Full wwPDB X-ray Structure Validation Report ⓘ

Aug 9, 2020 – 10:12 AM BST

PDB ID	:	6S76
Title	:	Crystal structure of human Nek7
Authors	:	Nasir, N.; Bayliss, R.
Deposited on	:	2019-07-04
Resolution	:	3.38 Å(reported)

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

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

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

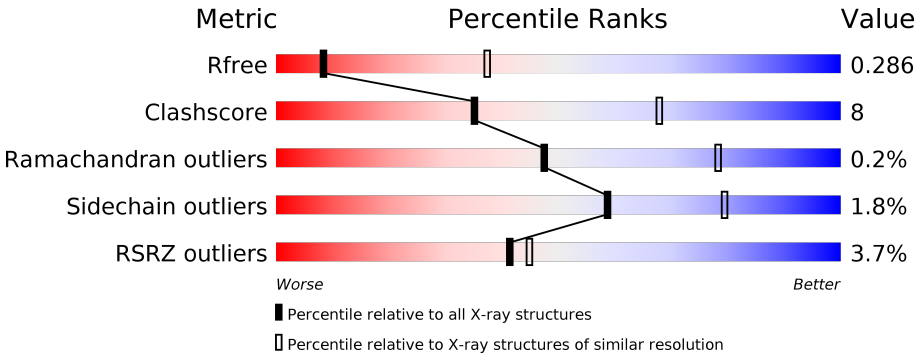
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.13.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.13.1

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 3.38 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	1691 (3.46-3.30)
Clashscore	141614	1762 (3.46-3.30)
Ramachandran outliers	138981	1732 (3.46-3.30)
Sidechain outliers	138945	1731 (3.46-3.30)
RSRZ outliers	127900	1635 (3.46-3.30)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=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	310	4% 71% 15% 14%
1	B	310	67% 19% 14%
1	C	310	3% 74% 11% 15%
1	D	310	5% 73% 11% 17%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 13565 atoms, of which 6168 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 Serine/threonine-protein kinase Nek7.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	266	Total	C	H	N	O	S	0	0	0
			3528	1210	1632	321	348	17			
1	B	267	Total	C	H	N	O	S	0	0	0
			3686	1245	1741	338	345	17			
1	C	264	Total	C	H	N	O	S	0	0	0
			3290	1168	1465	306	337	14			
1	D	258	Total	C	H	N	O	S	0	0	0
			3044	1095	1320	298	319	12			

There are 32 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	303	LEU	-	expression tag	UNP Q8TDX7
A	304	GLU	-	expression tag	UNP Q8TDX7
A	305	HIS	-	expression tag	UNP Q8TDX7
A	306	HIS	-	expression tag	UNP Q8TDX7
A	307	HIS	-	expression tag	UNP Q8TDX7
A	308	HIS	-	expression tag	UNP Q8TDX7
A	309	HIS	-	expression tag	UNP Q8TDX7
A	310	HIS	-	expression tag	UNP Q8TDX7
B	303	LEU	-	expression tag	UNP Q8TDX7
B	304	GLU	-	expression tag	UNP Q8TDX7
B	305	HIS	-	expression tag	UNP Q8TDX7
B	306	HIS	-	expression tag	UNP Q8TDX7
B	307	HIS	-	expression tag	UNP Q8TDX7
B	308	HIS	-	expression tag	UNP Q8TDX7
B	309	HIS	-	expression tag	UNP Q8TDX7
B	310	HIS	-	expression tag	UNP Q8TDX7
C	303	LEU	-	expression tag	UNP Q8TDX7
C	304	GLU	-	expression tag	UNP Q8TDX7
C	305	HIS	-	expression tag	UNP Q8TDX7
C	306	HIS	-	expression tag	UNP Q8TDX7
C	307	HIS	-	expression tag	UNP Q8TDX7

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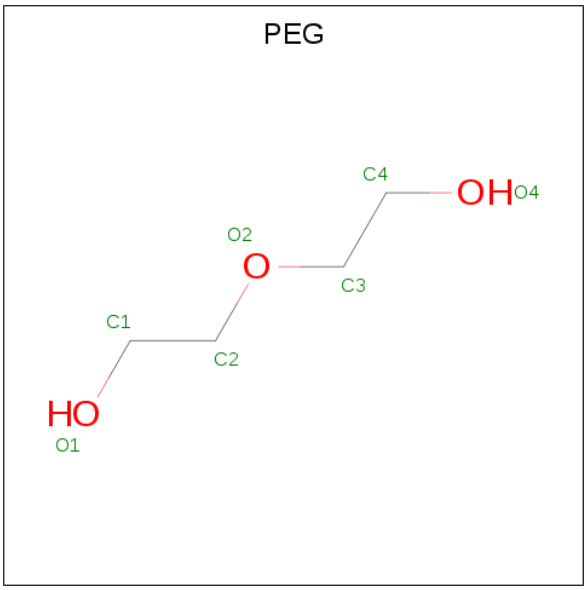
Chain	Residue	Modelled	Actual	Comment	Reference
C	308	HIS	-	expression tag	UNP Q8TDX7
C	309	HIS	-	expression tag	UNP Q8TDX7
C	310	HIS	-	expression tag	UNP Q8TDX7
D	303	LEU	-	expression tag	UNP Q8TDX7
D	304	GLU	-	expression tag	UNP Q8TDX7
D	305	HIS	-	expression tag	UNP Q8TDX7
D	306	HIS	-	expression tag	UNP Q8TDX7
D	307	HIS	-	expression tag	UNP Q8TDX7
D	308	HIS	-	expression tag	UNP Q8TDX7
D	309	HIS	-	expression tag	UNP Q8TDX7
D	310	HIS	-	expression tag	UNP Q8TDX7

- Molecule 2 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: $C_4H_{10}O_3$).



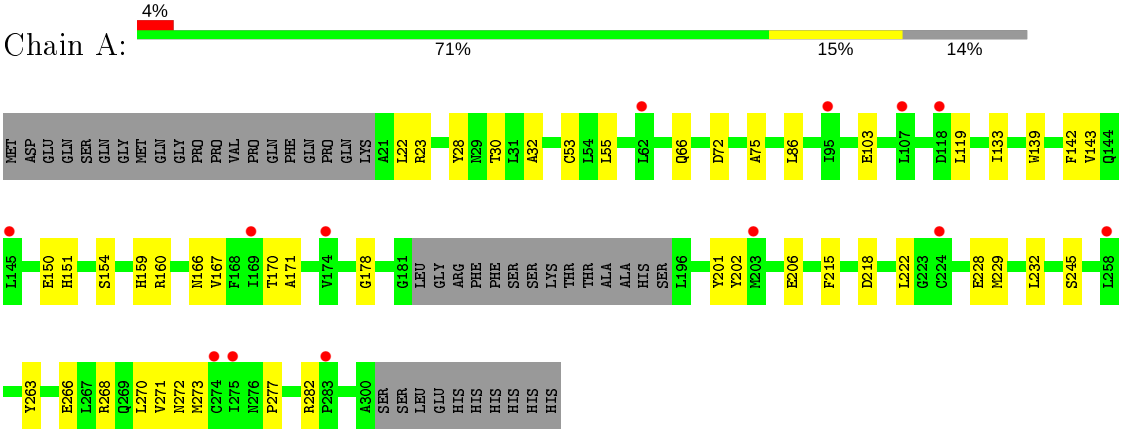
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	H	O		
2	A	1	17	4	10	3	0	0

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.

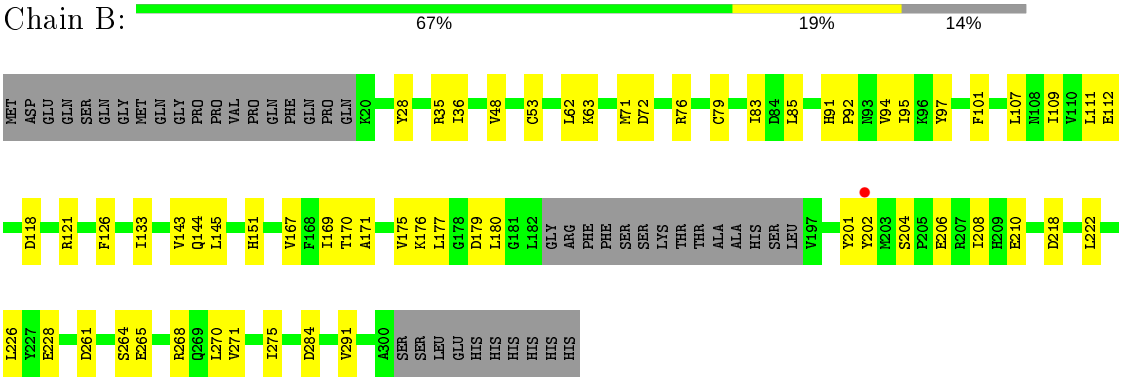
- Molecule 1: Serine/threonine-protein kinase Nek7

Chain A:



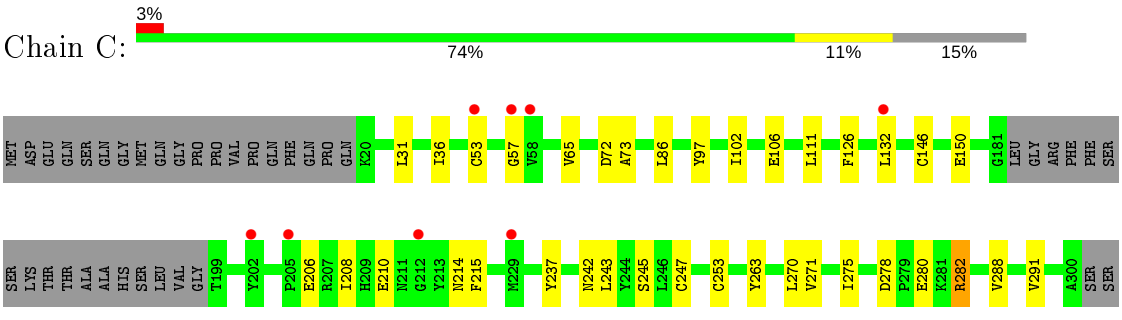
- Molecule 1: Serine/threonine-protein kinase Nek7

Chain B:

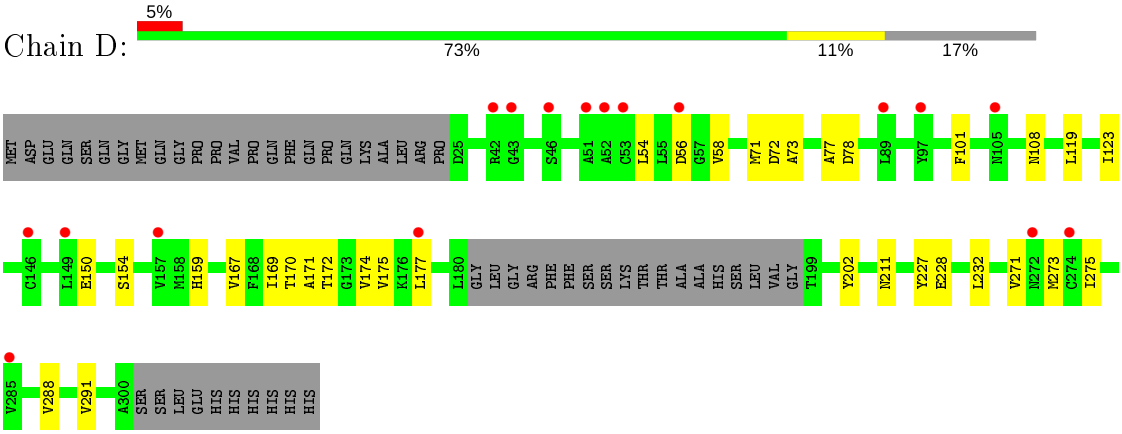


- Molecule 1: Serine/threonine-protein kinase Nek7

Chain C:



• Molecule 1: Serine/threonine-protein kinase Nek7



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	50.25Å 168.06Å 83.44Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	74.74 – 3.38 74.74 – 3.38	Depositor EDS
% Data completeness (in resolution range)	99.5 (74.74-3.38) 99.4 (74.74-3.38)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.77 (at 3.41Å)	Xtriage
Refinement program	PHENIX 1.14_3260	Depositor
R, R_{free}	0.262 , 0.286 0.262 , 0.286	Depositor DCC
R_{free} test set	985 reflections (5.11%)	wwPDB-VP
Wilson B-factor (Å^2)	88.3	Xtriage
Anisotropy	0.562	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.33 , 87.1	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.34$	Xtriage
Estimated twinning fraction	0.029 for h,-k,-l	Xtriage
F_o,F_c correlation	0.90	EDS
Total number of atoms	13565	wwPDB-VP
Average B, all atoms (Å^2)	99.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.78% 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

5.1 Standard geometry

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

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	0.25	0/1941	0.41	0/2659
1	B	0.25	0/1989	0.44	0/2714
1	C	0.25	0/1868	0.41	0/2569
1	D	0.24	0/1764	0.42	0/2431
All	All	0.25	0/7562	0.42	0/10373

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1896	1632	1652	30	0
1	B	1945	1741	1768	40	0
1	C	1825	1465	1539	19	0
1	D	1724	1320	1376	24	0
2	A	7	10	10	0	0
All	All	7397	6168	6345	112	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 (112) 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:C:102:ILE:H	1:D:54:LEU:HD11	1.47	0.78
1:B:202:TYR:OH	1:B:228:GLU:OE2	2.10	0.69
1:D:71:MET:CB	1:D:77:ALA:HB1	2.21	0.68
1:D:169:ILE:HA	1:D:175:VAL:HG12	1.76	0.67
1:A:151:HIS:O	1:A:154:SER:OG	2.14	0.66
1:B:167:VAL:HG12	1:B:177:LEU:HD12	1.79	0.65
1:D:228:GLU:O	1:D:232:LEU:N	2.29	0.64
1:D:202:TYR:OH	1:D:228:GLU:OE2	2.12	0.64
1:D:159:HIS:CE1	1:D:177:LEU:HD22	2.33	0.63
1:B:92:PRO:O	1:B:176:LYS:HE3	1.98	0.63
1:B:270:LEU:HD13	1:B:291:VAL:HG11	1.82	0.62
1:A:30:THR:HG23	1:A:103:GLU:OE2	2.00	0.62
1:A:277:PRO:O	1:A:282:ARG:NH2	2.35	0.60
1:C:36:ILE:O	1:C:36:ILE:HG22	2.03	0.58
1:A:139:TRP:O	1:A:143:VAL:HG12	2.03	0.58
1:D:119:LEU:HD23	1:D:123:ILE:HG23	1.85	0.58
1:A:263:TYR:O	1:A:268:ARG:NH1	2.36	0.58
1:B:72:ASP:O	1:B:76:ARG:N	2.38	0.57
1:A:66:GLN:HG2	1:A:66:GLN:O	2.05	0.57
1:C:208:ILE:HD12	1:C:247:CYS:SG	2.44	0.56
1:B:48:VAL:HG12	1:B:63:LYS:HA	1.88	0.56
1:D:227:TYR:HB2	1:D:271:VAL:HG21	1.89	0.55
1:D:167:VAL:HG23	1:D:167:VAL:O	2.08	0.54
1:B:145:LEU:CD2	1:B:222:LEU:HD11	2.37	0.54
1:A:72:ASP:O	1:A:75:ALA:N	2.41	0.54
1:C:31:LEU:HD23	1:C:31:LEU:O	2.06	0.54
1:A:266:GLU:OE2	1:A:266:GLU:N	2.42	0.53
1:B:261:ASP:OD1	1:B:261:ASP:N	2.41	0.53
1:D:288:VAL:HA	1:D:291:VAL:HG12	1.89	0.53
1:D:119:LEU:HB2	1:D:167:VAL:HG23	1.92	0.52
1:A:28:TYR:HE1	1:A:53:CYS:HG	1.58	0.52
1:B:126:PHE:CD2	1:B:133:ILE:HD13	2.45	0.52
1:D:167:VAL:HG12	1:D:177:LEU:HD23	1.91	0.51
1:B:28:TYR:HE1	1:B:53:CYS:HG	1.59	0.51
1:C:243:LEU:O	1:C:247:CYS:N	2.43	0.51
1:B:83:ILE:HG22	1:B:83:ILE:O	2.10	0.50
1:C:206:GLU:OE1	1:C:282:ARG:NH2	2.41	0.50
1:A:30:THR:HG22	1:A:32:ALA:H	1.76	0.50
1:C:242:ASN:HD21	1:C:245:SER:HB3	1.77	0.50
1:A:133:ILE:HG13	1:A:232:LEU:HD11	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:169:ILE:HG22	1:B:175:VAL:HG23	1.94	0.50
1:B:35:ARG:O	1:B:35:ARG:HG3	2.12	0.50
1:B:83:ILE:HD12	1:B:83:ILE:N	2.28	0.49
1:B:226:LEU:CD2	1:B:270:LEU:HD23	2.41	0.49
1:B:91:HIS:HB3	1:B:94:VAL:HG12	1.94	0.49
1:A:66:GLN:CG	1:A:66:GLN:O	2.61	0.49
1:B:206:GLU:OE1	1:B:206:GLU:N	2.46	0.48
1:C:132:LEU:HD12	1:C:263:TYR:OH	2.13	0.48
1:A:119:LEU:O	1:A:119:LEU:HD23	2.14	0.48
1:C:132:LEU:H	1:C:132:LEU:HD23	1.79	0.47
1:D:72:ASP:O	1:D:73:ALA:HB3	2.15	0.47
1:C:270:LEU:HD13	1:C:291:VAL:HG11	1.97	0.47
1:B:268:ARG:O	1:B:271:VAL:HG22	2.14	0.47
1:B:118:ASP:OD2	1:B:121:ARG:NH2	2.49	0.46
1:B:79:CYS:O	1:B:83:ILE:HD13	2.16	0.46
1:C:271:VAL:HG22	1:C:275:ILE:HD12	1.98	0.46
1:C:53:CYS:O	1:C:57:GLY:N	2.48	0.46
1:B:264:SER:O	1:B:265:GLU:CB	2.64	0.46
1:B:79:CYS:O	1:B:83:ILE:CD1	2.63	0.46
1:B:143:VAL:HG13	1:B:144:GLN:N	2.31	0.46
1:B:275:ILE:HG22	1:B:275:ILE:O	2.16	0.45
1:D:275:ILE:O	1:D:275:ILE:HG22	2.16	0.45
1:A:166:ASN:O	1:A:178:GLY:N	2.49	0.45
1:B:126:PHE:HD2	1:B:133:ILE:HD13	1.81	0.45
1:A:271:VAL:HG23	1:A:272:ASN:N	2.31	0.45
1:A:22:LEU:HD21	1:A:55:LEU:HD21	1.98	0.45
1:B:169:ILE:HD12	1:B:170:THR:N	2.32	0.45
1:A:86:LEU:HD23	1:A:86:LEU:C	2.37	0.45
1:B:91:HIS:HB2	1:B:151:HIS:ND1	2.32	0.45
1:C:72:ASP:O	1:C:73:ALA:HB3	2.17	0.45
1:B:204:SER:O	1:B:208:ILE:HG13	2.16	0.45
1:C:253:CYS:SG	1:C:275:ILE:HG22	2.57	0.45
1:D:172:THR:HG23	1:D:174:VAL:HG12	1.98	0.44
1:A:215:PHE:O	1:A:218:ASP:N	2.50	0.44
1:B:85:LEU:HD12	1:B:97:TYR:CZ	2.53	0.44
1:B:62:LEU:HD12	1:B:62:LEU:O	2.18	0.44
1:D:150:GLU:O	1:D:154:SER:N	2.48	0.44
1:B:85:LEU:HD13	1:B:180:LEU:HD13	1.99	0.44
1:A:150:GLU:O	1:A:154:SER:N	2.47	0.44
1:D:170:THR:HG22	1:D:171:ALA:N	2.33	0.44
1:A:142:PHE:HE1	1:A:222:LEU:HD11	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:71:MET:O	1:B:71:MET:HG3	2.17	0.43
1:D:56:ASP:OD1	1:D:58:VAL:HG12	2.18	0.43
1:C:146:CYS:O	1:C:150:GLU:N	2.43	0.43
1:C:97:TYR:HA	1:C:111:LEU:HD23	1.99	0.43
1:A:159:HIS:O	1:A:160:ARG:HB2	2.19	0.42
1:B:284:ASP:N	1:B:284:ASP:OD1	2.43	0.42
1:C:214:ASN:OD1	1:C:215:PHE:N	2.52	0.42
1:C:270:LEU:HD11	1:C:288:VAL:HG23	2.01	0.42
1:B:95:ILE:HD11	1:B:179:ASP:H	1.83	0.42
1:B:36:ILE:HG12	1:B:62:LEU:HD21	2.01	0.42
1:A:119:LEU:HB2	1:A:167:VAL:HG13	2.01	0.42
1:A:133:ILE:HD12	1:A:229:MET:O	2.18	0.42
1:C:65:VAL:O	1:C:106:GLU:CB	2.67	0.42
1:B:170:THR:OG1	1:B:171:ALA:N	2.52	0.42
1:D:271:VAL:C	1:D:273:MET:H	2.22	0.42
1:A:232:LEU:N	1:A:232:LEU:HD12	2.35	0.42
1:D:119:LEU:HD13	1:D:167:VAL:HG21	2.01	0.41
1:B:101:PHE:O	1:B:107:LEU:HD12	2.21	0.41
1:A:170:THR:HG22	1:A:171:ALA:N	2.36	0.41
1:A:206:GLU:OE2	1:A:282:ARG:NH2	2.50	0.41
1:B:109:ILE:CG2	1:B:111:LEU:HD21	2.50	0.41
1:B:95:ILE:HB	1:B:112:GLU:HG2	2.02	0.41
1:A:270:LEU:HD12	1:A:273:MET:HE3	2.03	0.41
1:A:142:PHE:CE1	1:A:222:LEU:HD11	2.55	0.41
1:A:202:TYR:OH	1:A:228:GLU:OE1	2.34	0.41
1:B:63:LYS:N	1:B:109:ILE:O	2.42	0.41
1:D:101:PHE:N	1:D:108:ASN:O	2.48	0.40
1:D:159:HIS:HE1	1:D:177:LEU:HD22	1.86	0.40
1:D:77:ALA:O	1:D:78:ASP:CB	2.70	0.40
1:D:56:ASP:N	1:D:56:ASP:OD1	2.49	0.40
1:A:22:LEU:HD23	1:A:23:ARG:N	2.37	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	262/310 (84%)	244 (93%)	18 (7%)	0	100	100
1	B	263/310 (85%)	248 (94%)	14 (5%)	1 (0%)	34	68
1	C	260/310 (84%)	226 (87%)	33 (13%)	1 (0%)	34	68
1	D	254/310 (82%)	224 (88%)	30 (12%)	0	100	100
All	All	1039/1240 (84%)	942 (91%)	95 (9%)	2 (0%)	47	78

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	86	LEU
1	B	210	GLU

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	168/274 (61%)	166 (99%)	2 (1%)	71	85
1	B	177/274 (65%)	175 (99%)	2 (1%)	73	86
1	C	152/274 (56%)	146 (96%)	6 (4%)	32	62
1	D	130/274 (47%)	129 (99%)	1 (1%)	81	91
All	All	627/1096 (57%)	616 (98%)	11 (2%)	59	79

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	201	TYR
1	A	245	SER
1	B	201	TYR
1	B	218	ASP
1	C	126	PHE
1	C	210	GLU

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Mol	Chain	Res	Type
1	C	237	TYR
1	C	278	ASP
1	C	280	GLU
1	C	282	ARG
1	D	211	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	151	HIS

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 monosaccharides in this entry.

5.6 Ligand geometry

1 ligand is 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	PEG	A	401	-	6,6,6	0.49	0	5,5,5	0.29	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	PEG	A	401	-	-	2/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	401	PEG	C4-C3-O2-C2
2	A	401	PEG	O1-C1-C2-O2

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^{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	266/310 (85%)	0.35	13 (4%) 29 33	49, 84, 131, 156	0
1	B	267/310 (86%)	0.30	1 (0%) 92 95	48, 79, 130, 171	0
1	C	264/310 (85%)	0.21	8 (3%) 50 54	48, 91, 142, 222	0
1	D	258/310 (83%)	0.33	17 (6%) 18 22	63, 103, 164, 244	0
All	All	1055/1240 (85%)	0.30	39 (3%) 41 45	48, 89, 144, 244	0

All (39) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	177	LEU	3.7
1	D	89	LEU	3.6
1	C	53	CYS	3.3
1	D	53	CYS	3.2
1	D	105	ASN	3.2
1	D	146	CYS	3.1
1	A	169	ILE	3.0
1	D	97	TYR	2.9
1	D	149	LEU	2.7
1	A	118	ASP	2.7
1	C	212	GLY	2.7
1	A	274	CYS	2.7
1	A	224	CYS	2.7
1	A	62	LEU	2.6
1	D	52	ALA	2.6
1	A	107	LEU	2.6
1	C	132	LEU	2.6
1	D	285	VAL	2.5
1	D	51	ALA	2.5
1	C	229	MET	2.5
1	A	203	MET	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	283	PRO	2.4
1	C	205	PRO	2.4
1	D	46	SER	2.4
1	C	58	VAL	2.3
1	D	42	ARG	2.3
1	C	57	GLY	2.3
1	A	174	VAL	2.3
1	C	202	TYR	2.2
1	A	95	ILE	2.2
1	A	258	LEU	2.1
1	A	145	LEU	2.1
1	D	272	ASN	2.1
1	D	56	ASP	2.1
1	B	202	TYR	2.0
1	D	274	CYS	2.0
1	D	157	VAL	2.0
1	D	43	GLY	2.0
1	A	275	ILE	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, 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	B-factors(Å^2)	Q<0.9
2	PEG	A	401	7/7	0.73	0.31	83,106,124,124	0

6.5 Other polymers (i)

There are no such residues in this entry.