Full wwPDB X-ray Structure Validation Report (i)

Jun 22, 2024 – 08:51 PM EDT

PDB ID	:	6IXV
Title	:	Crystal structure of SH3BP5-Rab11a
Authors	:	Goto-Ito, S.; Yamagata, A.; Sato, Y.; Fukai, S.
Deposited on	:	2018-12-12
Resolution	:	3.80 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

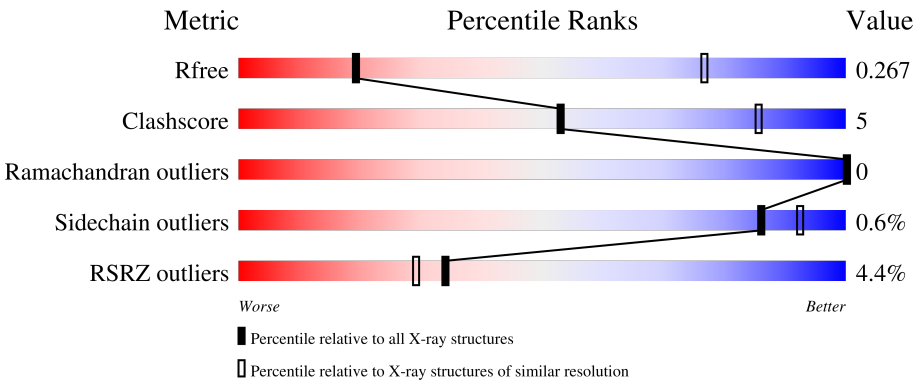
MolProbity	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	2.37.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

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 3.80 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1212 (4.00-3.60)
Clashscore	141614	1288 (4.00-3.60)
Ramachandran outliers	138981	1243 (4.00-3.60)
Sidechain outliers	138945	1237 (4.00-3.60)
RSRZ outliers	127900	1121 (4.00-3.60)

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 of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=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	269	74% 9% 17%
1	B	269	72% 12% 16%
1	C	269	71% 12% 17%
1	D	269	74% 10% 16%
2	E	175	2% 81% 17% •

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Mol	Chain	Length	Quality of chain
2	F	175	11% 76% 21% •
2	G	175	17% 81% 14% 6%
2	H	175	8% 78% 17% 5%

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 12750 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 SH3 domain-binding protein 5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	224	1840	1138	343	353	6	0	0	0
1	B	226	1860	1150	345	359	6	0	0	0
1	C	222	1830	1134	341	349	6	0	0	0
1	D	226	1852	1145	345	355	7	0	0	0

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	8	SER	-	expression tag	UNP O60239
A	9	HIS	-	expression tag	UNP O60239
B	8	SER	-	expression tag	UNP O60239
B	9	HIS	-	expression tag	UNP O60239
C	8	SER	-	expression tag	UNP O60239
C	9	HIS	-	expression tag	UNP O60239
D	8	SER	-	expression tag	UNP O60239
D	9	HIS	-	expression tag	UNP O60239

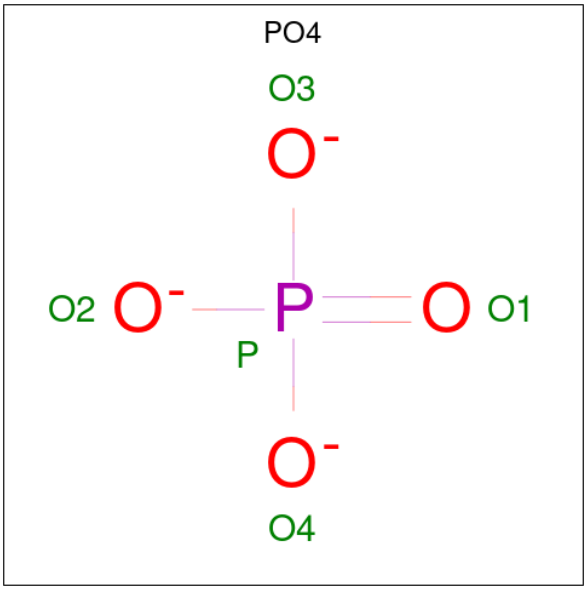
- Molecule 2 is a protein called Ras-related protein Rab-11A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	E	170	1356	856	235	264	1	0	0	0
2	F	170	1356	856	235	264	1	0	0	0
2	G	165	1312	831	224	256	1	0	0	0
2	H	167	1329	840	229	259	1	0	0	0

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	-1	SER	-	expression tag	UNP P62491
E	0	HIS	-	expression tag	UNP P62491
F	-1	SER	-	expression tag	UNP P62491
F	0	HIS	-	expression tag	UNP P62491
G	-1	SER	-	expression tag	UNP P62491
G	0	HIS	-	expression tag	UNP P62491
H	-1	SER	-	expression tag	UNP P62491
H	0	HIS	-	expression tag	UNP P62491

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



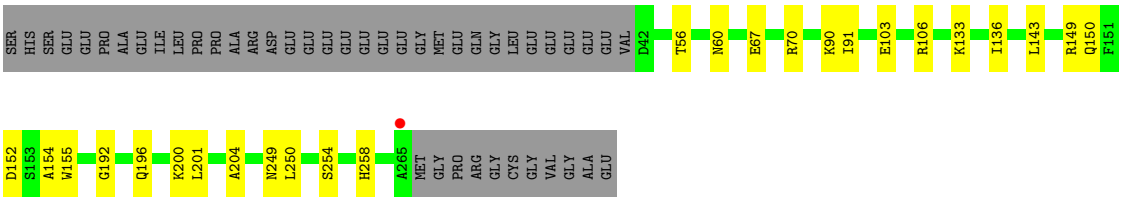
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	E	1	Total	O	P		0	0
			5	4	1			
3	F	1	Total	O	P		0	0
			5	4	1			
3	H	1	Total	O	P		0	0
			5	4	1			

3 Residue-property plots (i)

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

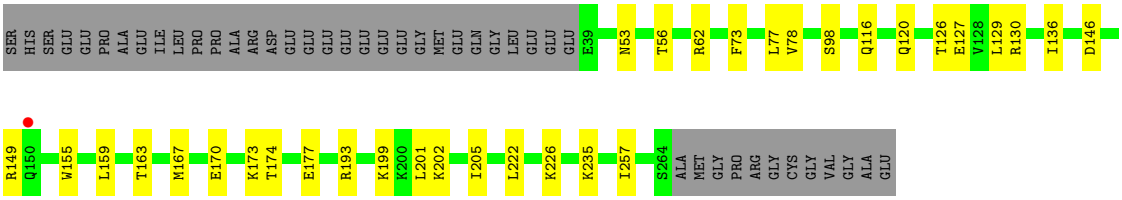
• Molecule 1: SH3 domain-binding protein 5

Chain A:



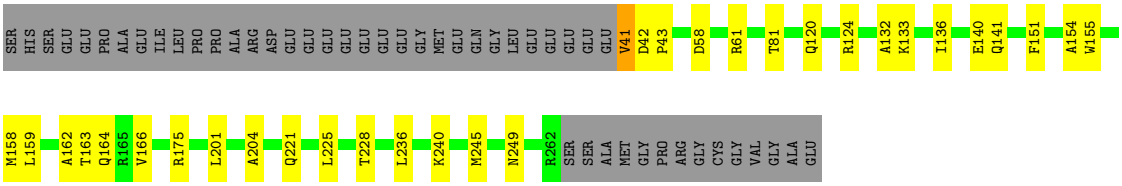
• Molecule 1: SH3 domain-binding protein 5

Chain B:



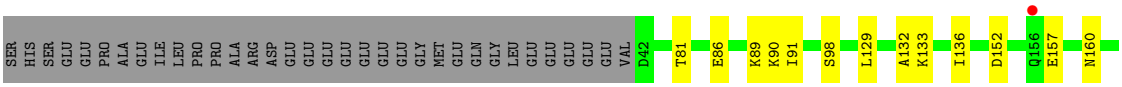
• Molecule 1: SH3 domain-binding protein 5

Chain C:



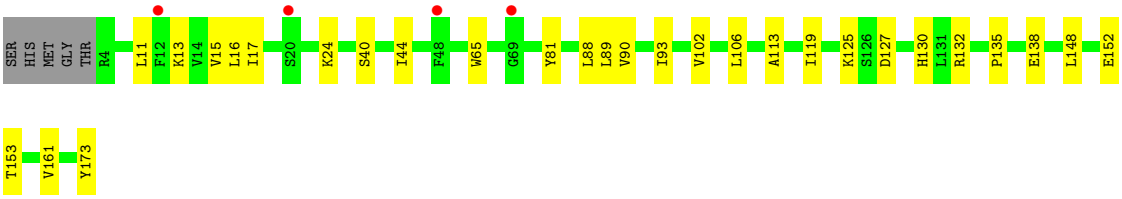
• Molecule 1: SH3 domain-binding protein 5

Chain D:



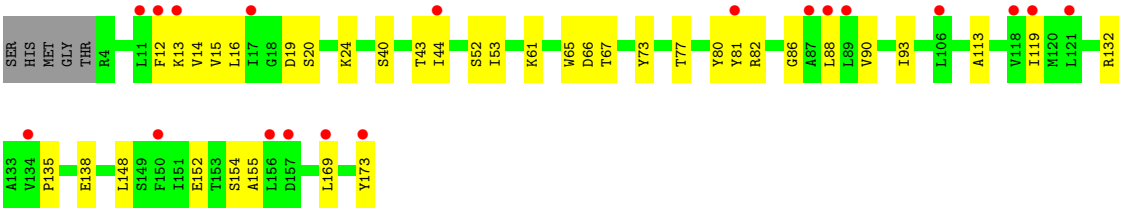
• Molecule 2: Ras-related protein Rab-11A

Chain E:



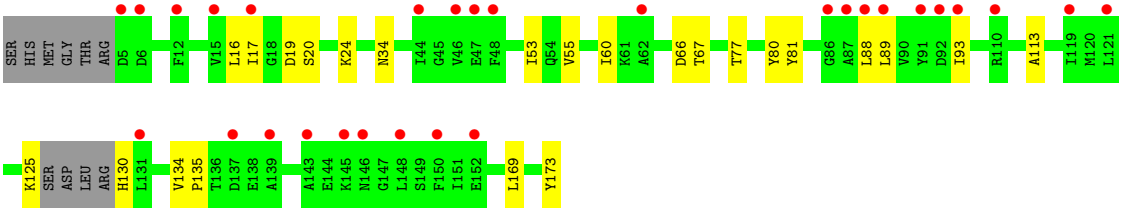
• Molecule 2: Ras-related protein Rab-11A

Chain F:



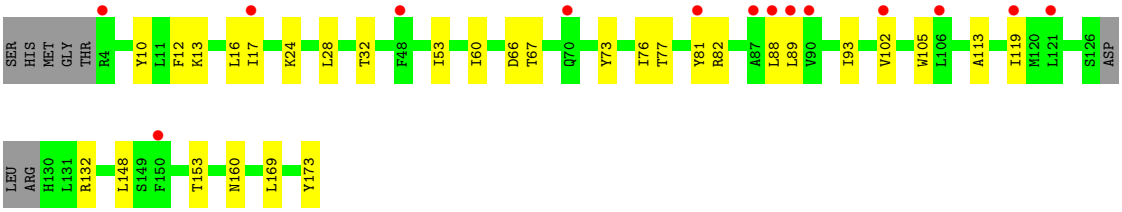
• Molecule 2: Ras-related protein Rab-11A

Chain G:



• Molecule 2: Ras-related protein Rab-11A

Chain H:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α, β, γ	117.81Å 199.07Å 303.90Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.77 – 3.80 49.77 – 3.80	Depositor EDS
% Data completeness (in resolution range)	99.9 (49.77-3.80) 99.7 (49.77-3.80)	Depositor EDS
R_{merge}	0.16	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.15 (at 3.77Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.229 , 0.259 0.243 , 0.267	Depositor DCC
R_{free} test set	1755 reflections (4.93%)	wwPDB-VP
Wilson B-factor (Å^2)	167.3	Xtriage
Anisotropy	0.084	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.31 , 160.8	EDS
L-test for twinning[2]	$< \|L\| > = 0.33$, $< L^2 > = 0.16$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	12750	wwPDB-VP
Average B, all atoms (Å^2)	224.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.84% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: 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	0.20	0/1859	0.34	0/2485
1	B	0.20	0/1879	0.35	0/2512
1	C	0.20	0/1849	0.34	0/2472
1	D	0.20	0/1871	0.35	0/2500
2	E	0.20	0/1378	0.36	0/1863
2	F	0.20	0/1378	0.34	0/1863
2	G	0.20	0/1333	0.35	0/1802
2	H	0.20	0/1350	0.34	0/1824
All	All	0.20	0/12897	0.35	0/17321

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 (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1840	0	1883	16	0
1	B	1860	0	1899	20	0
1	C	1830	0	1877	22	0
1	D	1852	0	1895	15	0
2	E	1356	0	1340	17	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	F	1356	0	1340	25	0
2	G	1312	0	1293	15	0
2	H	1329	0	1311	17	0
3	E	5	0	0	0	0
3	F	5	0	0	1	0
3	H	5	0	0	1	0
All	All	12750	0	12838	137	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 5.

All (137) 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:B:159:LEU:HD21	1:D:81:THR:HG21	1.73	0.69
1:C:159:LEU:HB2	1:C:163:THR:HG23	1.76	0.68
1:B:53:ASN:ND2	2:F:82:ARG:O	2.28	0.66
1:D:157:GLU:O	1:D:160:ASN:ND2	2.29	0.66
1:B:98:SER:HA	1:B:201:LEU:HD23	1.77	0.65
1:C:136:ILE:HD11	1:C:163:THR:HA	1.78	0.64
2:H:119:ILE:HB	2:H:148:LEU:HD22	1.80	0.62
1:D:245:MET:O	1:D:249:ASN:ND2	2.32	0.61
1:A:192:GLY:HA3	1:C:175:ARG:HH21	1.66	0.60
2:G:24:LYS:HZ2	2:G:67:THR:HG21	1.68	0.58
2:E:93:ILE:HD13	2:E:132:ARG:HG2	1.84	0.58
2:G:24:LYS:NZ	2:G:67:THR:HG21	2.19	0.58
1:A:254:SER:O	1:A:258:HIS:ND1	2.37	0.58
2:H:81:TYR:HB3	2:H:113:ALA:HB2	1.85	0.58
1:A:90:LYS:HG2	1:A:91:ILE:HG13	1.84	0.57
1:B:167:MET:HG3	1:D:226:LYS:HD3	1.86	0.57
2:F:66:ASP:OD1	2:F:67:THR:N	2.38	0.57
2:G:125:LYS:HE3	2:G:130:HIS:HB2	1.86	0.57
1:B:146:ASP:HB3	1:B:149:ARG:NH1	2.20	0.56
1:C:133:LYS:O	1:C:141:GLN:NE2	2.38	0.56
2:G:16:LEU:HD23	2:G:88:LEU:HB2	1.87	0.56
1:A:155:TRP:HH2	1:C:81:THR:HG21	1.71	0.56
1:D:98:SER:HA	1:D:201:LEU:HD13	1.88	0.56
1:C:136:ILE:HG23	1:C:140:GLU:HB2	1.88	0.55
2:E:15:VAL:HG12	2:E:65:TRP:HB2	1.87	0.55
2:E:93:ILE:HD11	2:E:125:LYS:HG3	1.88	0.55
1:D:132:ALA:HB1	1:D:166:VAL:HG12	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:201:LEU:HB3	1:D:204:ALA:HB3	1.88	0.55
2:F:20:SER:HA	2:F:24:LYS:HZ1	1.72	0.55
2:H:66:ASP:OD1	2:H:67:THR:N	2.41	0.54
2:E:135:PRO:HG2	2:E:138:GLU:HB2	1.90	0.54
2:F:16:LEU:HD23	2:F:88:LEU:HB2	1.88	0.53
2:F:132:ARG:NH1	2:F:152:GLU:OE1	2.35	0.53
1:B:257:ILE:HD12	2:F:43:THR:HB	1.90	0.53
1:D:91:ILE:HD13	1:D:207:LYS:HD2	1.91	0.53
1:D:133:LYS:HD2	1:D:136:ILE:HD11	1.90	0.53
2:H:102:VAL:HA	2:H:105:TRP:HD1	1.74	0.53
2:G:81:TYR:HB3	2:G:113:ALA:HB2	1.91	0.53
2:G:17:ILE:HG13	2:G:89:LEU:HD23	1.92	0.52
1:A:67:GLU:OE1	1:A:70:ARG:NH2	2.43	0.52
1:D:86:GLU:HA	1:D:89:LYS:HE3	1.91	0.52
1:B:136:ILE:HD11	1:B:163:THR:HA	1.91	0.52
2:F:19:ASP:O	2:F:24:LYS:NZ	2.38	0.51
1:C:155:TRP:CE2	1:C:164:GLN:HG2	2.45	0.51
1:A:56:THR:HG23	2:E:11:LEU:HD22	1.93	0.51
2:G:20:SER:HA	2:G:24:LYS:HE2	1.93	0.50
2:E:16:LEU:HD23	2:E:88:LEU:HB2	1.93	0.50
1:B:127:GLU:HG3	1:B:130:ARG:HH21	1.77	0.50
1:A:56:THR:O	1:A:60:ASN:ND2	2.44	0.49
2:H:16:LEU:HD23	2:H:88:LEU:HB2	1.92	0.49
2:H:89:LEU:HD22	2:H:102:VAL:HB	1.94	0.49
2:E:119:ILE:HB	2:E:148:LEU:HD22	1.95	0.49
2:H:13:LYS:NZ	2:H:82:ARG:O	2.44	0.49
1:C:245:MET:O	1:C:249:ASN:ND2	2.36	0.49
2:F:24:LYS:HG2	2:F:90:VAL:HB	1.95	0.49
1:A:200:LYS:HB2	1:A:201:LEU:HD22	1.95	0.49
1:C:201:LEU:HB3	1:C:204:ALA:HB3	1.95	0.48
2:E:24:LYS:NZ	2:E:90:VAL:O	2.45	0.48
2:H:17:ILE:HG13	2:H:89:LEU:HD23	1.94	0.48
1:A:201:LEU:HB3	1:A:204:ALA:HB3	1.96	0.48
1:C:132:ALA:HB1	1:C:166:VAL:HG22	1.96	0.48
2:H:73:TYR:HB3	2:H:77:THR:HG23	1.94	0.48
1:A:143:LEU:HD11	1:A:150:GLN:HE21	1.76	0.48
2:H:73:TYR:HD1	2:H:76:ILE:HD12	1.78	0.48
1:D:90:LYS:HG2	1:D:91:ILE:HG13	1.96	0.48
2:E:132:ARG:NH1	2:E:152:GLU:OE1	2.46	0.48
2:E:81:TYR:HB3	2:E:113:ALA:HB2	1.96	0.47
2:G:53:ILE:HD11	2:G:169:LEU:HD12	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:66:ASP:OD1	2:G:67:THR:N	2.42	0.47
1:D:129:LEU:HD21	1:D:170:GLU:HG2	1.97	0.47
2:F:135:PRO:HG2	2:F:138:GLU:HB2	1.96	0.47
1:B:56:THR:HG21	2:F:13:LYS:HE3	1.96	0.47
2:H:53:ILE:HD11	2:H:169:LEU:HD12	1.97	0.47
2:F:15:VAL:HG12	2:F:65:TRP:HB2	1.97	0.46
2:H:93:ILE:HD13	2:H:132:ARG:HG2	1.97	0.46
1:C:236:LEU:HG	1:C:240:LYS:HE3	1.97	0.46
1:C:158:MET:HB2	1:C:163:THR:HG21	1.97	0.46
1:B:129:LEU:HD21	1:B:170:GLU:HG2	1.97	0.46
1:C:225:LEU:O	1:C:228:THR:OG1	2.31	0.46
2:F:14:VAL:HG12	2:F:86:GLY:HA3	1.98	0.46
2:G:93:ILE:HD11	2:G:125:LYS:HB2	1.98	0.46
1:D:218:TYR:O	1:D:222:LEU:HG	2.16	0.46
2:F:77:THR:HA	2:F:80:TYR:HB3	1.98	0.46
1:C:159:LEU:HD13	1:C:162:ALA:HB3	1.97	0.45
1:C:58:ASP:HA	1:C:61:ARG:HD2	1.99	0.45
2:F:24:LYS:NZ	3:F:201:PO4:O2	2.49	0.45
2:F:93:ILE:HD13	2:F:132:ARG:HG2	1.98	0.45
2:E:17:ILE:HG13	2:E:89:LEU:HD23	1.99	0.45
1:B:174:THR:HA	1:B:177:GLU:HG2	1.99	0.45
1:A:196:GLN:HG2	1:A:200:LYS:HE3	1.98	0.45
2:F:52:SER:HA	2:F:61:LYS:HA	1.99	0.45
2:H:24:LYS:NZ	3:H:201:PO4:O4	2.48	0.45
2:H:153:THR:HG22	2:H:160:ASN:HB2	1.99	0.45
2:F:13:LYS:HZ3	2:F:65:TRP:HZ2	1.65	0.44
1:A:249:ASN:OD1	1:A:250:LEU:N	2.50	0.44
1:B:62:ARG:HH11	1:B:235:LYS:HB3	1.82	0.44
1:B:193:ARG:HH21	1:D:175:ARG:HH12	1.65	0.44
1:D:259:GLU:OE2	1:D:262:ARG:NH1	2.51	0.44
2:E:89:LEU:HD13	2:E:102:VAL:HB	2.00	0.44
1:C:221:GLN:O	1:C:225:LEU:HG	2.18	0.44
1:A:200:LYS:HD3	1:C:155:TRP:CZ2	2.52	0.44
2:G:77:THR:HA	2:G:80:TYR:HB3	2.00	0.44
1:B:126:THR:HG22	1:B:173:LYS:HE3	1.99	0.44
1:C:151:PHE:HD2	1:C:154:ALA:HB2	1.82	0.43
2:E:40:SER:O	2:E:44:ILE:N	2.51	0.43
2:H:28:LEU:O	2:H:32:THR:OG1	2.27	0.43
1:B:199:LYS:HD2	1:B:202:LYS:HD2	1.99	0.43
2:E:13:LYS:HE3	2:E:65:TRP:CD2	2.53	0.43
2:F:81:TYR:HB3	2:F:113:ALA:HB2	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:12:PHE:HD2	2:F:169:LEU:HD22	1.83	0.43
1:A:103:GLU:HG3	1:A:106:ARG:HE	1.84	0.43
1:A:152:ASP:OD2	1:A:154:ALA:HB3	2.19	0.43
2:E:89:LEU:HD11	2:E:106:LEU:HG	2.01	0.42
2:G:34:ASN:OD1	2:G:34:ASN:N	2.52	0.42
2:H:10:TYR:HB2	2:H:60:ILE:HG12	2.02	0.42
1:C:120:GLN:O	1:C:124:ARG:HG3	2.20	0.42
2:E:153:THR:HG21	2:E:161:VAL:HG22	2.02	0.42
1:B:222:LEU:O	1:B:226:LYS:N	2.53	0.42
1:C:41:VAL:HG12	1:C:42:ASP:H	1.84	0.42
1:B:116:GLN:O	1:B:120:GLN:HG2	2.19	0.42
2:E:127:ASP:OD1	2:E:130:HIS:ND1	2.53	0.42
2:F:40:SER:HB2	2:F:44:ILE:HB	2.02	0.42
2:F:119:ILE:HB	2:F:148:LEU:HD22	2.02	0.42
2:G:55:VAL:HB	2:G:60:ILE:HD12	2.02	0.42
1:B:98:SER:HB2	1:B:205:ILE:HG22	2.02	0.41
1:C:41:VAL:HB	1:C:43:PRO:HD2	2.02	0.41
1:C:159:LEU:O	1:C:163:THR:OG1	2.34	0.41
1:A:133:LYS:HA	1:A:136:ILE:HG22	2.03	0.41
2:F:154:SER:OG	2:F:155:ALA:N	2.54	0.41
2:F:53:ILE:HD11	2:F:169:LEU:HD12	2.02	0.40
2:G:19:ASP:C	2:G:24:LYS:HZ3	2.24	0.40
1:B:73:PHE:CE1	1:B:222:LEU:HB2	2.55	0.40
1:B:77:LEU:HD12	1:B:78:VAL:HG13	2.03	0.40
2:F:73:TYR:HB3	2:F:77:THR:HG23	2.02	0.40
2:G:134:VAL:N	2:G:135:PRO:HD3	2.36	0.40
2:H:12:PHE:HD2	2:H:169:LEU:HD22	1.86	0.40
2:F:73:TYR:O	2:F:77:THR:OG1	2.39	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	222/269 (82%)	218 (98%)	4 (2%)	0	100	100
1	B	224/269 (83%)	221 (99%)	3 (1%)	0	100	100
1	C	220/269 (82%)	216 (98%)	4 (2%)	0	100	100
1	D	224/269 (83%)	221 (99%)	3 (1%)	0	100	100
2	E	168/175 (96%)	162 (96%)	6 (4%)	0	100	100
2	F	168/175 (96%)	158 (94%)	10 (6%)	0	100	100
2	G	161/175 (92%)	152 (94%)	9 (6%)	0	100	100
2	H	163/175 (93%)	156 (96%)	7 (4%)	0	100	100
All	All	1550/1776 (87%)	1504 (97%)	46 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains (i)

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	195/231 (84%)	194 (100%)	1 (0%)	88	94
1	B	198/231 (86%)	197 (100%)	1 (0%)	88	94
1	C	194/231 (84%)	193 (100%)	1 (0%)	88	94
1	D	196/231 (85%)	195 (100%)	1 (0%)	88	94
2	E	144/148 (97%)	143 (99%)	1 (1%)	84	91
2	F	144/148 (97%)	143 (99%)	1 (1%)	84	91
2	G	139/148 (94%)	138 (99%)	1 (1%)	84	91
2	H	141/148 (95%)	140 (99%)	1 (1%)	84	91
All	All	1351/1516 (89%)	1343 (99%)	8 (1%)	86	92

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	149	ARG
1	B	155	TRP

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Mol	Chain	Res	Type
1	C	41	VAL
1	D	152	ASP
2	E	173	TYR
2	F	173	TYR
2	G	173	TYR
2	H	173	TYR

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

Mol	Chain	Res	Type
1	A	150	GLN
1	B	150	GLN
1	B	180	HIS
1	C	221	GLN
2	F	63	GLN
2	G	63	GLN

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 monosaccharides in this entry.

5.6 Ligand geometry (i)

3 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	E	201	-	4,4,4	0.96	0	6,6,6	0.47	0
3	PO4	H	201	-	4,4,4	0.96	0	6,6,6	0.46	0
3	PO4	F	201	-	4,4,4	0.96	0	6,6,6	0.46	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.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	H	201	PO4	1	0
3	F	201	PO4	1	0

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	224/269 (83%)	-0.14	1 (0%)	92	89	145, 190, 235, 283	0
1	B	226/269 (84%)	-0.12	1 (0%)	92	89	154, 194, 255, 284	0
1	C	222/269 (82%)	-0.03	0	100	100	153, 202, 261, 289	0
1	D	226/269 (84%)	-0.05	1 (0%)	92	89	144, 204, 292, 339	0
2	E	170/175 (97%)	0.20	4 (2%)	59	50	175, 218, 261, 315	0
2	F	170/175 (97%)	0.42	19 (11%)	5	5	194, 261, 296, 326	0
2	G	165/175 (94%)	0.80	29 (17%)	1	1	191, 272, 314, 334	0
2	H	167/175 (95%)	0.64	14 (8%)	11	9	176, 267, 303, 310	0
All	All	1570/1776 (88%)	0.17	69 (4%)	34	29	144, 218, 296, 339	0

All (69) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	G	17	ILE	6.4
2	H	70	GLN	5.8
2	H	89	LEU	5.2
2	G	46	VAL	4.8
2	E	69	GLY	4.7
2	G	44	ILE	4.4
2	H	17	ILE	4.4
2	G	121	LEU	4.3
2	F	150	PHE	4.3
2	G	152	GLU	4.2
2	H	119	ILE	4.2
2	H	87	ALA	4.0
2	H	121	LEU	4.0
2	G	150	PHE	3.9
2	G	48	PHE	3.9
2	F	12	PHE	3.8

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Mol	Chain	Res	Type	RSRZ
2	H	4	ARG	3.8
2	G	146	ASN	3.5
2	F	87	ALA	3.5
2	H	88	LEU	3.5
2	F	81	TYR	3.4
2	G	91	TYR	3.3
2	G	93	ILE	3.3
2	G	110	ARG	3.2
2	H	48	PHE	3.2
2	G	119	ILE	3.1
2	F	119	ILE	3.0
1	B	150	GLN	3.0
2	H	90	VAL	3.0
2	G	89	LEU	3.0
2	G	12	PHE	2.9
2	H	150	PHE	2.9
2	H	81	TYR	2.9
2	G	137	ASP	2.9
2	F	17	ILE	2.8
2	G	6	ASP	2.8
2	F	156	LEU	2.8
2	G	87	ALA	2.7
2	G	5	ASP	2.6
2	F	13	LYS	2.6
2	G	139	ALA	2.6
2	G	148	LEU	2.6
2	F	121	LEU	2.6
2	G	88	LEU	2.6
2	F	169	LEU	2.6
1	D	156	GLN	2.4
2	F	118	VAL	2.4
2	G	131	LEU	2.4
2	G	15	VAL	2.4
2	F	173	TYR	2.4
2	H	106	LEU	2.4
2	G	145	LYS	2.4
2	F	11	LEU	2.4
2	H	102	VAL	2.3
2	F	88	LEU	2.3
2	F	134	VAL	2.2
2	F	44	ILE	2.2
2	G	47	GLU	2.2

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Mol	Chain	Res	Type	RSRZ
2	G	92	ASP	2.2
1	A	265	ALA	2.2
2	G	86	GLY	2.1
2	F	89	LEU	2.1
2	F	106	LEU	2.1
2	G	143	ALA	2.1
2	E	12	PHE	2.1
2	G	62	ALA	2.0
2	E	48	PHE	2.0
2	F	157	ASP	2.0
2	E	20	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 monosaccharides 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. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	PO4	E	201	5/5	0.89	0.52	210,225,274,284	0
3	PO4	H	201	5/5	0.94	0.17	266,276,293,294	0
3	PO4	F	201	5/5	0.95	0.22	263,273,286,289	0

6.5 Other polymers (i)

There are no such residues in this entry.