:253:CYS:HB2	1.97	0.46
1:E:895:GLN:HG2	1:E:902:ILE:HG22	1.97	0.46
1:E:945:ARG:HG3	3:E:141:HOH:O	2.15	0.46
1:E:871:VAL:HA	1:E:903:ALA:O	2.16	0.46
1:E:895:GLN:O	1:E:896:GLU:CB	2.64	0.46
1:B:219:THR:O	1:B:223:VAL:HG23	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:685:SER:HB3	1:D:688:VAL:HB	1.98	0.46
1:G:1283:SER:HB3	1:G:1314:ALA:CB	2.45	0.46
1:D:612:LYS:HA	1:D:644:VAL:HG13	1.96	0.46
1:E:820:VAL:HG21	1:F:1020:VAL:HG21	1.97	0.46
1:G:1315:HIS:O	1:G:1316:GLU:C	2.53	0.46
1:G:1274:GLY:HA3	1:G:1306:CYS:HB3	1.97	0.46
1:G:1269:VAL:HA	1:G:1301:LEU:O	2.17	0.46
1:B:216:GLU:HG3	1:B:246:CYS:CB	2.46	0.45
1:D:664:GLU:O	1:D:665:GLY:O	2.34	0.45
1:G:1275:GLY:O	1:G:1276:ASN:CB	2.65	0.45
1:D:613:GLY:HA3	1:D:677:LEU:HB3	1.97	0.45
1:E:930:LYS:HE3	1:E:941:TYR:CD2	2.52	0.45
1:C:526:HIS:HE1	1:D:784:PRO:O	1.99	0.45
1:G:1319:PHE:CD1	1:G:1338:HIS:HB3	2.51	0.45
1:E:893:LYS:O	1:E:897:ASN:HB3	2.16	0.45
1:F:1010:LEU:HG	1:F:1044:VAL:HG11	1.98	0.45
1:E:816:GLU:HG3	1:E:846:CYS:HB2	1.97	0.45
1:G:1276:ASN:HB3	1:G:1277:LEU:HD23	1.98	0.45
1:F:1008:VAL:HA	1:F:1071:VAL:HG22	1.98	0.45
1:E:817:MSE:SE	1:F:1162:PHE:CZ	3.20	0.45
1:G:1261:ALA:O	1:G:1264:GLU:HB2	2.17	0.45
1:E:901:LEU:HD23	1:E:951:LEU:O	2.16	0.45
1:E:858:LEU:HD11	1:E:891:ILE:CD1	2.47	0.45
1:G:1355:SER:HB2	1:G:1364:PHE:CD1	2.52	0.45
1:E:904:ALA:O	1:E:954:THR:HA	2.17	0.45
1:D:614:ALA:O	1:D:646:CYS:HB3	2.16	0.45
1:G:1352:ILE:O	1:G:1352:ILE:HG22	2.16	0.45
1:G:1304:ALA:O	1:G:1354:THR:HA	2.17	0.45
1:D:621:ILE:CB	1:D:622:PRO:HD3	2.45	0.45
1:F:1022:PRO:HA	1:F:1165:ALA:CB	2.47	0.45
1:C:587:LEU:HD23	1:D:759:GLY:CA	2.47	0.45
1:A:29:ALA:HA	1:A:181:VAL:HG21	1.99	0.45
1:E:889:LYS:O	1:E:893:LYS:HG2	2.17	0.44
1:C:489:LYS:HG3	1:C:515:HIS:HB3	1.99	0.44
1:A:176:GLU:O	1:A:180:GLN:HG3	2.17	0.44
1:F:1113:LEU:HD12	1:F:1113:LEU:O	2.17	0.44
1:C:552:ILE:HD12	1:C:552:ILE:N	2.31	0.44
1:G:1364:PHE:O	1:G:1368:ILE:HG13	2.17	0.44
1:A:71:VAL:HA	1:A:103:ALA:O	2.17	0.44
1:G:1221:ILE:HB	1:G:1222:PRO:CD	2.34	0.44
1:C:416:GLU:HG2	1:C:450:VAL:CG2	2.47	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:62:LYS:NZ	1:A:90:GLU:OE2	2.51	0.44
1:G:1247:SER:HA	1:G:1277:LEU:CD1	2.48	0.44
1:D:618:GLU:OE1	1:D:706:CYS:HB2	2.17	0.44
1:G:1226:MSE:O	1:G:1231:ILE:HG22	2.17	0.44
1:E:945:ARG:NH1	1:F:1186:VAL:O	2.51	0.44
1:C:576:GLU:O	1:C:580:GLN:HG3	2.18	0.44
1:A:131:ASP:HB2	3:A:207:HOH:O	2.17	0.44
1:E:811:ALA:O	1:E:812:LYS:C	2.54	0.44
1:A:113:LEU:HD22	1:A:133:MSE:HE3	1.99	0.44
1:A:145:ARG:NH1	1:B:388:LYS:N	2.65	0.44
1:E:853:CYS:HB2	1:F:1051:VAL:HB	1.99	0.44
1:F:1058:LEU:C	1:F:1058:LEU:HD13	2.39	0.44
1:D:699:LYS:C	1:D:751:LEU:HD13	2.38	0.44
1:C:495:GLN:OE1	1:C:495:GLN:HA	2.18	0.44
1:D:726:HIS:HD2	1:D:728:LEU:H	1.66	0.44
1:G:1221:ILE:HG21	1:G:1361:SER:HB3	2.00	0.43
1:A:184:PRO:O	1:A:186:VAL:HG23	2.18	0.43
1:C:502:ILE:HG21	1:C:512:LEU:HD21	2.00	0.43
1:E:909:PRO:CG	1:E:925:THR:HG22	2.48	0.43
1:G:1276:ASN:O	1:G:1280:GLN:HB2	2.18	0.43
1:G:1231:ILE:HD12	1:G:1372:LEU:HD12	2.01	0.43
1:D:723:VAL:HG21	1:D:733:MSE:HE2	2.00	0.43
1:F:1004:LYS:HB3	1:F:1172:LEU:HD23	1.99	0.43
1:A:153:LEU:HD23	1:A:168:ILE:HG12	2.01	0.43
1:C:530:LYS:HG3	1:C:541:TYR:CE1	2.53	0.43
1:F:1099:LYS:C	1:F:1151:LEU:HD13	2.39	0.43
1:A:145:ARG:NH1	1:B:386:VAL:O	2.51	0.43
1:E:958:PRO:O	1:E:961:SER:HB2	2.19	0.43
1:A:152:ILE:N	1:A:152:ILE:HD12	2.32	0.43
1:D:709:PRO:O	1:D:712:LEU:HB2	2.19	0.43
1:F:1097:ASN:N	1:F:1097:ASN:HD22	2.16	0.43
1:C:559:GLY:HA2	1:D:787:LEU:HD23	2.01	0.43
1:D:671:VAL:C	1:D:672:LEU:HD12	2.39	0.43
1:C:506:CYS:SG	1:C:507:ALA:N	2.91	0.43
1:E:909:PRO:HG2	1:E:925:THR:HG22	2.00	0.43
1:A:17:MSE:HE2	1:B:224:ASP:CG	2.39	0.43
1:G:1277:LEU:CD2	1:G:1277:LEU:H	2.24	0.43
1:G:1325:THR:HG21	1:G:1333:MSE:CB	2.49	0.43
1:B:264:GLU:O	1:B:265:GLY:O	2.36	0.43
1:C:416:GLU:CG	1:C:450:VAL:HG13	2.47	0.42
1:C:492:LEU:CB	1:C:517:ILE:CD1	2.97	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:1277:LEU:HD23	1:G:1277:LEU:H	1.84	0.42
1:A:53:CYS:HA	1:A:54:PRO:HD3	1.81	0.42
1:E:926:HIS:HD2	1:E:928:LEU:H	1.65	0.42
1:B:277:LEU:HD13	1:B:281:ASN:ND2	2.34	0.42
1:C:419:THR:O	1:C:423:VAL:HG23	2.19	0.42
1:D:604:LYS:HD2	1:D:604:LYS:N	2.34	0.42
1:D:616:GLU:O	1:D:619:THR:HG23	2.18	0.42
1:F:1016:GLU:CD	1:F:1048:ARG:H	2.22	0.42
1:G:1304:ALA:HB1	1:G:1309:PRO:N	2.35	0.42
1:D:696:GLU:CD	1:D:717:ILE:HG23	2.40	0.42
1:A:184:PRO:O	1:B:326:HIS:HE1	2.02	0.42
1:C:533:MSE:HE2	1:C:533:MSE:HA	2.01	0.42
1:E:945:ARG:HA	1:E:956:ARG:HG3	2.02	0.42
1:E:869:VAL:HG23	1:E:901:LEU:HB3	2.01	0.42
1:E:988:LYS:CB	1:F:1145:ARG:NH2	2.82	0.42
1:D:776:GLU:O	1:D:780:GLN:HG3	2.20	0.42
1:C:462:LYS:HE3	3:C:83:HOH:O	2.20	0.42
1:E:850:VAL:HA	3:E:276:HOH:O	2.19	0.42
1:D:722:LYS:HD3	1:D:747:GLU:OE2	2.20	0.42
1:A:18:GLU:O	1:A:22:PRO:HG2	2.20	0.42
1:D:653:CYS:HA	1:D:654:PRO:HD3	1.59	0.42
1:F:1010:LEU:HD21	1:F:1052:ILE:HB	2.01	0.42
1:F:1007:LEU:HD12	1:F:1067:TYR:CD2	2.55	0.42
1:B:318:GLY:HA2	3:B:407:HOH:O	2.19	0.41
1:C:513:LEU:CB	1:C:533:MSE:HE1	2.50	0.41
1:C:452:ILE:O	1:C:454:PRO:HD3	2.20	0.41
1:G:1346:VAL:O	1:G:1346:VAL:HG23	2.20	0.41
1:C:458:LEU:HA	1:C:458:LEU:HD23	1.94	0.41
1:B:207:LEU:HB2	1:B:267:TYR:CG	2.54	0.41
1:G:1208:VAL:HG22	1:G:1271:VAL:HG22	2.02	0.41
1:C:416:GLU:HG3	1:C:446:CYS:HB3	2.01	0.41
1:E:822:PRO:HA	1:E:965:ALA:HB2	2.02	0.41
1:B:299:LYS:C	1:B:351:LEU:HD13	2.40	0.41
1:C:412:LYS:O	1:C:481:ASN:ND2	2.53	0.41
1:A:166:LEU:HA	1:A:166:LEU:HD23	1.84	0.41
1:A:16:GLU:OE2	1:A:48:ARG:HB2	2.20	0.41
1:B:206:ALA:HB3	1:B:233:VAL:HG22	2.02	0.41
1:G:1283:SER:O	1:G:1315:HIS:CE1	2.74	0.41
1:C:489:LYS:HG2	1:C:493:LYS:HE3	2.03	0.41
1:C:489:LYS:HE3	1:C:493:LYS:HE2	2.03	0.41
1:G:1288:VAL:O	1:G:1292:LEU:HG	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:472:LEU:HD22	1:C:482:LEU:HD13	2.03	0.41
1:G:1247:SER:C	1:G:1248:ARG:HD2	2.40	0.41
1:G:1382:LYS:HG3	1:G:1387:LEU:HD12	2.01	0.41
1:C:534:MSE:HE1	1:C:539:TYR:O	2.20	0.41
1:A:23:VAL:O	1:A:27:ARG:HG3	2.22	0.40
1:F:1172:LEU:C	1:F:1173:ASN:HD22	2.23	0.40
1:C:537:GLY:O	1:C:539:TYR:N	2.54	0.40
1:F:1126:HIS:CD2	1:F:1128:LEU:H	2.40	0.40
1:F:1076:ASN:C	1:F:1076:ASN:HD22	2.24	0.40
1:C:422:PRO:O	1:C:426:MSE:HG3	2.20	0.40
1:E:817:MSE:O	1:E:821:ILE:HG13	2.21	0.40
1:B:247:SER:C	1:B:248:ARG:HD2	2.42	0.40
1:G:1227:ARG:HD3	3:G:167:HOH:O	2.20	0.40
1:G:1387:LEU:O	1:G:1388:LYS:C	2.59	0.40
1:G:1283:SER:O	1:G:1315:HIS:HE1	2.04	0.40
1:B:322:LYS:HA	1:B:340:THR:HB	2.04	0.40
1:F:1016:GLU:OE1	1:F:1048:ARG:N	2.54	0.40
1:C:408:VAL:HG22	1:C:471:VAL:HG21	2.02	0.40
1:F:1103:ALA:HA	1:F:1153:LEU:O	2.21	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	186/189 (98%)	179 (96%)	3 (2%)	4 (2%)	8	9
1	B	185/189 (98%)	180 (97%)	3 (2%)	2 (1%)	17	25
1	C	186/189 (98%)	173 (93%)	10 (5%)	3 (2%)	12	16
1	D	184/189 (97%)	177 (96%)	6 (3%)	1 (0%)	34	48
1	E	186/189 (98%)	172 (92%)	9 (5%)	5 (3%)	6	6

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	F	184/189 (97%)	176 (96%)	6 (3%)	2 (1%)	17	25
1	G	184/189 (97%)	158 (86%)	19 (10%)	7 (4%)	4	3
All	All	1295/1323 (98%)	1215 (94%)	56 (4%)	24 (2%)	10	12

All (24) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	665	GLY
1	E	864	GLU
1	G	1265	GLY
1	A	2	ALA
1	B	265	GLY
1	C	538	HIS
1	E	865	GLY
1	G	1337	GLY
1	G	1356	ARG
1	A	65	GLY
1	A	137	GLY
1	B	276	ASN
1	C	402	ALA
1	C	531	ASP
1	E	896	GLU
1	F	1065	GLY
1	G	1264	GLU
1	E	906	CYS
1	F	1106	CYS
1	G	1269	VAL
1	G	1331	ASP
1	A	106	CYS
1	E	937	GLY
1	G	1266	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	142/142 (100%)	134 (94%)	8 (6%)	26	41
1	B	142/142 (100%)	133 (94%)	9 (6%)	22	35
1	C	142/142 (100%)	128 (90%)	14 (10%)	10	14
1	D	142/142 (100%)	133 (94%)	9 (6%)	22	35
1	E	137/142 (96%)	125 (91%)	12 (9%)	12	18
1	F	140/142 (99%)	133 (95%)	7 (5%)	30	48
1	G	136/142 (96%)	131 (96%)	5 (4%)	41	62
All	All	981/994 (99%)	917 (94%)	64 (6%)	21	33

All (64) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	19	THR
1	A	31	ILE
1	A	50	VAL
1	A	58	LEU
1	A	77	LEU
1	A	93	LYS
1	A	140	THR
1	A	155	SER
1	B	219	THR
1	B	250	VAL
1	B	270	VAL
1	B	271	VAL
1	B	272	LEU
1	B	277	LEU
1	B	321	SER
1	B	333	MSE
1	B	355	SER
1	C	407	LEU
1	C	410	LEU
1	C	419	THR
1	C	431	ILE
1	C	432	LYS
1	C	448	ARG
1	C	450	VAL
1	C	458	LEU
1	C	462	LYS
1	C	470	VAL
1	C	477	LEU
1	C	493	LYS

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Mol	Chain	Res	Type
1	C	531	ASP
1	C	533	MSE
1	D	604	LYS
1	D	619	THR
1	D	631	ILE
1	D	650	VAL
1	D	653	CYS
1	D	658	LEU
1	D	664	GLU
1	D	671	VAL
1	D	677	LEU
1	E	810	LEU
1	E	819	THR
1	E	831	ILE
1	E	842	ASP
1	E	864	GLU
1	E	870	VAL
1	E	890	GLU
1	E	895	GLN
1	E	898	ARG
1	E	901	LEU
1	E	942	SER
1	E	961	SER
1	F	1019	THR
1	F	1048	ARG
1	F	1070	VAL
1	F	1071	VAL
1	F	1076	ASN
1	F	1077	LEU
1	F	1130	LYS
1	G	1205	ARG
1	G	1250	VAL
1	G	1270	VAL
1	G	1277	LEU
1	G	1316	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (30) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	80	GLN
1	A	97	ASN
1	A	126	HIS

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Mol	Chain	Res	Type
1	A	173	ASN
1	B	245	GLN
1	B	281	ASN
1	B	297	ASN
1	B	326	HIS
1	B	373	ASN
1	C	497	ASN
1	C	526	HIS
1	C	573	ASN
1	D	645	GLN
1	D	697	ASN
1	D	726	HIS
1	E	845	GLN
1	E	895	GLN
1	E	926	HIS
1	E	935	ASN
1	E	973	ASN
1	F	1076	ASN
1	F	1097	ASN
1	F	1126	HIS
1	F	1173	ASN
1	G	1245	GLN
1	G	1281	ASN
1	G	1295	GLN
1	G	1326	HIS
1	G	1344	ASN
1	G	1373	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 ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry

7 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	$\# Z  > 2$
2	PO4	A	190	-	4,4,4	1.56	0	6,6,6	0.27	0
2	PO4	A	191	-	4,4,4	1.59	0	6,6,6	0.27	0
2	PO4	C	3	-	4,4,4	1.47	0	6,6,6	0.27	0
2	PO4	D	1	-	4,4,4	1.36	0	6,6,6	0.27	0
2	PO4	E	6	-	4,4,4	1.39	0	6,6,6	0.27	0
2	PO4	F	4	-	4,4,4	1.32	0	6,6,6	0.27	0
2	PO4	F	5	-	4,4,4	1.30	0	6,6,6	0.27	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
2	PO4	A	190	-	-	0/0/0/0	0/0/0/0
2	PO4	A	191	-	-	0/0/0/0	0/0/0/0
2	PO4	C	3	-	-	0/0/0/0	0/0/0/0
2	PO4	D	1	-	-	0/0/0/0	0/0/0/0
2	PO4	E	6	-	-	0/0/0/0	0/0/0/0
2	PO4	F	4	-	-	0/0/0/0	0/0/0/0
2	PO4	F	5	-	-	0/0/0/0	0/0/0/0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 6 Fit of model and data

### 6.1 Protein, DNA and RNA chains

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	A	183/189 (96%)	0.02	1 (0%) 91 91	13, 24, 37, 46	0
1	B	183/189 (96%)	0.01	0 100 100	13, 23, 34, 42	0
1	C	183/189 (96%)	0.07	2 (1%) 82 82	13, 25, 34, 44	0
1	D	182/189 (96%)	0.04	0 100 100	14, 26, 36, 40	0
1	E	184/189 (97%)	0.30	7 (3%) 44 45	20, 34, 43, 47	0
1	F	182/189 (96%)	0.13	2 (1%) 82 82	19, 30, 38, 45	0
1	G	182/189 (96%)	0.27	8 (4%) 38 39	26, 36, 45, 50	0
All	All	1279/1323 (96%)	0.12	20 (1%) 74 74	13, 28, 41, 50	0

All (20) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	942	SER	4.5
1	E	935	ASN	3.3
1	F	1065	GLY	3.2
1	G	1275	GLY	3.1
1	E	831	ILE	3.0
1	G	1265	GLY	3.0
1	G	1297	ASN	2.8
1	E	937	GLY	2.7
1	F	1149	ASP	2.7
1	A	2	ALA	2.5
1	E	941	TYR	2.4
1	C	465	GLY	2.4
1	G	1323	VAL	2.3
1	G	1335	ASN	2.3
1	G	1231	ILE	2.2
1	E	955	SER	2.1
1	E	924	THR	2.1

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Mol	Chain	Res	Type	RSRZ
1	G	1213	GLY	2.1
1	C	402	ALA	2.0
1	G	1319	PHE	2.0

## 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](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
2	PO4	A	191	5/5	0.96	0.22	3.80	33,33,34,35	0
2	PO4	C	3	5/5	0.99	0.21	3.36	32,33,35,35	0
2	PO4	D	1	5/5	0.98	0.19	1.62	39,40,41,43	0
2	PO4	A	190	5/5	0.97	0.19	0.98	29,30,32,33	0
2	PO4	F	4	5/5	0.98	0.14	-0.61	37,37,38,38	0
2	PO4	F	5	5/5	0.98	0.17	-0.62	43,44,44,45	0
2	PO4	E	6	5/5	0.99	0.14	-0.98	35,35,35,36	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.