



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 06:46 AM UTC

PDB ID : 4XH9 / pdb_00004xh9
Title : CRYSTAL STRUCTURE OF HUMAN RHOA IN COMPLEX WITH DH/PH
FRAGMENT OF THE GUANINE NUCLEOTIDE EXCHANGE FACTOR
NET1
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Deposited on : 2015-01-05
Resolution : 2.00 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 types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

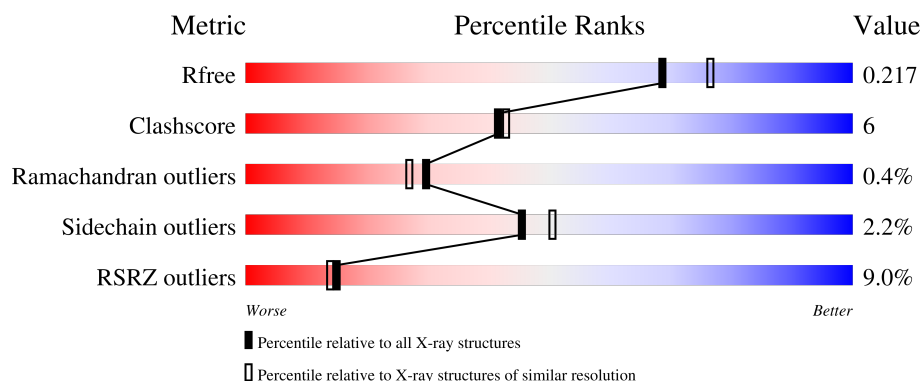
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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}	180053	10052 (2.00-2.00)
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (2.00-2.00)

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 $\leq 5\%$. 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	361	8% 75% 17% • 7%
1	D	361	11% 79% 13% • 6%
2	B	180	6% 85% 12% •
2	E	180	6% 88% 8% • •

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 9206 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 Neuroepithelial cell-transforming gene 1 protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	336	Total	C	N	O	S	0	0	0
			2753	1751	487	504	11			
1	D	338	Total	C	N	O	S	0	1	0
			2784	1769	497	508	10			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	147	MET	-	initiating methionine	UNP Q7Z628
A	148	GLY	-	expression tag	UNP Q7Z628
A	502	HIS	-	expression tag	UNP Q7Z628
A	503	HIS	-	expression tag	UNP Q7Z628
A	504	HIS	-	expression tag	UNP Q7Z628
A	505	HIS	-	expression tag	UNP Q7Z628
A	506	HIS	-	expression tag	UNP Q7Z628
A	507	HIS	-	expression tag	UNP Q7Z628
D	147	MET	-	initiating methionine	UNP Q7Z628
D	148	GLY	-	expression tag	UNP Q7Z628
D	502	HIS	-	expression tag	UNP Q7Z628
D	503	HIS	-	expression tag	UNP Q7Z628
D	504	HIS	-	expression tag	UNP Q7Z628
D	505	HIS	-	expression tag	UNP Q7Z628
D	506	HIS	-	expression tag	UNP Q7Z628
D	507	HIS	-	expression tag	UNP Q7Z628

- Molecule 2 is a protein called Transforming protein RhoA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	174	Total	C	N	O	S	0	0	0
			1374	865	234	265	10			
2	E	174	Total	C	N	O	S	0	0	0
			1374	865	234	265	10			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	1	GLY	-	expression tag	UNP P61586
B	25	ASN	PHE	engineered mutation	UNP P61586
E	1	GLY	-	expression tag	UNP P61586
E	25	ASN	PHE	engineered mutation	UNP P61586

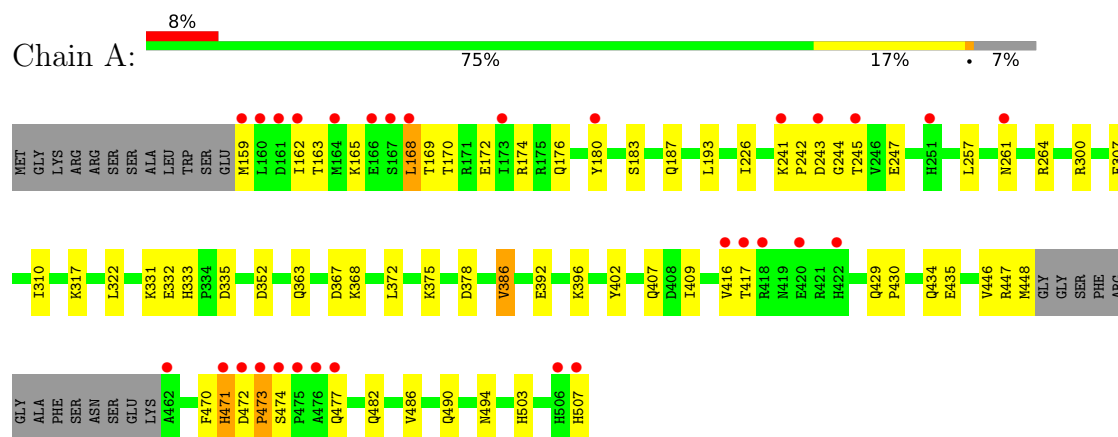
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	337	Total 337	O 337	0	0
3	B	170	Total 170	O 170	0	0
3	D	291	Total 291	O 291	0	0
3	E	123	Total 123	O 123	0	0

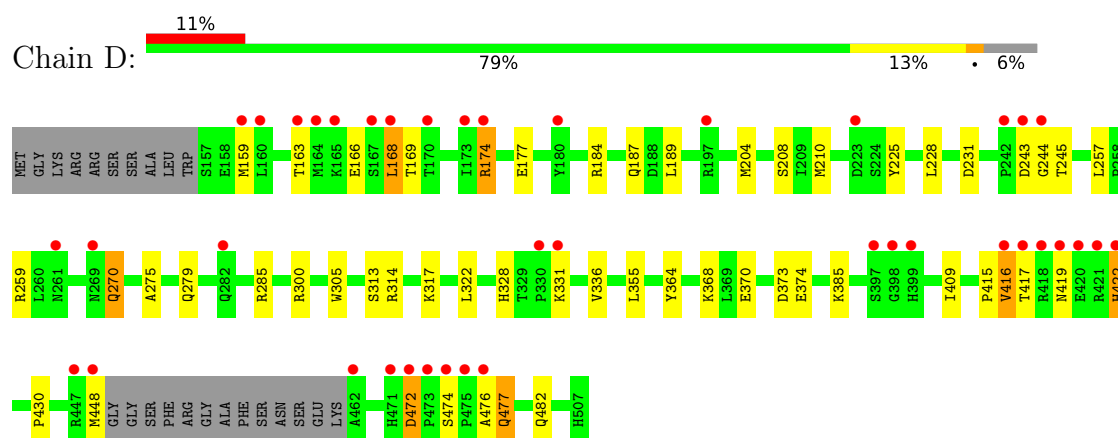
3 Residue-property plots [i](#)

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.

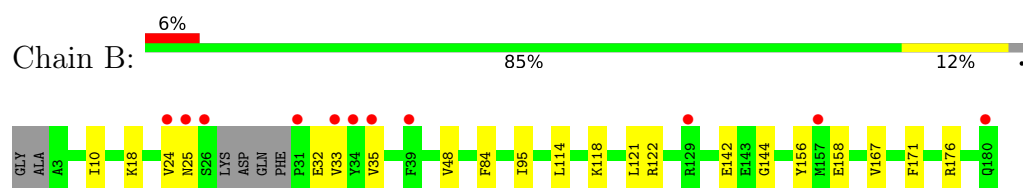
- Molecule 1: Neuroepithelial cell-transforming gene 1 protein



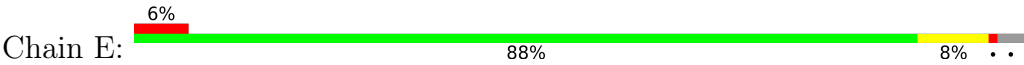
- Molecule 1: Neuroepithelial cell-transforming gene 1 protein



- Molecule 2: Transforming protein RhoA



- Molecule 2: Transforming protein RhoA



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	54.10Å 101.40Å 116.20Å 90.00° 94.30° 90.00°	Depositor
Resolution (Å)	34.69 – 2.00 34.69 – 2.00	Depositor EDS
% Data completeness (in resolution range)	99.4 (34.69-2.00) 99.4 (34.69-2.00)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.84 (at 2.00Å)	Xtriage
Refinement program	PHENIX (phenix.refine: dev_1702)	Depositor
R, R_{free}	0.189 , 0.217 0.190 , 0.217	Depositor DCC
R_{free} test set	4195 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	26.3	Xtriage
Anisotropy	0.330	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 54.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	9206	wwPDB-VP
Average B, all atoms (Å ²)	35.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.84% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ 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](#)

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	0.37	0/2813	0.73	3/3803 (0.1%)
1	D	0.36	0/2850	0.78	4/3851 (0.1%)
2	B	0.35	0/1399	0.79	1/1890 (0.1%)
2	E	0.41	0/1399	0.77	0/1890
All	All	0.37	0/8461	0.76	8/11434 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	D	0	1
2	E	0	1
All	All	0	2

There are no bond length outliers.

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	32	GLU	N-CA-C	-8.79	102.10	113.17
1	D	419	ASN	N-CA-C	-7.19	99.02	109.59
1	A	471	HIS	N-CA-C	-6.00	98.02	110.80
1	A	378	ASP	CA-C-N	5.53	125.89	119.47
1	A	378	ASP	C-N-CA	5.53	125.89	119.47
1	D	416	VAL	CB-CA-C	-5.50	102.98	110.90
1	D	244	GLY	N-CA-C	-5.23	108.12	114.92
1	D	270	GLN	N-CA-C	-5.10	107.61	113.88

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	D	472	ASP	Peptide
2	E	33	VAL	Peptide

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	2753	0	2745	49	0
1	D	2784	0	2782	34	0
2	B	1374	0	1368	14	0
2	E	1374	0	1368	12	0
3	A	337	0	0	6	0
3	B	170	0	0	4	0
3	D	291	0	0	5	0
3	E	123	0	0	0	0
All	All	9206	0	8263	106	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 6.

All (106) 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:241:LYS:NZ	1:A:247:GLU:OE2	2.02	0.92
1:A:392:GLU:OE1	3:A:601:HOH:O	1.97	0.82
1:A:429:GLN:H	1:A:477:GLN:HE22	1.30	0.79
1:A:300:ARG:NH1	3:A:694:HOH:O	2.18	0.76
1:A:470:PHE:CD1	1:A:477:GLN:HG2	2.22	0.75
2:E:122:ARG:NH2	2:E:158:GLU:OE1	2.19	0.71
1:D:416:VAL:HG12	1:D:417:THR:N	2.05	0.69
1:D:177:GLU:HG3	2:E:34:TYR:CE2	2.27	0.69
1:D:300:ARG:NH1	3:D:780:HOH:O	2.25	0.69
1:D:177:GLU:HG3	2:E:34:TYR:CZ	2.29	0.68
2:B:122:ARG:NH2	2:B:158:GLU:OE1	2.26	0.67
2:B:118:LYS:HB3	2:B:121:LEU:HD13	1.78	0.65
2:B:25:ASN:ND2	2:B:171:PHE:CD2	2.66	0.64
1:A:368:LYS:NZ	3:A:894:HOH:O	2.28	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:170:THR:O	1:A:174:ARG:HG3	2.00	0.62
1:D:189:LEU:HD22	1:D:314:ARG:HG2	1.83	0.61
1:A:243:ASP:HB3	1:A:245:THR:HG23	1.82	0.61
2:E:24:VAL:HG23	2:E:167:VAL:HG11	1.83	0.61
1:A:503:HIS:O	1:A:507:HIS:N	2.34	0.60
1:D:168:LEU:HD13	1:D:169:THR:H	1.66	0.60
2:E:125:GLU:HB3	2:E:129:ARG:NH2	2.17	0.60
1:A:375:LYS:NZ	3:A:898:HOH:O	2.29	0.60
1:A:168:LEU:HD12	1:A:169:THR:H	1.67	0.59
1:A:168:LEU:HD23	1:A:172:GLU:HG2	1.85	0.59
1:A:471:HIS:ND1	1:A:473:PRO:HG2	2.18	0.59
1:A:163:THR:HG22	1:A:165:LYS:H	1.67	0.59
1:D:174:ARG:NH2	3:D:716:HOH:O	2.30	0.59
1:A:264:ARG:NE	1:A:352:ASP:OD2	2.36	0.58
1:A:241:LYS:HE3	1:A:247:GLU:HG3	1.84	0.58
1:D:416:VAL:HG12	1:D:417:THR:H	1.68	0.58
1:A:470:PHE:CE1	1:A:477:GLN:HG2	2.39	0.57
2:E:118:LYS:HB3	2:E:121:LEU:HD13	1.85	0.57
1:D:231:ASP:OD2	1:D:259:ARG:NH1	2.39	0.56
1:A:448:MET:HE2	1:A:482:GLN:HB2	1.88	0.55
1:D:257:LEU:HD11	1:D:322:LEU:HD21	1.89	0.54
1:D:331:LYS:HA	1:D:336:VAL:HG21	1.88	0.54
1:D:275:ALA:O	1:D:279:GLN:HG3	2.09	0.53
2:B:84:PHE:HB3	2:B:95:ILE:HD11	1.90	0.53
2:B:122:ARG:HH22	2:B:158:GLU:CD	2.18	0.52
2:B:10:ILE:HG12	2:B:18:LYS:HG2	1.91	0.52
1:D:448:MET:HE2	1:D:482:GLN:HB2	1.92	0.51
2:B:176:ARG:NH1	3:B:203:HOH:O	2.41	0.51
1:D:184:ARG:NH1	3:D:850:HOH:O	2.44	0.51
1:D:208:SER:O	1:D:285:ARG:NH2	2.43	0.51
1:D:417:THR:CG2	1:D:422:HIS:CE1	2.94	0.50
1:A:162:ILE:HD12	1:A:244:GLY:HA3	1.94	0.50
1:A:477:GLN:O	1:A:477:GLN:HG3	2.12	0.50
1:A:159:MET:HE3	1:A:180:TYR:CD2	2.47	0.50
1:A:470:PHE:HD1	1:A:477:GLN:HG2	1.76	0.49
1:A:193:LEU:HB2	1:A:226:ILE:HD11	1.95	0.49
1:A:490:GLN:HG2	3:B:207:HOH:O	2.13	0.49
1:D:177:GLU:HA	1:D:177:GLU:OE1	2.11	0.48
2:E:32:GLU:O	2:E:33:VAL:HG12	2.13	0.48
1:D:417:THR:HG22	1:D:422:HIS:CE1	2.47	0.48
1:A:257:LEU:HD11	1:A:322:LEU:HD21	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:476:ALA:O	1:D:477:GLN:NE2	2.47	0.48
1:A:392:GLU:HG2	1:A:402:TYR:CD2	2.49	0.48
1:A:486:VAL:HG23	3:A:780:HOH:O	2.13	0.48
1:A:434:GLN:HA	1:A:503:HIS:CD2	2.48	0.47
1:A:470:PHE:HB3	1:A:474:SER:OG	2.14	0.47
1:A:241:LYS:NZ	1:A:247:GLU:CD	2.72	0.47
1:D:416:VAL:CG1	1:D:417:THR:N	2.76	0.47
2:E:142:GLU:HG3	2:E:145:ARG:NH2	2.30	0.47
2:B:25:ASN:ND2	2:B:171:PHE:CG	2.81	0.47
1:A:386:VAL:HG13	1:A:407:GLN:HB2	1.96	0.47
1:D:370:GLU:OE2	3:D:875:HOH:O	2.20	0.46
1:A:363:GLN:NE2	1:A:367:ASP:OD1	2.45	0.46
1:D:243:ASP:HB3	1:D:245:THR:H	1.81	0.46
1:A:471:HIS:ND1	1:A:473:PRO:HD2	2.30	0.46
1:D:313:SER:OG	1:D:317:LYS:NZ	2.49	0.46
2:E:33:VAL:O	2:E:34:TYR:CG	2.69	0.46
1:A:183:SER:O	1:A:187:GLN:HG3	2.17	0.45
1:A:241:LYS:O	1:A:242:PRO:C	2.60	0.45
2:B:142:GLU:CD	2:B:142:GLU:H	2.25	0.44
2:B:24:VAL:HG23	2:B:167:VAL:HG11	2.00	0.44
1:D:174:ARG:HE	1:D:328:HIS:CE1	2.36	0.44
2:E:142:GLU:H	2:E:142:GLU:CD	2.26	0.44
1:D:225:TYR:O	1:D:228:LEU:HB3	2.16	0.44
1:A:435:GLU:O	1:A:471:HIS:N	2.45	0.44
2:B:95:ILE:HD13	2:B:114:LEU:HD11	2.00	0.43
1:A:490:GLN:HG3	1:A:494:ASN:ND2	2.33	0.43
1:D:270:GLN:HG2	1:D:305:TRP:CH2	2.54	0.43
1:D:364:TYR:O	1:D:368:LYS:HG3	2.19	0.43
1:D:373:ASP:OD1	1:D:374:GLU:N	2.51	0.43
1:A:241:LYS:C	1:A:243:ASP:N	2.74	0.43
1:A:470:PHE:HE1	1:A:477:GLN:CD	2.27	0.42
1:D:417:THR:HG22	1:D:422:HIS:ND1	2.34	0.42
2:B:176:ARG:NH2	3:B:206:HOH:O	2.51	0.42
1:A:300:ARG:NE	3:A:869:HOH:O	2.35	0.42
1:A:261:ASN:O	1:A:264:ARG:HG3	2.20	0.42
1:D:159:MET:SD	2:E:34:TYR:CE2	3.12	0.42
1:A:416:VAL:HG12	1:A:417:THR:O	2.20	0.42
1:D:415:PRO:HB3	1:D:422:HIS:CD2	2.55	0.42
1:A:310:ILE:HA	1:A:310:ILE:HD13	1.84	0.41
1:A:409:ILE:HD11	1:A:430:PRO:HB2	2.02	0.41
1:D:409:ILE:HD11	1:D:430:PRO:HB2	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:241:LYS:HZ1	1:A:247:GLU:CD	2.19	0.41
1:A:396:LYS:HD3	1:A:446:VAL:CG1	2.51	0.41
2:B:48:VAL:HG12	3:B:223:HOH:O	2.20	0.41
1:A:307:PHE:HA	1:A:310:ILE:HG12	2.03	0.41
1:D:385:LYS:NZ	3:D:610:HOH:O	2.53	0.41
1:A:172:GLU:OE2	1:A:176:GLN:NE2	2.54	0.40
2:E:168:ARG:HE	2:E:168:ARG:HB2	1.69	0.40
2:B:144:GLY:HA3	2:B:156:TYR:CZ	2.55	0.40
1:A:333:HIS:ND1	1:A:335:ASP:HB2	2.37	0.40
1:D:204:MET:SD	1:D:210:MET:HE2	2.61	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	332/361 (92%)	321 (97%)	10 (3%)	1 (0%)	36	35
1	D	336/361 (93%)	328 (98%)	6 (2%)	2 (1%)	21	17
2	B	170/180 (94%)	168 (99%)	2 (1%)	0	100	100
2	E	170/180 (94%)	164 (96%)	5 (3%)	1 (1%)	21	17
All	All	1008/1082 (93%)	981 (97%)	23 (2%)	4 (0%)	30	27

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	472	ASP
1	D	472	ASP
1	D	166	GLU
2	E	33	VAL

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	304/328 (93%)	296 (97%)	8 (3%)	40	44
1	D	307/328 (94%)	299 (97%)	8 (3%)	40	44
2	B	152/156 (97%)	150 (99%)	2 (1%)	61	68
2	E	152/156 (97%)	150 (99%)	2 (1%)	61	68
All	All	915/968 (94%)	895 (98%)	20 (2%)	45	50

All (20) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	168	LEU
1	A	317	LYS
1	A	331	LYS
1	A	332	GLU
1	A	372	LEU
1	A	386	VAL
1	A	447	ARG
1	A	473	PRO
2	B	33	VAL
2	B	35	VAL
1	D	163	THR
1	D	168	LEU
1	D	174	ARG
1	D	187	GLN
1	D	355	LEU
1	D	422	HIS
1	D	474	SER
1	D	477	GLN
2	E	135	LYS
2	E	162	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	269	ASN
1	A	429	GLN
1	A	477	GLN
2	B	126	HIS
1	D	337	GLN
1	D	422	HIS
1	D	477	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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	336/361 (93%)	0.35	30 (8%) 15 14	16, 29, 69, 81	0
1	D	338/361 (93%)	0.39	40 (11%) 9 8	12, 31, 66, 80	1 (0%)
2	B	174/180 (96%)	0.22	11 (6%) 26 24	14, 29, 57, 121	0
2	E	174/180 (96%)	0.28	11 (6%) 26 24	16, 31, 60, 122	0
All	All	1022/1082 (94%)	0.33	92 (9%) 15 14	12, 30, 67, 122	1 (0%)

All (92) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	E	34	TYR	6.9
1	D	474	SER	6.3
2	E	31	PRO	5.8
2	E	33	VAL	5.4
2	B	31	PRO	5.3
1	A	160	LEU	5.3
2	B	34	TYR	4.9
2	B	33	VAL	4.8
1	A	161	ASP	4.8
1	A	474	SER	4.8
1	A	471	HIS	4.6
1	A	473	PRO	4.4
2	E	26	SER	4.4
1	A	420	GLU	4.2
1	A	243	ASP	4.2
1	A	475	PRO	4.2
1	D	475	PRO	4.1
1	D	168	LEU	4.1
1	A	159	MET	4.1
1	A	417	THR	4.0
1	D	244	GLY	3.9

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Mol	Chain	Res	Type	RSRZ
1	A	462	ALA	3.9
1	A	477	GLN	3.8
1	A	472	ASP	3.8
1	D	167	SER	3.7
1	D	473	PRO	3.7
1	A	167	SER	3.7
1	D	397	SER	3.6
1	D	422	HIS	3.5
2	B	35	VAL	3.5
1	D	269	ASN	3.5
1	D	398	GLY	3.5
1	A	164	MET	3.4
1	A	180	TYR	3.4
1	A	168	LEU	3.3
1	D	165	LYS	3.3
1	D	243	ASP	3.3
1	D	159	MET	3.1
1	D	170	THR	3.1
1	D	471	HIS	3.1
1	D	416	VAL	3.1
1	D	418	ARG	3.0
1	A	261	ASN	3.0
2	E	25	ASN	2.9
2	B	26	SER	2.9
1	A	251	HIS	2.9
1	A	507	HIS	2.8
2	E	24	VAL	2.8
1	D	448	MET	2.8
1	D	173	ILE	2.7
1	D	419	ASN	2.7
1	A	166	GLU	2.7
1	A	416	VAL	2.7
1	A	418	ARG	2.7
2	E	14	GLY	2.7
1	D	476	ALA	2.6
1	D	174	ARG	2.6
1	D	160	LEU	2.6
2	B	39	PHE	2.6
1	D	180	TYR	2.6
1	A	476	ALA	2.6
1	A	162	ILE	2.5
1	A	173	ILE	2.5

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Mol	Chain	Res	Type	RSRZ
1	D	447	ARG	2.5
2	E	157	MET	2.5
2	E	129	ARG	2.5
1	D	223	ASP	2.5
1	D	421	ARG	2.4
1	D	163	THR	2.4
2	E	15	ALA	2.4
1	D	462	ALA	2.4
1	D	331	LYS	2.3
1	D	420	GLU	2.3
1	A	422	HIS	2.3
2	B	24	VAL	2.3
1	D	242	PRO	2.3
1	D	399	HIS	2.3
2	E	39	PHE	2.2
1	A	506	HIS	2.2
1	D	261	ASN	2.2
2	B	25	ASN	2.2
1	D	164	MET	2.2
1	D	472	ASP	2.2
1	D	282	GLN	2.1
1	D	197[A]	ARG	2.1
2	B	129	ARG	2.1
1	D	330	PRO	2.1
1	A	241	LYS	2.1
2	B	180	GLN	2.0
1	A	245	THR	2.0
1	D	417	THR	2.0
2	B	157	MET	2.0

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 oligosaccharides 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.