Full wwPDB X-ray Structure Validation Report (i)

May 9, 2016 – 02:05 PM EDT

PDB ID	:	5FI0
Title	:	Crystal Structure of the P-Rex1 DH/PH tandem in complex with Rac1
Authors	:	Cash, J.N.; Tesmer, J.J.G.
Deposited on	:	2015-12-22
Resolution	:	3.28 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 (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

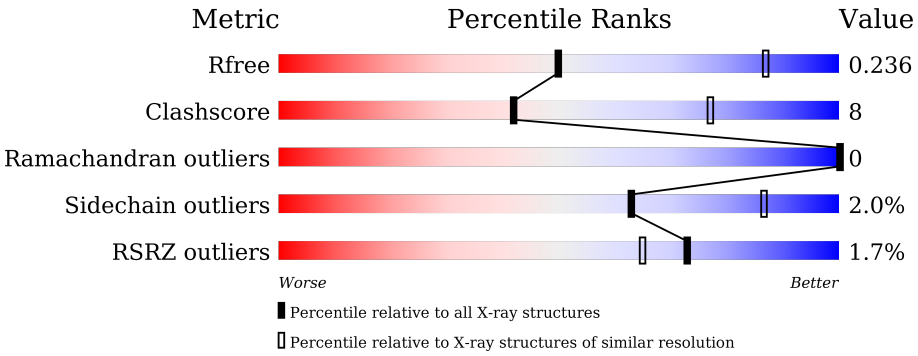
MolProbity	:	4.02b-467
Mogul	:	1.7.1 (RC1), CSD as537be (2016)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20027457
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	rb-20027457

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 3.28 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	1756 (3.36-3.20)
Clashscore	102246	1941 (3.36-3.20)
Ramachandran outliers	100387	1905 (3.36-3.20)
Sidechain outliers	100360	1903 (3.36-3.20)
RSRZ outliers	91569	1764 (3.36-3.20)

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	374	2% 75% 16% • 8%
1	C	374	2% 69% 22% • 8%
1	E	374	3% 69% 22% 9%
1	G	374	2% 75% 17% • 7%
2	B	195	77% 13% • 10%
2	D	195	73% 18% • 9%

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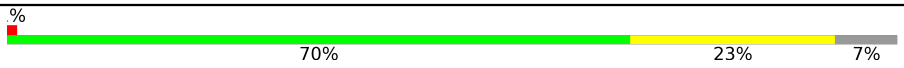
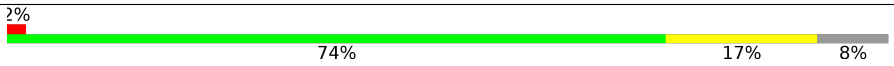
Mol	Chain	Length	Quality of chain
2	F	195	
2	H	195	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 16731 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 Phosphatidylinositol 3,4,5-trisphosphate-dependent Rac exchanger 1 protein,Phosphatidylinositol 3,4,5-trisphosphate-dependent Rac exchanger 1 protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	344	Total	C	N	O	S	0	0	0
			2792	1772	491	514	15			
1	C	344	Total	C	N	O	S	0	0	0
			2789	1769	491	514	15			
1	E	341	Total	C	N	O	S	0	0	0
			2762	1753	483	511	15			
1	G	346	Total	C	N	O	S	0	0	0
			2805	1779	493	518	15			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	GLY	-	expression tag	UNP Q8TCU6
A	-1	GLU	-	expression tag	UNP Q8TCU6
A	0	PHE	-	expression tag	UNP Q8TCU6
C	35	GLY	-	expression tag	UNP Q8TCU6
C	36	GLU	-	expression tag	UNP Q8TCU6
C	37	PHE	-	expression tag	UNP Q8TCU6
E	-2	GLY	-	expression tag	UNP Q8TCU6
E	-1	GLU	-	expression tag	UNP Q8TCU6
E	0	PHE	-	expression tag	UNP Q8TCU6
G	-2	GLY	-	expression tag	UNP Q8TCU6
G	-1	GLU	-	expression tag	UNP Q8TCU6
G	0	PHE	-	expression tag	UNP Q8TCU6

- Molecule 2 is a protein called Ras-related C3 botulinum toxin substrate 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	176	Total	C	N	O	S	0	0	0
			1372	882	226	256	8			

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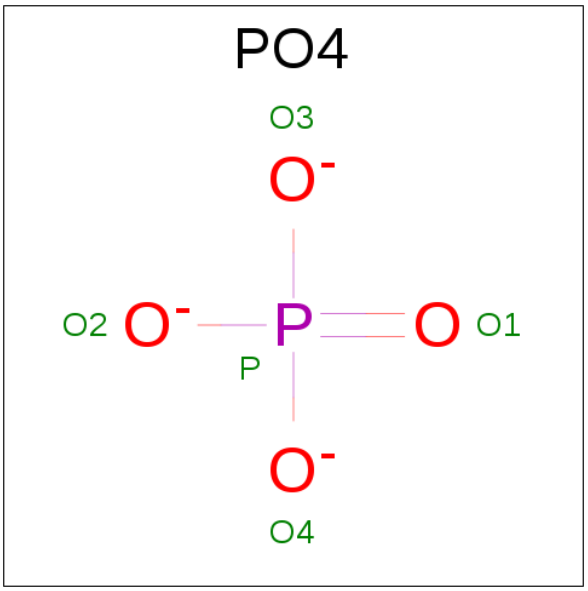
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	178	Total	C	N	O	S	0	0	0
			1388	892	229	259	8			
2	F	181	Total	C	N	O	S	0	0	0
			1410	907	232	262	9			
2	H	179	Total	C	N	O	S	0	0	0
			1393	897	229	259	8			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-2	GLY	-	expression tag	UNP P63000
B	-1	GLU	-	expression tag	UNP P63000
B	0	PHE	-	expression tag	UNP P63000
D	-2	GLY	-	expression tag	UNP P63000
D	-1	GLU	-	expression tag	UNP P63000
D	0	PHE	-	expression tag	UNP P63000
F	-2	GLY	-	expression tag	UNP P63000
F	-1	GLU	-	expression tag	UNP P63000
F	0	PHE	-	expression tag	UNP P63000
H	-2	GLY	-	expression tag	UNP P63000
H	-1	GLU	-	expression tag	UNP P63000
H	0	PHE	-	expression tag	UNP P63000

- Molecule 3 is PHOSPHATE ION (three-letter code: PO4) (formula: O_4P).



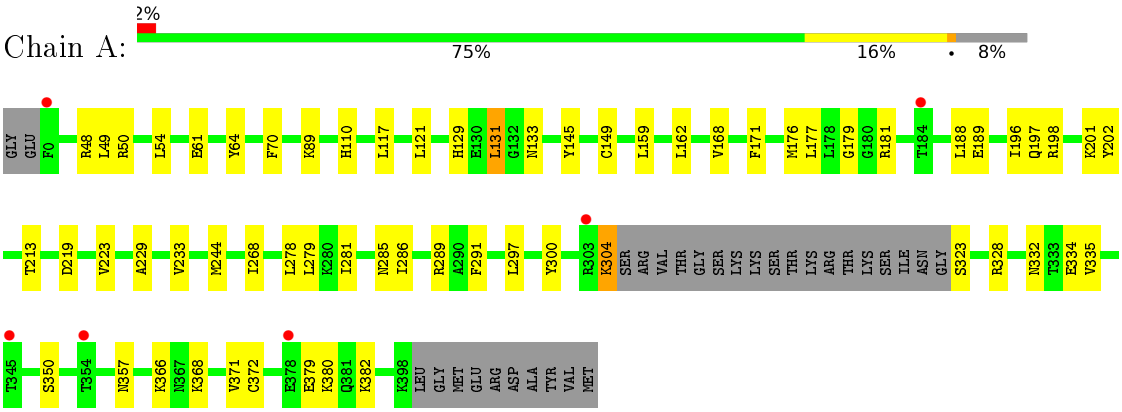
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total O P 5 4 1	0	0
3	C	1	Total O P 5 4 1	0	0
3	E	1	Total O P 5 4 1	0	0
3	G	1	Total O P 5 4 1	0	0

3 Residue-property plots (i)

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.

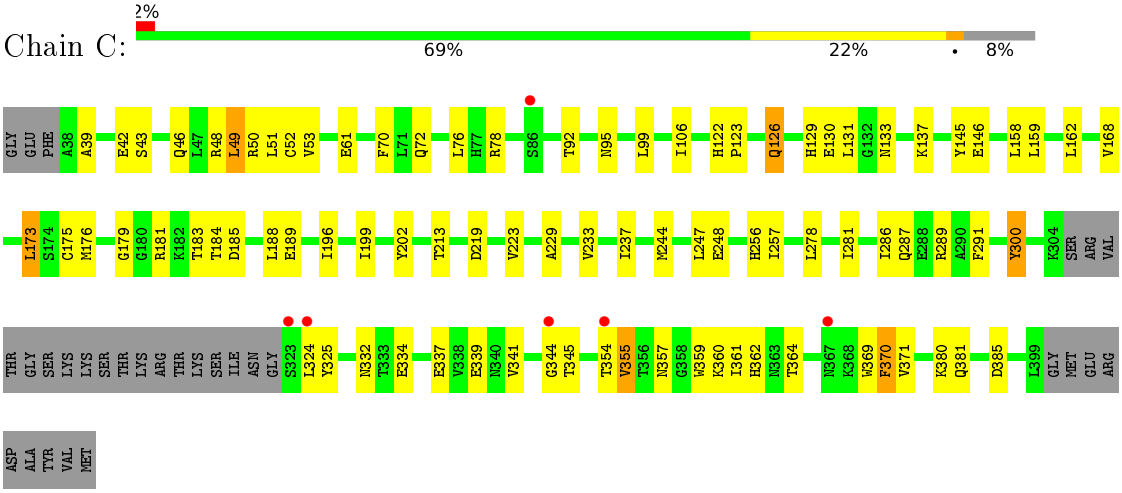
• Molecule 1: Phosphatidylinositol 3,4,5-trisphosphate-dependent Rac exchanger 1 protein,Phosphatidylinositol 3,4,5-trisphosphate-dependent Rac exchanger 1 protein

Chain A:



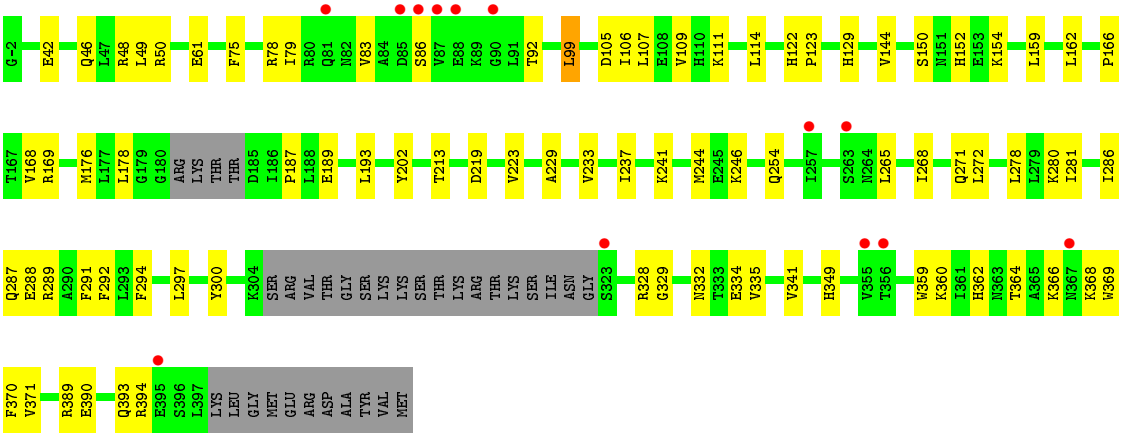
• Molecule 1: Phosphatidylinositol 3,4,5-trisphosphate-dependent Rac exchanger 1 protein,Phosphatidylinositol 3,4,5-trisphosphate-dependent Rac exchanger 1 protein

Chain C:



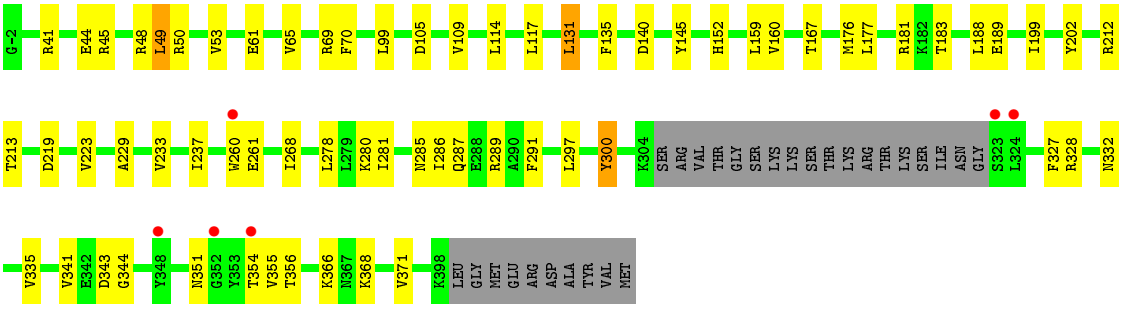
• Molecule 1: Phosphatidylinositol 3,4,5-trisphosphate-dependent Rac exchanger 1 protein,Phosphatidylinositol 3,4,5-trisphosphate-dependent Rac exchanger 1 protein

Chain E:



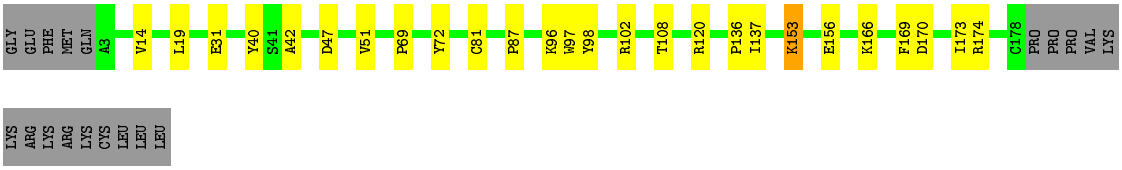
• Molecule 1: Phosphatidylinositol 3,4,5-trisphosphate-dependent Rac exchanger 1 protein,Phosphatidylinositol 3,4,5-trisphosphate-dependent Rac exchanger 1 protein

Chain G:



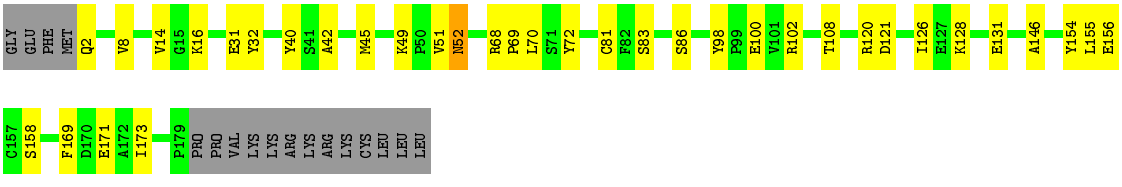
• Molecule 2: Ras-related C3 botulinum toxin substrate 1

Chain B:



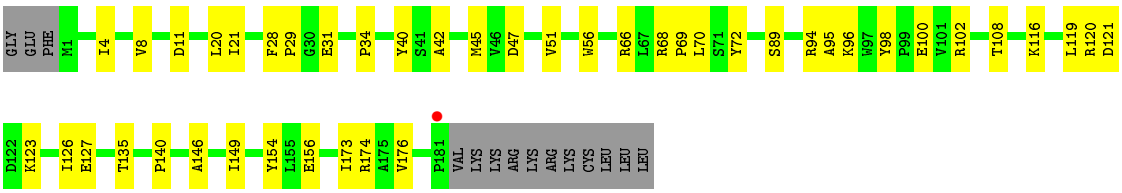
• Molecule 2: Ras-related C3 botulinum toxin substrate 1

Chain D:

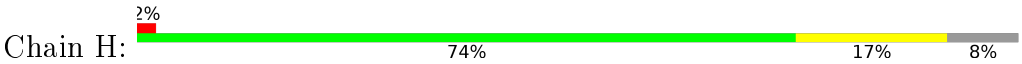


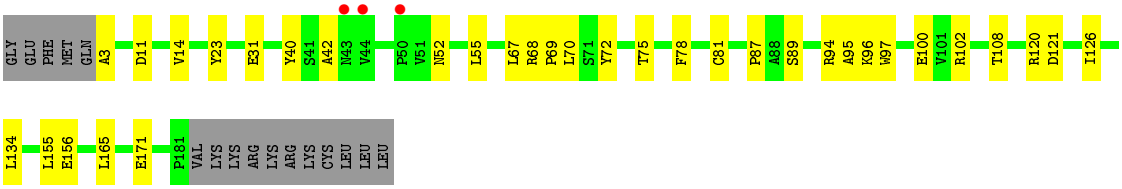
• Molecule 2: Ras-related C3 botulinum toxin substrate 1

Chain F:



• Molecule 2: Ras-related C3 botulinum toxin substrate 1





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	81.37Å 107.05Å 323.57Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	34.85 – 3.28 34.85 – 3.28	Depositor EDS
% Data completeness (in resolution range)	96.8 (34.85-3.28) 96.9 (34.85-3.28)	Depositor EDS
R_{merge}	0.17	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.62 (at 3.32Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.190 , 0.235 0.192 , 0.236	Depositor DCC
R_{free} test set	2104 reflections (4.92%)	DCC
Wilson B-factor (Å^2)	63.5	Xtriage
Anisotropy	0.761	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.27 , 41.3	EDS
L-test for twinning[2]	$< \|L\| > = 0.47$, $< L^2 > = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	16731	wwPDB-VP
Average B, all atoms (Å^2)	81.0	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 22.07 % 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 6.1463e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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	0.29	0/2841	0.51	0/3828
1	C	0.30	0/2837	0.54	0/3823
1	E	0.30	0/2810	0.56	1/3786 (0.0%)
1	G	0.30	0/2854	0.52	0/3845
2	B	0.29	0/1402	0.53	0/1908
2	D	0.28	0/1419	0.52	0/1932
2	F	0.27	0/1443	0.50	0/1966
2	H	0.29	0/1426	0.55	0/1944
All	All	0.29	0/17032	0.53	1/23032 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	E	99	LEU	CA-CB-CG	6.20	129.57	115.30

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	2792	0	2829	43	0
1	C	2789	0	2828	63	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	E	2762	0	2784	61	0
1	G	2805	0	2838	41	0
2	B	1372	0	1390	21	0
2	D	1388	0	1405	21	0
2	F	1410	0	1431	28	0
2	H	1393	0	1411	25	0
3	A	5	0	0	0	0
3	C	5	0	0	0	0
3	E	5	0	0	0	0
3	G	5	0	0	1	0
All	All	16731	0	16916	283	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 8.

All (283) 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)
2:B:174:ARG:HG2	1:C:137:LYS:HE3	1.54	0.88
2:F:102:ARG:NH2	2:F:108:THR:O	2.11	0.83
1:E:281:ILE:HG12	1:E:286:ILE:HG12	1.67	0.76
1:C:48:ARG:NH1	2:D:31:GLU:OE2	2.20	0.75
2:H:102:ARG:NH2	2:H:108:THR:O	2.22	0.73
1:G:48:ARG:NH1	2:H:31:GLU:OE2	2.21	0.73
1:A:110:HIS:NE2	1:A:145:TYR:OH	2.20	0.73
2:H:40:TYR:CE2	2:H:42:ALA:HB2	2.25	0.71
1:C:70:PHE:HE1	1:C:179:GLY:HA3	1.55	0.71
2:D:51:VAL:HG21	2:D:173:ILE:HD13	1.72	0.70
2:B:14:VAL:HG11	2:B:81:CYS:HB3	1.74	0.70
1:G:281:ILE:HB	1:G:371:VAL:HG12	1.75	0.69
2:H:23:TYR:HB2	2:H:165:LEU:HD21	1.75	0.68
1:C:281:ILE:HG12	1:C:286:ILE:HD12	1.76	0.68
2:F:116:LYS:HB3	2:F:119:LEU:HD12	1.75	0.67
1:G:287:GLN:OE1	1:G:289:ARG:NH2	2.27	0.67
1:G:50:ARG:NH1	1:G:213:THR:OG1	2.28	0.67
2:B:51:VAL:HG21	2:B:173:ILE:HD13	1.76	0.67
1:E:390:GLU:OE1	1:E:394:ARG:NH2	2.27	0.67
2:B:153:LYS:NZ	1:C:133:ASN:OD1	2.28	0.66
1:A:379:GLU:OE2	1:A:382:LYS:NZ	2.22	0.66
2:D:102:ARG:NH2	2:D:108:THR:O	2.28	0.66
1:C:50:ARG:NH1	1:C:213:THR:OG1	2.28	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:184:THR:O	2:D:52:ASN:ND2	2.29	0.65
1:E:281:ILE:HB	1:E:371:VAL:HB	1.79	0.65
1:E:48:ARG:NH1	2:F:31:GLU:OE2	2.29	0.65
1:E:287:GLN:OE1	1:E:289:ARG:NH2	2.30	0.64
1:A:50:ARG:NH1	1:A:213:THR:OG1	2.31	0.64
1:A:281:ILE:HG21	1:A:350:SER:HA	1.80	0.64
2:B:102:ARG:NH2	2:B:108:THR:O	2.31	0.63
1:C:344:GLY:HA2	1:C:354:THR:HG23	1.80	0.63
1:A:50:ARG:NH2	1:A:129:HIS:O	2.32	0.63
1:E:272:LEU:HD13	1:E:294:PHE:HE2	1.63	0.63
1:C:50:ARG:NH2	1:C:129:HIS:O	2.32	0.63
1:A:281:ILE:HB	1:A:371:VAL:HB	1.81	0.62
1:C:95:ASN:HD22	1:C:158:LEU:HD21	1.64	0.62
1:E:152:HIS:HD2	2:F:70:LEU:HD22	1.62	0.62
1:A:54:LEU:HD22	1:A:131:LEU:HD13	1.82	0.62
1:C:332:ASN:OD1	1:C:334:GLU:HG2	1.98	0.62
1:E:360:LYS:HD2	1:E:369:TRP:CE3	2.34	0.62
1:G:281:ILE:HG12	1:G:286:ILE:HG12	1.80	0.62
1:C:357:ASN:HA	1:C:380:LYS:HD2	1.81	0.62
2:F:40:TYR:CE2	2:F:42:ALA:HB2	2.34	0.62
1:G:61:GLU:OE1	1:G:202:TYR:OH	2.18	0.62
1:E:272:LEU:HD13	1:E:294:PHE:CE2	2.35	0.61
1:E:362:HIS:CE1	1:E:364:THR:HG22	2.34	0.61
2:H:40:TYR:HE2	2:H:42:ALA:HB2	1.65	0.61
1:C:176:MET:HE1	1:C:188:LEU:HB2	1.82	0.61
2:F:120:ARG:NH2	2:F:156:GLU:OE2	2.30	0.61
1:A:121:LEU:HD11	1:A:131:LEU:HD11	1.82	0.61
1:A:304:LYS:NZ	1:A:323:SER:O	2.35	0.60
2:D:14:VAL:HG11	2:D:81:CYS:HB3	1.82	0.60
1:G:281:ILE:HB	1:G:371:VAL:CG1	2.31	0.60
2:B:166:LYS:NZ	2:B:170:ASP:OD2	2.35	0.59
1:E:61:GLU:OE1	1:E:202:TYR:OH	2.20	0.59
1:C:244:MET:HA	1:C:247:LEU:HD12	1.84	0.59
2:B:120:ARG:NH2	2:B:156:GLU:OE2	2.36	0.59
1:G:278:LEU:HB2	1:G:291:PHE:CD1	2.38	0.58
1:C:361:ILE:HB	1:C:370:PHE:HE2	1.67	0.58
2:H:121:ASP:HA	2:H:126:ILE:HD11	1.84	0.58
1:A:48:ARG:NH1	2:B:31:GLU:OE2	2.35	0.58
1:C:361:ILE:HB	1:C:370:PHE:CE2	2.38	0.58
1:E:50:ARG:NH2	1:E:129:HIS:O	2.37	0.57
2:B:98:TYR:CE1	2:B:102:ARG:HD2	2.39	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:159:LEU:HD23	1:C:189:GLU:HG3	1.86	0.57
1:C:257:ILE:HG12	1:C:325:TYR:HB2	1.87	0.57
1:A:289:ARG:HH21	1:A:328:ARG:HD3	1.69	0.57
1:C:70:PHE:CE1	1:C:179:GLY:HA3	2.39	0.57
1:E:332:ASN:OD1	1:E:334:GLU:HG2	2.04	0.57
1:G:176:MET:HE1	1:G:188:LEU:HB2	1.86	0.56
1:G:99:LEU:HD21	1:G:159:LEU:HB2	1.85	0.56
1:E:362:HIS:HB2	1:E:369:TRP:CZ3	2.40	0.56
2:H:14:VAL:HG11	2:H:81:CYS:HB3	1.86	0.56
1:E:254:GLN:HB2	1:E:265:LEU:HD12	1.88	0.56
2:F:120:ARG:HH22	2:F:156:GLU:CD	2.08	0.56
1:C:233:VAL:O	1:C:237:ILE:HG13	2.06	0.56
1:A:159:LEU:HD23	1:A:189:GLU:HG3	1.87	0.55
1:E:289:ARG:NH1	1:E:328:ARG:HG2	2.20	0.55
1:C:362:HIS:CE1	1:C:364:THR:HG22	2.42	0.54
1:G:159:LEU:HD23	1:G:189:GLU:HG3	1.87	0.54
1:C:146:GLU:HG2	1:C:237:ILE:HA	1.87	0.54
1:E:332:ASN:HB3	1:E:335:VAL:HG22	1.90	0.54
2:B:51:VAL:HG21	2:B:173:ILE:HG21	1.90	0.54
1:C:173:LEU:HD12	1:C:183:THR:HG22	1.90	0.54
1:A:197:GLN:O	1:A:201:LYS:HG2	2.08	0.53
1:A:70:PHE:CE1	1:A:181:ARG:HD3	2.43	0.53
2:F:21:ILE:HD13	2:F:34:PRO:HD2	1.90	0.53
1:C:291:PHE:CE2	1:C:300:TYR:HB3	2.44	0.53
1:G:229:ALA:O	1:G:233:VAL:HG23	2.09	0.53
1:E:75:PHE:HZ	1:E:176:MET:HE2	1.72	0.53
2:D:69:PRO:HA	2:D:72:TYR:CD2	2.44	0.53
1:A:196:ILE:H	1:A:196:ILE:HD12	1.74	0.52
1:A:281:ILE:HG23	1:A:286:ILE:HD11	1.89	0.52
1:C:345:THR:O	1:C:355:VAL:HG22	2.09	0.52
1:C:61:GLU:OE1	1:C:202:TYR:OH	2.24	0.52
1:A:278:LEU:HB2	1:A:291:PHE:CD1	2.44	0.52
2:B:87:PRO:HA	2:B:137:ILE:HD11	1.90	0.52
1:E:278:LEU:HB2	1:E:291:PHE:HD2	1.74	0.52
2:F:69:PRO:HA	2:F:72:TYR:CD2	2.44	0.52
1:A:61:GLU:HG2	1:A:117:LEU:HD12	1.90	0.52
1:C:341:VAL:HG23	1:C:359:TRP:HA	1.91	0.52
1:A:278:LEU:HB2	1:A:291:PHE:HD1	1.73	0.52
1:C:337:GLU:HB2	1:C:362:HIS:HB3	1.92	0.52
2:F:8:VAL:HG21	2:F:20:LEU:HD21	1.91	0.52
2:D:68:ARG:NH1	2:D:100:GLU:OE1	2.43	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:14:VAL:HG11	2:B:81:CYS:CB	2.40	0.51
1:E:152:HIS:CD2	2:F:70:LEU:HD22	2.45	0.51
1:G:268:ILE:HD11	1:G:297:LEU:HD22	1.93	0.51
1:C:122:HIS:CG	1:C:123:PRO:HA	2.46	0.51
1:C:287:GLN:HB3	1:C:289:ARG:NH1	2.26	0.50
1:E:61:GLU:HB3	1:E:114:LEU:HD13	1.93	0.50
2:F:51:VAL:HG21	2:F:173:ILE:HG21	1.92	0.50
1:E:107:LEU:HG	1:E:111:LYS:HE3	1.91	0.50
1:A:149:CYS:SG	1:A:196:ILE:HG13	2.52	0.50
1:E:105:ASP:O	1:E:109:VAL:HG23	2.12	0.50
2:D:155:LEU:HD21	2:D:171:GLU:HG3	1.94	0.50
1:A:89:LYS:HD3	1:A:171:PHE:HB2	1.94	0.50
1:E:292:PHE:HB3	1:E:294:PHE:CE2	2.47	0.50
1:G:278:LEU:HB2	1:G:291:PHE:HD1	1.75	0.50
2:B:40:TYR:CE2	2:B:42:ALA:HB2	2.47	0.49
1:C:162:LEU:HD22	1:C:168:VAL:HG11	1.93	0.49
1:E:341:VAL:HG23	1:E:359:TRP:HA	1.94	0.49
2:B:40:TYR:HE2	2:B:42:ALA:HB2	1.78	0.49
1:E:79:ILE:HG23	1:E:86:SER:HB2	1.95	0.49
2:H:96:LYS:HE2	2:H:97:TRP:CZ2	2.48	0.49
1:C:278:LEU:HB2	1:C:291:PHE:CD1	2.47	0.49
2:D:128:LYS:O	2:D:131:GLU:HB2	2.13	0.49
1:C:176:MET:HG3	1:C:181:ARG:HB2	1.94	0.49
2:B:136:PRO:HD2	1:E:122:HIS:CE1	2.48	0.49
1:C:126:GLN:HG3	1:C:129:HIS:CE1	2.48	0.49
1:E:109:VAL:HG21	1:E:144:VAL:HG21	1.95	0.49
1:E:349:HIS:ND1	1:E:360:LYS:HD3	2.27	0.49
2:F:4:ILE:HG12	2:F:176:VAL:HG11	1.95	0.49
1:G:65:VAL:HG12	1:G:69:ARG:HD2	1.95	0.49
2:H:94:ARG:HG3	2:H:95:ALA:N	2.28	0.49
2:F:121:ASP:HA	2:F:126:ILE:HD11	1.95	0.48
1:A:281:ILE:HA	1:A:286:ILE:HD12	1.94	0.48
1:E:241:LYS:HD3	2:F:66:ARG:HB3	1.94	0.48
1:E:288:GLU:O	1:E:289:ARG:HD3	2.14	0.48
1:A:121:LEU:HD23	1:A:129:HIS:HD2	1.78	0.48
1:E:150:SER:HA	1:E:241:LYS:HG3	1.95	0.48
1:C:145:TYR:CE2	1:C:199:ILE:HB	2.49	0.48
1:E:187:PRO:HB2	1:E:189:GLU:OE1	2.14	0.48
2:H:87:PRO:HG2	2:H:134:LEU:HD22	1.95	0.48
1:C:196:ILE:HD13	2:D:70:LEU:HD13	1.96	0.48
1:G:131:LEU:HD23	1:G:135:PHE:HE2	1.78	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:121:LEU:HD23	1:A:129:HIS:CD2	2.49	0.48
2:B:120:ARG:HH22	2:B:156:GLU:CD	2.17	0.48
1:C:39:ALA:O	1:C:42:GLU:HB3	2.14	0.48
1:G:280:LYS:HD3	1:G:289:ARG:HE	1.78	0.48
1:C:92:THR:O	1:C:95:ASN:HB2	2.14	0.47
2:D:83:SER:HB3	2:D:86:SER:HB3	1.95	0.47
1:A:61:GLU:OE1	1:A:202:TYR:OH	2.24	0.47
1:E:233:VAL:O	1:E:237:ILE:HG13	2.14	0.47
1:A:121:LEU:HA	1:A:129:HIS:CD2	2.50	0.47
1:C:381:GLN:HG3	1:C:385:ASP:OD2	2.15	0.47
2:H:75:THR:HG21	2:H:78:PHE:CE1	2.50	0.47
1:A:332:ASN:HB3	1:A:335:VAL:HG22	1.96	0.47
2:F:123:LYS:O	2:F:127:GLU:HG2	2.14	0.47
2:F:94:ARG:HG3	2:F:95:ALA:N	2.29	0.47
1:E:278:LEU:HB2	1:E:291:PHE:CD2	2.50	0.47
1:C:219:ASP:O	1:C:223:VAL:HG23	2.14	0.47
1:G:152:HIS:HD2	2:H:70:LEU:HD22	1.80	0.47
1:C:278:LEU:HB2	1:C:291:PHE:HD1	1.80	0.46
1:C:341:VAL:HG11	1:C:355:VAL:HG21	1.98	0.46
2:H:40:TYR:HD2	2:H:55:LEU:HD12	1.81	0.46
1:C:72:GLN:HA	1:C:76:LEU:HD12	1.96	0.46
1:G:237:ILE:HG22	2:H:67:LEU:HD21	1.98	0.46
1:C:51:LEU:HD21	1:C:126:GLN:HA	1.97	0.46
1:G:145:TYR:CG	1:G:199:ILE:HD12	2.50	0.46
2:D:14:VAL:HG11	2:D:81:CYS:CB	2.45	0.46
1:E:193:LEU:HD23	2:F:56:TRP:HZ3	1.79	0.46
1:C:300:TYR:CD2	1:C:300:TYR:N	2.83	0.46
2:H:23:TYR:HB2	2:H:165:LEU:CD2	2.44	0.46
2:H:69:PRO:HA	2:H:72:TYR:CD2	2.51	0.46
2:H:14:VAL:HG11	2:H:81:CYS:CB	2.46	0.46
1:E:169:ARG:HB3	1:E:169:ARG:CZ	2.46	0.45
2:H:11:ASP:OD2	2:H:89:SER:HA	2.15	0.45
1:C:99:LEU:HD11	1:C:159:LEU:HB2	1.98	0.45
1:A:291:PHE:CD2	1:A:300:TYR:HB3	2.52	0.45
1:G:70:PHE:CE1	1:G:181:ARG:HD3	2.51	0.45
2:B:169:PHE:O	2:B:173:ILE:HG13	2.17	0.45
1:A:64:TYR:CD2	1:A:198:ARG:HG2	2.51	0.45
1:C:256:HIS:CD2	1:C:324:LEU:HD12	2.52	0.45
1:E:42:GLU:OE2	1:E:46:GLN:NE2	2.42	0.45
1:G:260:TRP:HA	1:G:327:PHE:CD1	2.51	0.45
2:H:120:ARG:NH2	2:H:156:GLU:OE2	2.50	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:344:GLY:HA2	1:G:354:THR:HG23	1.98	0.45
1:A:229:ALA:O	1:A:233:VAL:HG23	2.17	0.45
1:C:291:PHE:CD2	1:C:300:TYR:HB3	2.52	0.45
1:C:339:GLU:HB3	1:C:360:LYS:HB2	1.98	0.45
1:E:268:ILE:HD11	1:E:297:LEU:HD22	1.99	0.45
1:E:50:ARG:NH1	1:E:213:THR:OG1	2.50	0.45
2:H:3:ALA:HA	2:H:52:ASN:O	2.17	0.45
1:C:131:LEU:HA	1:C:131:LEU:HD23	1.75	0.44
2:D:8:VAL:HG12	2:D:16:LYS:HD2	1.98	0.44
2:F:68:ARG:HB2	2:F:69:PRO:HD3	1.99	0.44
2:B:96:LYS:HE2	2:B:97:TRP:CZ2	2.53	0.44
1:A:176:MET:HE1	1:A:188:LEU:HB2	1.98	0.44
2:F:47:ASP:OD1	2:F:174:ARG:NH1	2.51	0.44
1:A:176:MET:HB2	1:A:176:MET:HE2	1.78	0.44
1:A:357:ASN:HA	1:A:380:LYS:HD2	2.00	0.44
2:D:146:ALA:CB	2:D:154:TYR:HB2	2.47	0.44
1:E:122:HIS:CG	1:E:123:PRO:HA	2.53	0.44
1:E:246:LYS:HD3	1:E:271:GLN:HB3	1.98	0.44
2:H:68:ARG:NH1	2:H:100:GLU:OE1	2.51	0.44
2:F:28:PHE:CD1	2:F:29:PRO:HD2	2.53	0.44
1:G:341:VAL:HG21	1:G:355:VAL:HG11	1.99	0.44
1:G:41:ARG:NE	1:G:41:ARG:HA	2.33	0.44
2:H:120:ARG:HH22	2:H:156:GLU:CD	2.21	0.44
2:H:155:LEU:HD11	2:H:171:GLU:HG3	1.99	0.44
1:G:41:ARG:NH2	1:G:44:GLU:OE1	2.47	0.44
1:A:219:ASP:O	1:A:223:VAL:HG23	2.18	0.43
1:G:177:LEU:HA	1:G:181:ARG:O	2.17	0.43
1:G:261:GLU:HB2	1:G:327:PHE:CZ	2.53	0.43
1:E:366:LYS:O	1:E:368:LYS:HG3	2.17	0.43
1:C:52:CYS:HB3	2:D:32:TYR:CD2	2.54	0.43
1:C:78:ARG:NH1	1:C:175:CYS:SG	2.92	0.43
1:C:362:HIS:HB2	1:C:369:TRP:CZ3	2.53	0.43
1:E:287:GLN:CB	1:E:289:ARG:HE	2.32	0.43
1:E:229:ALA:O	1:E:233:VAL:HG23	2.17	0.43
1:E:193:LEU:CD2	2:F:56:TRP:HZ3	2.32	0.43
1:A:289:ARG:NH2	1:A:328:ARG:HD3	2.34	0.43
1:G:61:GLU:HB3	1:G:114:LEU:HD13	2.01	0.43
1:G:343:ASP:HB3	1:G:356:THR:HG22	1.99	0.43
1:A:268:ILE:HD11	1:A:297:LEU:HD22	2.00	0.42
1:A:70:PHE:HE1	1:A:179:GLY:HA3	1.84	0.42
1:G:105:ASP:O	1:G:109:VAL:HG23	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:122:HIS:CD2	1:E:123:PRO:HA	2.53	0.42
1:G:332:ASN:HB3	1:G:335:VAL:HG22	2.01	0.42
1:G:152:HIS:CD2	2:H:70:LEU:HD22	2.54	0.42
1:C:300:TYR:HD2	1:C:300:TYR:N	2.17	0.42
2:D:98:TYR:CE1	2:D:102:ARG:HD2	2.54	0.42
1:E:287:GLN:HB3	1:E:289:ARG:HE	1.84	0.42
2:F:98:TYR:CE1	2:F:102:ARG:HD2	2.54	0.42
2:H:11:ASP:OD1	2:H:97:TRP:NE1	2.48	0.42
1:G:212:ARG:HA	1:G:212:ARG:HD3	1.94	0.42
1:E:389:ARG:O	1:E:393:GLN:HG2	2.20	0.42
1:G:219:ASP:O	1:G:223:VAL:HG23	2.19	0.42
1:E:106:ILE:HD13	1:E:144:VAL:HG23	2.01	0.42
1:G:45:ARG:NH2	3:G:501:PO4:O1	2.50	0.42
1:C:281:ILE:HB	1:C:371:VAL:HB	2.01	0.42
2:F:140:PRO:HD3	1:G:140:ASP:HB3	2.02	0.42
1:A:332:ASN:OD1	1:A:334:GLU:HG2	2.19	0.42
2:F:68:ARG:NH1	2:F:100:GLU:OE1	2.53	0.42
1:C:49:LEU:HD11	2:D:31:GLU:HG2	2.02	0.41
1:E:162:LEU:HD22	1:E:168:VAL:HG11	2.02	0.41
1:E:219:ASP:O	1:E:223:VAL:HG23	2.20	0.41
1:A:162:LEU:HD22	1:A:168:VAL:HG11	2.01	0.41
1:A:279:LEU:O	1:A:372:CYS:HA	2.20	0.41
1:E:166:PRO:HA	1:E:169:ARG:NH2	2.35	0.41
2:B:69:PRO:HA	2:B:72:TYR:CD2	2.56	0.41
1:E:289:ARG:HH11	1:E:328:ARG:HG2	1.84	0.41
2:F:98:TYR:CD1	2:F:149:ILE:HB	2.55	0.41
1:E:393:GLN:HA	1:E:393:GLN:OE1	2.20	0.41
2:D:121:ASP:HA	2:D:126:ILE:HD11	2.02	0.41
1:E:154:LYS:HZ2	1:E:154:LYS:HG3	1.29	0.41
1:A:366:LYS:O	1:A:368:LYS:HG3	2.20	0.41
1:E:280:LYS:HG3	1:E:370:PHE:CD1	2.56	0.41
2:F:11:ASP:OD2	2:F:89:SER:HA	2.21	0.41
2:D:169:PHE:O	2:D:173:ILE:HG13	2.21	0.41
1:C:287:GLN:HB3	1:C:289:ARG:HH12	1.84	0.41
1:A:285:ASN:C	1:A:286:ILE:HD13	2.41	0.41
1:C:43:SER:O	1:C:46:GLN:HB2	2.20	0.41
1:C:49:LEU:O	1:C:53:VAL:HG23	2.20	0.41
1:E:159:LEU:HD23	1:E:189:GLU:HG3	2.02	0.41
1:G:300:TYR:O	1:G:328:ARG:HB3	2.20	0.41
1:C:229:ALA:O	1:C:233:VAL:HG23	2.21	0.40
2:D:120:ARG:NH2	2:D:156:GLU:OE1	2.52	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:61:GLU:HG3	1:G:117:LEU:CD1	2.51	0.40
2:B:98:TYR:HE1	2:B:102:ARG:HD2	1.85	0.40
1:A:89:LYS:HD2	1:A:171:PHE:HD1	1.86	0.40
2:B:47:ASP:OD1	2:B:174:ARG:NH1	2.54	0.40
1:C:357:ASN:CA	1:C:380:LYS:HD2	2.49	0.40
2:D:40:TYR:CE2	2:D:42:ALA:HB2	2.57	0.40
1:E:300:TYR:CE2	1:E:329:GLY:HA3	2.56	0.40
2:F:146:ALA:CB	2:F:154:TYR:HB2	2.51	0.40
1:E:83:VAL:O	1:E:86:SER:HB3	2.21	0.40
1:G:366:LYS:O	1:G:368:LYS:HG3	2.21	0.40
1:G:49:LEU:O	1:G:53:VAL:HG23	2.21	0.40
1:C:106:ILE:HG23	1:C:145:TYR:CE1	2.57	0.40
1:C:122:HIS:CD2	1:C:123:PRO:HA	2.56	0.40
1:E:78:ARG:CZ	1:E:178:LEU:HD23	2.52	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	340/374 (91%)	329 (97%)	11 (3%)	0	100	100
1	C	340/374 (91%)	328 (96%)	12 (4%)	0	100	100
1	E	335/374 (90%)	325 (97%)	10 (3%)	0	100	100
1	G	342/374 (91%)	331 (97%)	11 (3%)	0	100	100
2	B	174/195 (89%)	168 (97%)	6 (3%)	0	100	100
2	D	176/195 (90%)	169 (96%)	7 (4%)	0	100	100
2	F	179/195 (92%)	174 (97%)	5 (3%)	0	100	100
2	H	177/195 (91%)	170 (96%)	7 (4%)	0	100	100
All	All	2063/2276 (91%)	1994 (97%)	69 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	307/332 (92%)	301 (98%)	6 (2%)	63	86
1	C	307/332 (92%)	298 (97%)	9 (3%)	50	81
1	E	303/332 (91%)	299 (99%)	4 (1%)	76	91
1	G	308/332 (93%)	300 (97%)	8 (3%)	54	83
2	B	152/170 (89%)	150 (99%)	2 (1%)	76	91
2	D	154/170 (91%)	149 (97%)	5 (3%)	46	80
2	F	157/170 (92%)	154 (98%)	3 (2%)	65	87
2	H	155/170 (91%)	155 (100%)	0	100	100
All	All	1843/2008 (92%)	1806 (98%)	37 (2%)	63	86

All (37) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	49	LEU
1	A	131	LEU
1	A	133	ASN
1	A	177	LEU
1	A	244	MET
1	A	304	LYS
2	B	19	LEU
2	B	153	LYS
1	C	49	LEU
1	C	126	GLN
1	C	130	GLU
1	C	173	LEU
1	C	185	ASP
1	C	248	GLU
1	C	300	TYR
1	C	355	VAL

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Mol	Chain	Res	Type
1	C	370	PHE
2	D	2	GLN
2	D	45	MET
2	D	49	LYS
2	D	52	ASN
2	D	158	SER
1	E	49	LEU
1	E	92	THR
1	E	99	LEU
1	E	244	MET
2	F	45	MET
2	F	96	LYS
2	F	135	THR
1	G	49	LEU
1	G	131	LEU
1	G	160	VAL
1	G	167	THR
1	G	183	THR
1	G	285	ASN
1	G	300	TYR
1	G	351	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	129	HIS
2	D	52	ASN
1	E	122	HIS
1	E	152	HIS
1	G	152	HIS
1	G	285	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)

4 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	PO4	A	501	-	4,4,4	0.67	0	6,6,6	0.23	0
3	PO4	C	501	-	4,4,4	0.68	0	6,6,6	0.23	0
3	PO4	E	501	-	4,4,4	0.70	0	6,6,6	0.23	0
3	PO4	G	501	-	4,4,4	0.68	0	6,6,6	0.23	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	PO4	A	501	-	-	0/0/0/0	0/0/0/0
3	PO4	C	501	-	-	0/0/0/0	0/0/0/0
3	PO4	E	501	-	-	0/0/0/0	0/0/0/0
3	PO4	G	501	-	-	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.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	G	501	PO4	1	0

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

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^{th} 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	344/374 (91%)	-0.21	6 (1%) 73 65	27, 73, 133, 150	0
1	C	344/374 (91%)	-0.11	6 (1%) 73 65	29, 84, 150, 173	0
1	E	341/374 (91%)	-0.04	13 (3%) 44 34	30, 99, 164, 189	0
1	G	346/374 (92%)	-0.05	6 (1%) 73 65	41, 95, 165, 201	0
2	B	176/195 (90%)	-0.45	0 100 100	26, 43, 74, 88	0
2	D	178/195 (91%)	-0.44	0 100 100	32, 50, 81, 100	0
2	F	181/195 (92%)	-0.37	1 (0%) 90 87	36, 65, 109, 145	0
2	H	179/195 (91%)	-0.23	3 (1%) 73 65	46, 73, 131, 160	0
All	All	2089/2276 (91%)	-0.19	35 (1%) 73 65	26, 71, 151, 201	0

All (35) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	90	GLY	4.8
1	E	323	SER	4.3
1	G	260	TRP	3.3
2	H	44	VAL	3.3
1	E	355	VAL	2.9
1	G	354	THR	2.9
1	G	324	LEU	2.8
1	A	0	PHE	2.8
1	E	257	ILE	2.6
2	H	43	ASN	2.6
1	C	324	LEU	2.6
1	E	263	SER	2.6
2	F	181	PRO	2.5
1	A	354	THR	2.5
2	H	50	PRO	2.5
1	G	323	SER	2.4

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Mol	Chain	Res	Type	RSRZ
1	E	356	THR	2.4
1	E	395	GLU	2.4
1	E	88	GLU	2.3
1	G	352	GLY	2.3
1	E	367	ASN	2.3
1	A	184	THR	2.2
1	C	323	SER	2.2
1	E	85	ASP	2.2
1	C	86	SER	2.2
1	A	345	THR	2.2
1	E	87	VAL	2.1
1	C	344	GLY	2.1
1	C	354	THR	2.1
1	E	81	GLN	2.1
1	A	378	GLU	2.1
1	A	303	ARG	2.1
1	C	367	ASN	2.0
1	G	348	TYR	2.0
1	E	86	SER	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^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å^2)	Q<0.9
3	PO4	E	501	5/5	0.89	0.21	-	83,92,93,97	0
3	PO4	C	501	5/5	0.88	0.16	-	97,100,103,111	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å^2)	Q<0.9
3	PO4	A	501	5/5	0.87	0.22	-	102,103,107,108	0
3	PO4	G	501	5/5	0.83	0.22	-	99,99,105,109	0

6.5 Other polymers (i)

There are no such residues in this entry.