Full wwPDB X-ray Structure Validation Report ⓘ

May 14, 2020 – 03:09 pm BST

PDB ID	:	4RFX
Title	:	Crystal Structure of the Dynactin DCTN1 Fragment involved in Dynein Interaction
Authors	:	Findeisen, P.; Eckert, C.; Kollmar, M.
Deposited on	:	2014-09-29
Resolution	:	2.90 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:

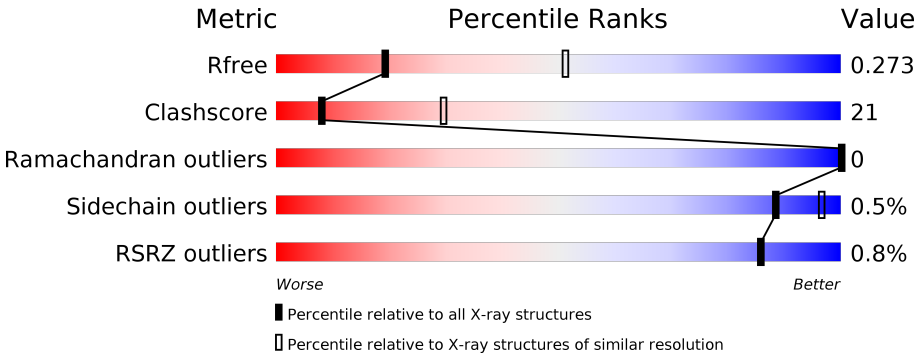
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

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 2.90 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	1957 (2.90-2.90)
Clashscore	141614	2172 (2.90-2.90)
Ramachandran outliers	138981	2115 (2.90-2.90)
Sidechain outliers	138945	2117 (2.90-2.90)
RSRZ outliers	127900	1906 (2.90-2.90)

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	141	47% 24% 29%
1	B	141	% 48% 21% 30%
1	C	141	57% 14% 28%
1	D	141	56% 15% 29%
1	E	141	2% 44% 23% 33%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 4065 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 Dynactin subunit 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	100	Total	C	N	O	S	0	0	0
			822	494	149	175	4			
1	B	98	Total	C	N	O	S	0	0	0
			807	484	147	173	3			
1	C	101	Total	C	N	O	S	0	0	0
			831	499	150	178	4			
1	D	100	Total	C	N	O	S	0	0	0
			823	494	149	177	3			
1	E	95	Total	C	N	O	S	0	0	0
			782	470	143	166	3			

There are 100 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	393	MET	-	initiating methionine	UNP P35458
A	394	ASP	-	expression tag	UNP P35458
A	395	HIS	-	expression tag	UNP P35458
A	396	HIS	-	expression tag	UNP P35458
A	397	HIS	-	expression tag	UNP P35458
A	398	HIS	-	expression tag	UNP P35458
A	399	HIS	-	expression tag	UNP P35458
A	400	HIS	-	expression tag	UNP P35458
A	401	HIS	-	expression tag	UNP P35458
A	402	HIS	-	expression tag	UNP P35458
A	403	THR	-	expression tag	UNP P35458
A	404	THR	-	expression tag	UNP P35458
A	405	GLU	-	expression tag	UNP P35458
A	406	THR	-	expression tag	UNP P35458
A	407	GLY	-	expression tag	UNP P35458
A	408	TYR	-	expression tag	UNP P35458
A	409	VAL	-	expression tag	UNP P35458
A	410	GLN	-	expression tag	UNP P35458
A	411	GLY	-	expression tag	UNP P35458

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Chain	Residue	Modelled	Actual	Comment	Reference
A	419	VAL	LEU	engineered mutation	UNP P35458
B	393	MET	-	initiating methionine	UNP P35458
B	394	ASP	-	expression tag	UNP P35458
B	395	HIS	-	expression tag	UNP P35458
B	396	HIS	-	expression tag	UNP P35458
B	397	HIS	-	expression tag	UNP P35458
B	398	HIS	-	expression tag	UNP P35458
B	399	HIS	-	expression tag	UNP P35458
B	400	HIS	-	expression tag	UNP P35458
B	401	HIS	-	expression tag	UNP P35458
B	402	HIS	-	expression tag	UNP P35458
B	403	THR	-	expression tag	UNP P35458
B	404	THR	-	expression tag	UNP P35458
B	405	GLU	-	expression tag	UNP P35458
B	406	THR	-	expression tag	UNP P35458
B	407	GLY	-	expression tag	UNP P35458
B	408	TYR	-	expression tag	UNP P35458
B	409	VAL	-	expression tag	UNP P35458
B	410	GLN	-	expression tag	UNP P35458
B	411	GLY	-	expression tag	UNP P35458
B	419	VAL	LEU	engineered mutation	UNP P35458
C	393	MET	-	initiating methionine	UNP P35458
C	394	ASP	-	expression tag	UNP P35458
C	395	HIS	-	expression tag	UNP P35458
C	396	HIS	-	expression tag	UNP P35458
C	397	HIS	-	expression tag	UNP P35458
C	398	HIS	-	expression tag	UNP P35458
C	399	HIS	-	expression tag	UNP P35458
C	400	HIS	-	expression tag	UNP P35458
C	401	HIS	-	expression tag	UNP P35458
C	402	HIS	-	expression tag	UNP P35458
C	403	THR	-	expression tag	UNP P35458
C	404	THR	-	expression tag	UNP P35458
C	405	GLU	-	expression tag	UNP P35458
C	406	THR	-	expression tag	UNP P35458
C	407	GLY	-	expression tag	UNP P35458
C	408	TYR	-	expression tag	UNP P35458
C	409	VAL	-	expression tag	UNP P35458
C	410	GLN	-	expression tag	UNP P35458
C	411	GLY	-	expression tag	UNP P35458
C	419	VAL	LEU	engineered mutation	UNP P35458
D	393	MET	-	initiating methionine	UNP P35458

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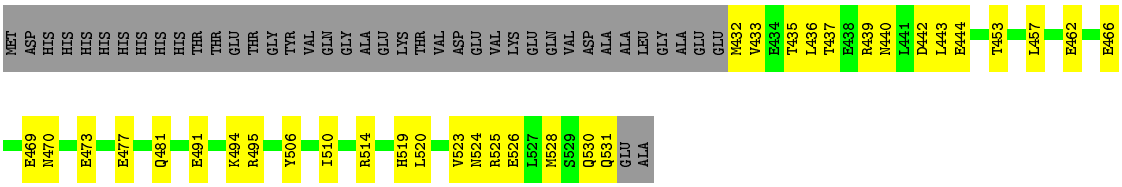
Chain	Residue	Modelled	Actual	Comment	Reference
D	394	ASP	-	expression tag	UNP P35458
D	395	HIS	-	expression tag	UNP P35458
D	396	HIS	-	expression tag	UNP P35458
D	397	HIS	-	expression tag	UNP P35458
D	398	HIS	-	expression tag	UNP P35458
D	399	HIS	-	expression tag	UNP P35458
D	400	HIS	-	expression tag	UNP P35458
D	401	HIS	-	expression tag	UNP P35458
D	402	HIS	-	expression tag	UNP P35458
D	403	THR	-	expression tag	UNP P35458
D	404	THR	-	expression tag	UNP P35458
D	405	GLU	-	expression tag	UNP P35458
D	406	THR	-	expression tag	UNP P35458
D	407	GLY	-	expression tag	UNP P35458
D	408	TYR	-	expression tag	UNP P35458
D	409	VAL	-	expression tag	UNP P35458
D	410	GLN	-	expression tag	UNP P35458
D	411	GLY	-	expression tag	UNP P35458
D	419	VAL	LEU	engineered mutation	UNP P35458
E	393	MET	-	initiating methionine	UNP P35458
E	394	ASP	-	expression tag	UNP P35458
E	395	HIS	-	expression tag	UNP P35458
E	396	HIS	-	expression tag	UNP P35458
E	397	HIS	-	expression tag	UNP P35458
E	398	HIS	-	expression tag	UNP P35458
E	399	HIS	-	expression tag	UNP P35458
E	400	HIS	-	expression tag	UNP P35458
E	401	HIS	-	expression tag	UNP P35458
E	402	HIS	-	expression tag	UNP P35458
E	403	THR	-	expression tag	UNP P35458
E	404	THR	-	expression tag	UNP P35458
E	405	GLU	-	expression tag	UNP P35458
E	406	THR	-	expression tag	UNP P35458
E	407	GLY	-	expression tag	UNP P35458
E	408	TYR	-	expression tag	UNP P35458
E	409	VAL	-	expression tag	UNP P35458
E	410	GLN	-	expression tag	UNP P35458
E	411	GLY	-	expression tag	UNP P35458
E	419	VAL	LEU	engineered mutation	UNP P35458

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 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.

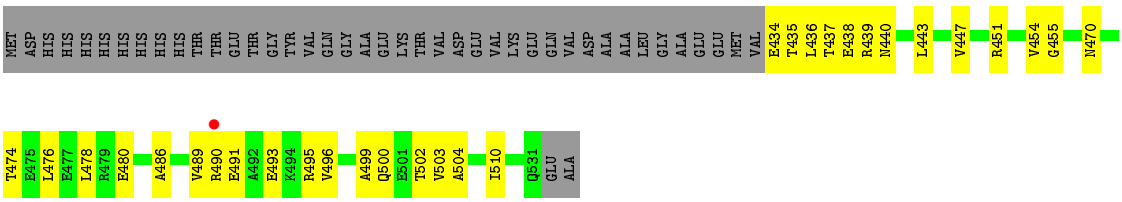
- Molecule 1: Dynactin subunit 1

Chain A:



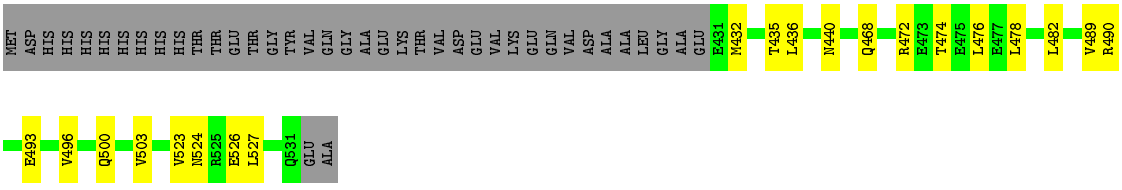
- Molecule 1: Dynactin subunit 1

Chain B:



- Molecule 1: Dynactin subunit 1

Chain C:

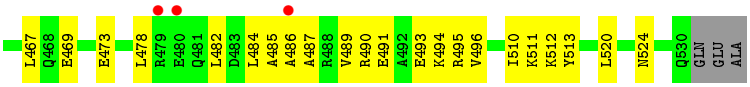


- Molecule 1: Dynactin subunit 1

Chain D:

- Molecule 1: Dynactin subunit 1

Chain E:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α, β, γ	155.32Å 155.32Å 129.26Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.70 – 2.90 49.68 – 2.80	Depositor EDS
% Data completeness (in resolution range)	96.9 (49.70-2.90) 89.0 (49.68-2.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	0.73 (at 2.81Å)	Xtriage
Refinement program	REFMAC 5.7.0029	Depositor
R, R_{free}	0.258 , 0.277 0.262 , 0.273	Depositor DCC
R_{free} test set	1760 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å^2)	95.4	Xtriage
Anisotropy	0.137	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.29 , 74.0	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	0.94	EDS
Total number of atoms	4065	wwPDB-VP
Average B, all atoms (Å^2)	109.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.81% 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

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	0.75	0/824	0.86	0/1106
1	B	0.76	0/809	0.88	0/1086
1	C	0.77	0/833	0.86	0/1118
1	D	0.83	0/825	0.90	0/1108
1	E	0.78	0/784	0.90	0/1052
All	All	0.78	0/4075	0.88	0/5470

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	822	0	804	67	0
1	B	807	0	786	35	0
1	C	831	0	810	20	0
1	D	823	0	801	15	0
1	E	782	0	765	55	2
All	All	4065	0	3966	171	2

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 21.

All (171) 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:432:MET:CE	1:A:435:THR:HG23	1.11	1.52
1:A:432:MET:CE	1:A:435:THR:CG2	1.88	1.47
1:A:432:MET:HE3	1:A:435:THR:CG2	1.49	1.42
1:A:432:MET:SD	1:A:435:THR:HG23	1.63	1.39
1:A:432:MET:HB2	1:A:435:THR:CG2	1.60	1.30
1:A:432:MET:HE1	1:A:435:THR:OG1	1.45	1.15
1:A:432:MET:CE	1:A:435:THR:C	2.16	1.14
1:A:432:MET:CE	1:A:435:THR:CB	2.26	1.13
1:A:444:GLU:OE2	1:B:439:ARG:NH2	1.84	1.11
1:E:438:GLU:HA	1:E:441:LEU:HD21	1.21	1.10
1:E:438:GLU:O	1:E:441:LEU:HG	1.50	1.09
1:A:432:MET:HE3	1:A:435:THR:C	1.71	1.09
1:A:432:MET:CB	1:A:435:THR:HG22	1.82	1.07
1:E:438:GLU:O	1:E:441:LEU:CD1	2.02	1.07
1:A:432:MET:CB	1:A:435:THR:CG2	2.34	1.04
1:A:432:MET:HE3	1:A:435:THR:CB	1.89	1.03
1:A:432:MET:SD	1:A:435:THR:CG2	2.37	1.02
1:C:432:MET:HA	1:C:435:THR:HG22	1.41	1.02
1:A:440:ASN:ND2	1:B:440:ASN:OD1	1.91	1.01
1:E:438:GLU:O	1:E:441:LEU:CG	2.09	1.01
1:A:432:MET:HE1	1:A:435:THR:CB	1.88	1.00
1:E:438:GLU:HA	1:E:441:LEU:CD2	1.90	0.98
1:C:493:GLU:O	1:C:496:VAL:HG12	1.63	0.98
1:B:499:ALA:O	1:B:502:THR:HG22	1.64	0.98
1:A:432:MET:HE1	1:A:435:THR:CG2	1.97	0.94
1:A:432:MET:HG3	1:A:436:LEU:HB2	1.50	0.91
1:A:514:ARG:HD3	1:E:452:GLU:HG3	1.52	0.89
1:A:432:MET:HE3	1:A:435:THR:CA	2.02	0.89
1:E:441:LEU:O	1:E:444:GLU:HG2	1.74	0.87
1:E:487:ALA:HA	1:E:490:ARG:NH1	1.89	0.86
1:A:432:MET:HB2	1:A:435:THR:HG22	0.88	0.85
1:E:438:GLU:C	1:E:441:LEU:HG	1.97	0.84
1:A:514:ARG:HD3	1:E:452:GLU:CG	2.06	0.84
1:B:470:ASN:O	1:B:474:THR:HG23	1.79	0.83
1:E:486:ALA:O	1:E:490:ARG:NH2	2.11	0.83
1:A:432:MET:HE2	1:A:435:THR:O	1.79	0.82
1:B:434:GLU:O	1:B:437:THR:OG1	1.97	0.82
1:A:432:MET:CG	1:A:435:THR:HG23	2.09	0.81
1:B:491:GLU:OE1	1:B:495:ARG:NH1	2.15	0.80
1:A:432:MET:HE2	1:A:435:THR:C	2.01	0.80
1:E:438:GLU:O	1:E:441:LEU:HD12	1.80	0.80
1:E:520:LEU:O	1:E:524:ASN:ND2	2.16	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:486:ALA:O	1:B:489:VAL:HG12	1.82	0.79
1:C:432:MET:O	1:C:435:THR:N	2.17	0.78
1:A:432:MET:O	1:A:436:LEU:CB	2.32	0.77
1:A:437:THR:CG2	1:B:436:LEU:HD11	2.16	0.76
1:A:432:MET:CG	1:A:435:THR:CG2	2.63	0.75
1:A:432:MET:HE3	1:A:435:THR:HG23	0.93	0.74
1:A:432:MET:CE	1:A:435:THR:O	2.34	0.74
1:C:432:MET:CA	1:C:435:THR:HG22	2.18	0.74
1:A:491:GLU:OE2	1:A:495:ARG:CZ	2.35	0.74
1:E:438:GLU:HA	1:E:441:LEU:CG	2.19	0.72
1:B:490:ARG:HG3	1:B:490:ARG:O	1.90	0.71
1:A:432:MET:O	1:A:436:LEU:HB3	1.89	0.71
1:B:476:LEU:O	1:B:480:GLU:HG3	1.90	0.71
1:A:432:MET:HE3	1:A:436:LEU:N	2.05	0.71
1:A:432:MET:CE	1:A:435:THR:CA	2.67	0.69
1:A:520:LEU:O	1:A:523:VAL:HG22	1.93	0.69
1:C:432:MET:O	1:C:436:LEU:N	2.24	0.69
1:C:523:VAL:O	1:C:526:GLU:HG2	1.94	0.68
1:E:487:ALA:CA	1:E:490:ARG:NH1	2.59	0.66
1:A:432:MET:O	1:A:436:LEU:HB2	1.95	0.66
1:B:499:ALA:HA	1:B:502:THR:HG22	1.78	0.64
1:E:487:ALA:HA	1:E:490:ARG:CZ	2.26	0.64
1:A:437:THR:HG22	1:B:436:LEU:HD11	1.78	0.64
1:B:486:ALA:O	1:B:489:VAL:CG1	2.47	0.63
1:C:432:MET:HA	1:C:435:THR:CG2	2.25	0.62
1:E:438:GLU:CA	1:E:441:LEU:HD21	2.13	0.62
1:B:451:ARG:O	1:B:454:VAL:HG22	1.99	0.62
1:A:432:MET:HG3	1:A:432:MET:O	1.99	0.62
1:E:486:ALA:O	1:E:490:ARG:CZ	2.47	0.62
1:E:437:THR:O	1:E:441:LEU:HD23	2.00	0.61
1:E:486:ALA:HB1	1:E:490:ARG:HH22	1.65	0.61
1:A:514:ARG:CD	1:E:452:GLU:HG3	2.26	0.61
1:E:486:ALA:C	1:E:490:ARG:NH2	2.54	0.60
1:A:437:THR:CG2	1:B:436:LEU:CD1	2.79	0.60
1:B:499:ALA:C	1:B:502:THR:HG22	2.23	0.59
1:E:439:ARG:O	1:E:442:ASP:OD1	2.20	0.59
1:A:432:MET:SD	1:A:435:THR:HG21	2.37	0.58
1:D:460:MET:HE1	1:E:512:LYS:C	2.24	0.58
1:B:490:ARG:HA	1:B:493:GLU:H	1.68	0.58
1:B:499:ALA:O	1:B:502:THR:CG2	2.47	0.57
1:E:438:GLU:CA	1:E:441:LEU:CG	2.83	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:486:ALA:C	1:B:489:VAL:HG12	2.25	0.56
1:B:491:GLU:O	1:B:495:ARG:HG3	2.06	0.56
1:E:490:ARG:O	1:E:494:LYS:HG3	2.06	0.56
1:B:499:ALA:CA	1:B:502:THR:HG22	2.36	0.56
1:A:437:THR:HG23	1:B:436:LEU:CD1	2.36	0.55
1:B:443:LEU:O	1:B:447:VAL:HG23	2.07	0.55
1:C:474:THR:O	1:C:478:LEU:HD13	2.07	0.54
1:E:469:GLU:O	1:E:473:GLU:HG3	2.08	0.54
1:A:433:VAL:HG12	1:A:433:VAL:O	2.07	0.54
1:D:526:GLU:OE2	1:D:530:GLN:NE2	2.40	0.54
1:E:438:GLU:CA	1:E:441:LEU:CD2	2.78	0.54
1:A:526:GLU:OE2	1:A:530:GLN:NE2	2.41	0.53
1:E:437:THR:O	1:E:441:LEU:CD2	2.55	0.53
1:A:481:GLN:OE1	1:A:481:GLN:HA	2.08	0.53
1:E:438:GLU:O	1:E:441:LEU:HD11	2.05	0.53
1:E:489:VAL:HG12	1:E:490:ARG:N	2.24	0.53
1:A:469:GLU:HG3	1:A:470:ASN:N	2.24	0.53
1:C:489:VAL:HG12	1:C:490:ARG:N	2.25	0.52
1:A:506:TYR:O	1:A:510:ILE:HG12	2.10	0.52
1:A:432:MET:CE	1:A:436:LEU:N	2.68	0.51
1:B:499:ALA:HA	1:B:502:THR:CG2	2.39	0.51
1:D:460:MET:HE1	1:E:513:TYR:N	2.25	0.51
1:A:525:ARG:HA	1:A:528:MET:HE2	1.92	0.51
1:A:437:THR:HG22	1:B:436:LEU:CD1	2.39	0.51
1:A:510:ILE:HD13	1:B:510:ILE:HD13	1.92	0.50
1:B:435:THR:O	1:B:438:GLU:N	2.45	0.50
1:A:437:THR:HG23	1:B:436:LEU:HD11	1.92	0.50
1:A:514:ARG:HD3	1:E:452:GLU:HG2	1.93	0.49
1:E:438:GLU:CA	1:E:441:LEU:HD11	2.43	0.49
1:B:435:THR:C	1:B:437:THR:N	2.63	0.49
1:B:474:THR:O	1:B:478:LEU:HD13	2.13	0.49
1:C:440:ASN:HB2	1:D:440:ASN:OD1	2.13	0.49
1:E:438:GLU:CA	1:E:441:LEU:HG	2.42	0.48
1:C:432:MET:CE	1:C:432:MET:HA	2.42	0.48
1:B:500:GLN:O	1:B:503:VAL:HG22	2.13	0.48
1:E:438:GLU:HA	1:E:441:LEU:HD11	1.95	0.48
1:E:438:GLU:C	1:E:441:LEU:CG	2.70	0.48
1:D:433:VAL:HG13	1:D:434:GLU:N	2.28	0.48
1:B:454:VAL:HG23	1:B:455:GLY:N	2.29	0.47
1:C:500:GLN:O	1:C:503:VAL:HG22	2.15	0.47
1:A:453:THR:HG22	1:A:457:LEU:HD12	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:525:ARG:HA	1:D:528:MET:HE2	1.96	0.47
1:A:528:MET:O	1:A:531:GLN:HG2	2.15	0.47
1:E:493:GLU:O	1:E:496:VAL:HG12	2.15	0.46
1:C:524:ASN:HB2	1:D:524:ASN:OD1	2.16	0.46
1:C:493:GLU:O	1:C:496:VAL:CG1	2.48	0.46
1:C:493:GLU:C	1:C:496:VAL:HG12	2.32	0.46
1:A:523:VAL:HG23	1:A:524:ASN:N	2.29	0.46
1:A:462:GLU:OE2	1:A:466:GLU:OE1	2.33	0.46
1:E:484:LEU:HD23	1:E:484:LEU:C	2.36	0.46
1:A:528:MET:SD	1:E:467:LEU:CD1	3.04	0.45
1:D:493:GLU:O	1:D:496:VAL:HG12	2.15	0.45
1:E:439:ARG:HA	1:E:442:ASP:OD1	2.16	0.45
1:A:466:GLU:O	1:A:469:GLU:HG2	2.16	0.45
1:D:453:THR:HG22	1:D:457:LEU:HD12	1.98	0.45
1:E:453:THR:HG22	1:E:457:LEU:HD12	1.97	0.45
1:A:439:ARG:O	1:A:442:ASP:HB2	2.17	0.45
1:E:438:GLU:HA	1:E:441:LEU:CD1	2.46	0.45
1:B:503:VAL:HG23	1:B:504:ALA:N	2.32	0.44
1:E:445:GLU:HA	1:E:448:ARG:NH2	2.32	0.44
1:A:473:GLU:O	1:A:477:GLU:HG3	2.18	0.44
1:A:519:HIS:O	1:A:523:VAL:HG13	2.18	0.44
1:C:526:GLU:HG3	1:C:527:LEU:N	2.32	0.44
1:E:482:LEU:O	1:E:485:ALA:HB3	2.18	0.44
1:E:510:ILE:O	1:E:511:LYS:C	2.55	0.43
1:D:510:ILE:O	1:D:511:LYS:C	2.56	0.43
1:A:491:GLU:O	1:A:494:LYS:HG2	2.19	0.43
1:C:432:MET:HA	1:C:432:MET:HE2	1.99	0.42
1:B:490:ARG:O	1:B:490:ARG:CG	2.65	0.42
1:D:486:ALA:HA	1:D:489:VAL:HG12	2.01	0.42
1:C:472:ARG:O	1:C:476:LEU:HG	2.20	0.42
1:A:439:ARG:CZ	1:A:443:LEU:HD11	2.49	0.42
1:A:433:VAL:O	1:A:433:VAL:CG1	2.68	0.42
1:C:468:GLN:HG3	1:D:468:GLN:OE1	2.20	0.42
1:E:437:THR:O	1:E:441:LEU:HG	2.20	0.41
1:E:491:GLU:OE2	1:E:495:ARG:HD2	2.20	0.41
1:E:478:LEU:O	1:E:482:LEU:N	2.45	0.41
1:B:493:GLU:O	1:B:496:VAL:HG12	2.21	0.41
1:E:438:GLU:C	1:E:441:LEU:CD1	2.82	0.41
1:A:528:MET:SD	1:E:467:LEU:HD11	2.61	0.41
1:D:435:THR:HG23	1:D:436:LEU:N	2.36	0.41
1:E:478:LEU:HD23	1:E:478:LEU:HA	1.77	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:493:GLU:C	1:E:496:VAL:HG12	2.42	0.41
1:A:439:ARG:O	1:A:443:LEU:HD13	2.21	0.40
1:C:432:MET:CE	1:C:432:MET:CA	2.98	0.40
1:D:460:MET:CE	1:E:512:LYS:HB3	2.51	0.40
1:D:434:GLU:HA	1:D:434:GLU:OE2	2.18	0.40
1:E:487:ALA:O	1:E:490:ARG:HG2	2.22	0.40

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:524:ASN:OD1	1:E:524:ASN:OD1[8_665]	1.50	0.70
1:E:524:ASN:CG	1:E:524:ASN:OD1[8_665]	2.01	0.19

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	98/141 (70%)	96 (98%)	2 (2%)	0	100	100
1	B	96/141 (68%)	96 (100%)	0	0	100	100
1	C	99/141 (70%)	99 (100%)	0	0	100	100
1	D	98/141 (70%)	98 (100%)	0	0	100	100
1	E	93/141 (66%)	91 (98%)	2 (2%)	0	100	100
All	All	484/705 (69%)	480 (99%)	4 (1%)	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	89/122 (73%)	89 (100%)	0	100	100
1	B	87/122 (71%)	87 (100%)	0	100	100
1	C	90/122 (74%)	89 (99%)	1 (1%)	73	92
1	D	89/122 (73%)	88 (99%)	1 (1%)	73	92
1	E	84/122 (69%)	84 (100%)	0	100	100
All	All	439/610 (72%)	437 (100%)	2 (0%)	88	96

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	482	LEU
1	D	520	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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

There are no ligands in this entry.

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	100/141 (70%)	0.21	0 100 100	64, 104, 162, 207	0
1	B	98/141 (69%)	0.06	1 (1%) 82 82	57, 100, 161, 184	0
1	C	101/141 (71%)	0.05	0 100 100	57, 95, 152, 177	0
1	D	100/141 (70%)	-0.03	0 100 100	47, 95, 156, 193	0
1	E	95/141 (67%)	0.33	3 (3%) 47 43	58, 115, 177, 218	1 (1%)
All	All	494/705 (70%)	0.12	4 (0%) 86 86	47, 102, 166, 218	1 (0%)

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	480	GLU	3.1
1	E	479	ARG	2.6
1	E	486	ALA	2.5
1	B	490	ARG	2.1

6.2 Non-standard residues in protein, DNA, RNA chains

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

6.3 Carbohydrates

There are no carbohydrates in this entry.

6.4 Ligands

There are no ligands in this entry.

6.5 Other polymers (i)

There are no such residues in this entry.