



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 13, 2017 – 10:20 am GMT

PDB ID : 1XIU
Title : Crystal structure of the agonist-bound ligand-binding domain of Biomphalaria glabrata RXR
Authors : De Groot, A.; De Rosny, E.; Juillan-Binard, C.; Ferrer, J.-L.; Laudet, V.; Pebay-Peroula, E.; Fontecilla-Camps, J.-C.; Borel, F.
Deposited on : 2004-09-22
Resolution : 2.50 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 ⓘ symbol.

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

MolProbity	:	4.02b-467
Mogul	:	1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix)	:	1.9-1692
EDS	:	trunk28620
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
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)	:	recalc28949

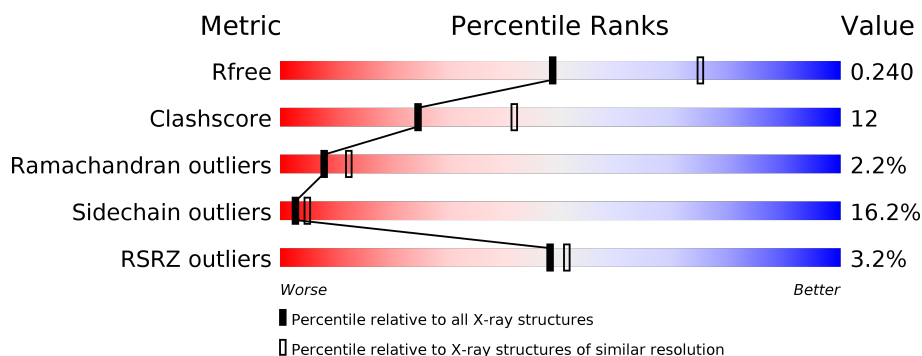
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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}	100719	3846 (2.50-2.50)
Clashscore	112137	4554 (2.50-2.50)
Ramachandran outliers	110173	4463 (2.50-2.50)
Sidechain outliers	110143	4465 (2.50-2.50)
RSRZ outliers	101464	3876 (2.50-2.50)

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 $\leq 5\%$. 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	230	<div> <div>0%</div> <div>67% 20% 7% . .</div> </div>
1	B	230	<div> <div>3%</div> <div>64% 26% 6% . .</div> </div>
2	E	15	<div> <div>20%</div> <div>33% 40% 7% 20%</div> </div>
2	F	15	<div> <div>13%</div> <div>27% 27% 13% 33%</div> </div>

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 3782 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.

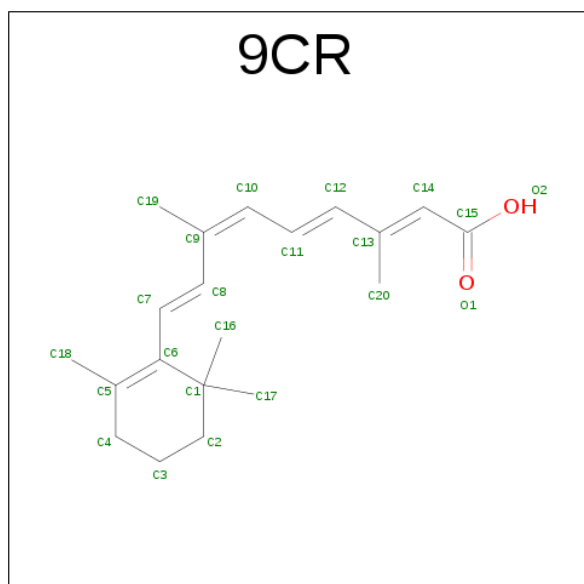
- Molecule 1 is a protein called RXR-like protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	221	Total	C	N	O	S	0	0	0
			1748	1124	297	317	10			
1	B	224	Total	C	N	O	S	0	0	0
			1759	1132	300	317	10			

- Molecule 2 is a protein called Nuclear receptor coactivator 1.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	E	12	Total	C	N	O	0	0	0
			100	63	21	16			
2	F	10	Total	C	N	O	0	0	0
			84	54	17	13			

- Molecule 3 is (9CIS)-RETINOIC ACID (three-letter code: 9CR) (formula: C₂₀H₂₈O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			22	20	2		
3	B	1	Total	C	O	0	0
			22	20	2		

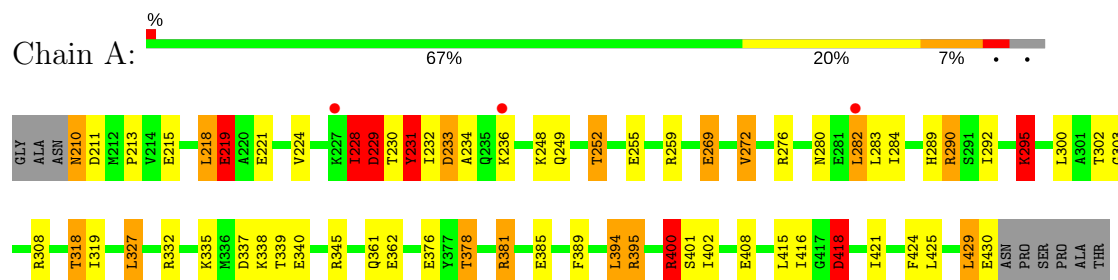
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	28	Total	O	0	0
			28	28		
4	B	17	Total	O	0	0
			17	17		
4	E	1	Total	O	0	0
			1	1		
4	F	1	Total	O	0	0
			1	1		

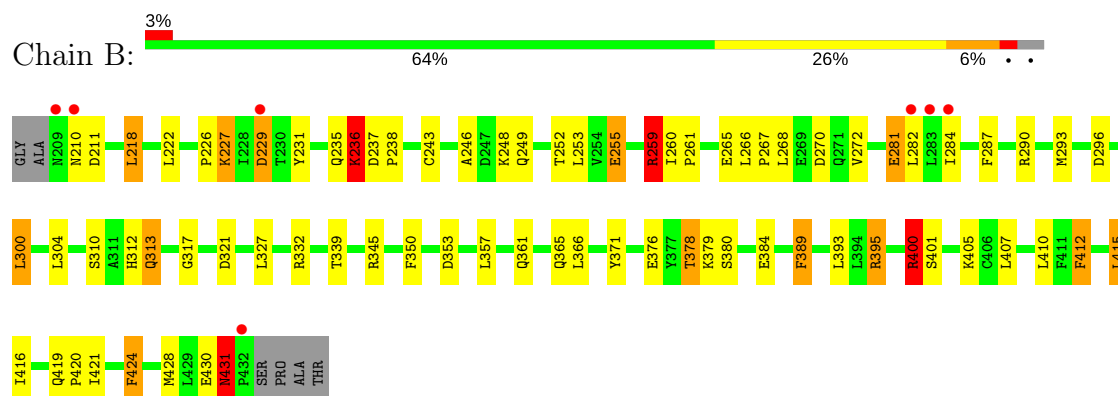
3 Residue-property plots [i](#)

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.

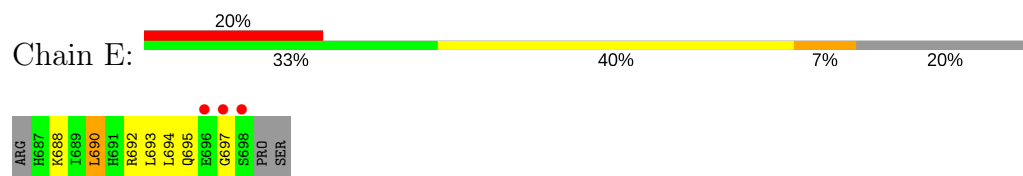
• Molecule 1: RXR-like protein



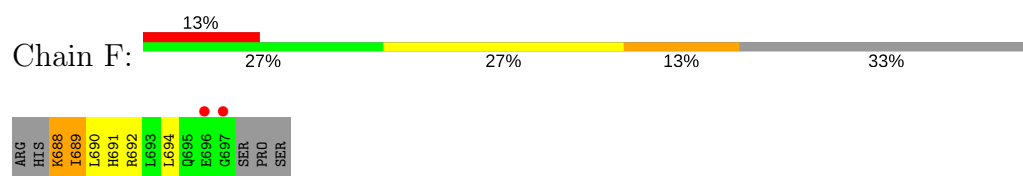
• Molecule 1: RXR-like protein



• Molecule 2: Nuclear receptor coactivator 1



• Molecule 2: Nuclear receptor coactivator 1



4 Data and refinement statistics

Property	Value	Source
Space group	P 61 2 2	Depositor
Cell constants a, b, c, α , β , γ	87.10Å 87.10Å 320.40Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	24.40 – 2.50 24.42 – 2.50	Depositor EDS
% Data completeness (in resolution range)	100.0 (24.40-2.50) 99.7 (24.42-2.50)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.09	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.73 (at 2.50Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.193 , 0.243 0.190 , 0.240	Depositor DCC
R_{free} test set	1292 reflections (5.27%)	DCC
Wilson B-factor (Å ²)	47.5	Xtriage
Anisotropy	0.488	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 40.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	3782	wwPDB-VP
Average B, all atoms (Å ²)	46.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.60% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 9CR

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	1.42	9/1781 (0.5%)	1.29	19/2409 (0.8%)
1	B	1.30	4/1793 (0.2%)	1.30	19/2428 (0.8%)
2	E	1.18	0/101	1.34	1/133 (0.8%)
2	F	1.30	0/84	1.74	2/110 (1.8%)
All	All	1.36	13/3759 (0.3%)	1.30	41/5080 (0.8%)

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	A	0	1

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	219	GLU	CG-CD	8.50	1.64	1.51
1	A	229	ASP	CB-CG	8.03	1.68	1.51
1	A	362	GLU	CG-CD	7.66	1.63	1.51
1	A	385	GLU	CD-OE1	6.08	1.32	1.25
1	A	219	GLU	CD-OE1	5.85	1.32	1.25
1	A	295	LYS	CD-CE	5.79	1.65	1.51
1	A	408	GLU	CG-CD	5.77	1.60	1.51
1	B	412	PHE	CE2-CZ	5.72	1.48	1.37
1	B	389	PHE	CB-CG	-5.62	1.41	1.51
1	B	384	GLU	CB-CG	-5.30	1.42	1.52
1	A	224	VAL	CB-CG1	5.27	1.64	1.52
1	A	269	GLU	CG-CD	5.22	1.59	1.51
1	B	281	GLU	CG-CD	5.19	1.59	1.51

All (41) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	395	ARG	NE-CZ-NH1	13.39	126.99	120.30
1	B	395	ARG	NE-CZ-NH2	-10.33	115.13	120.30
1	B	345	ARG	NE-CZ-NH2	-9.95	115.33	120.30
1	A	332	ARG	NE-CZ-NH2	-9.79	115.41	120.30
1	A	395	ARG	NE-CZ-NH1	8.92	124.76	120.30
1	B	400	ARG	NE-CZ-NH1	-8.67	115.97	120.30
1	A	276	ARG	NE-CZ-NH2	8.35	124.47	120.30
1	A	229	ASP	CB-CG-OD2	8.17	125.65	118.30
1	B	332	ARG	NE-CZ-NH2	-7.70	116.45	120.30
1	B	332	ARG	NE-CZ-NH1	7.50	124.05	120.30
1	B	345	ARG	NE-CZ-NH1	7.28	123.94	120.30
1	B	243	CYS	CA-CB-SG	-7.09	101.23	114.00
1	B	384	GLU	CB-CA-C	-6.87	96.66	110.40
1	A	332	ARG	NE-CZ-NH1	6.85	123.72	120.30
1	A	400	ARG	CG-CD-NE	-6.49	98.17	111.80
2	E	692	ARG	NE-CZ-NH1	6.36	123.48	120.30
1	B	211	ASP	N-CA-CB	-6.19	99.46	110.60
1	B	248	LYS	CD-CE-NZ	-6.14	97.57	111.70
1	B	281	GLU	OE1-CD-OE2	-6.12	115.95	123.30
1	A	290	ARG	NE-CZ-NH2	-6.10	117.25	120.30
1	B	253	LEU	CA-CB-CG	-5.97	101.56	115.30
1	A	282	LEU	CB-CG-CD1	5.80	120.87	111.00
1	A	290	ARG	NE-CZ-NH1	5.67	123.14	120.30
1	A	327	LEU	CB-CG-CD1	5.64	120.58	111.00
2	F	689	ILE	CB-CA-C	-5.54	100.52	111.60
1	A	233	ASP	CB-CG-OD2	-5.52	113.33	118.30
1	B	395	ARG	CD-NE-CZ	5.50	131.30	123.60
1	A	228	ILE	C-N-CA	5.47	135.38	121.70
1	A	228	ILE	CG1-CB-CG2	5.45	123.40	111.40
1	A	401	SER	N-CA-CB	-5.44	102.33	110.50
1	B	259	ARG	NE-CZ-NH1	5.37	122.98	120.30
1	B	415	LEU	CB-CG-CD2	-5.31	101.97	111.00
2	F	688	LYS	N-CA-C	-5.29	96.72	111.00
1	A	308	ARG	CG-CD-NE	-5.26	100.75	111.80
1	A	229	ASP	N-CA-CB	-5.19	101.26	110.60
1	B	353	ASP	CB-CG-OD1	5.18	122.96	118.30
1	A	338	LYS	CD-CE-NZ	-5.05	100.08	111.70
1	B	304	LEU	CB-CG-CD1	-5.03	102.46	111.00
1	A	231	TYR	CB-CG-CD1	5.01	124.00	121.00
1	B	415	LEU	CB-CG-CD1	5.01	119.52	111.00
1	A	395	ARG	NE-CZ-NH2	-5.00	117.80	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	233	ASP	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	1748	0	1786	42	1
1	B	1759	0	1792	40	1
2	E	100	0	105	4	0
2	F	84	0	93	5	0
3	A	22	0	27	2	0
3	B	22	0	27	7	0
4	A	28	0	0	11	0
4	B	17	0	0	3	0
4	E	1	0	0	0	0
4	F	1	0	0	2	0
All	All	3782	0	3830	93	1

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 12.

All (93) 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:229:ASP:HA	4:A:40:HOH:O	1.32	1.25
1:A:210:ASN:HB3	4:A:46:HOH:O	1.48	1.13
2:F:688:LYS:HB2	4:F:31:HOH:O	1.47	1.11
1:A:234:ALA:HB1	4:A:33:HOH:O	1.52	1.06
1:A:381:ARG:HG2	4:A:43:HOH:O	1.68	0.94
1:A:381:ARG:CG	4:A:43:HOH:O	2.20	0.90
1:A:210:ASN:CB	4:A:46:HOH:O	2.11	0.89
1:B:255:GLU:OE2	1:B:255:GLU:HA	1.73	0.87
1:A:255:GLU:HG3	4:A:38:HOH:O	1.78	0.83
1:B:431:ASN:ND2	1:B:431:ASN:O	2.14	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:202:9CR:H19	3:B:202:9CR:C8	2.13	0.77
2:F:690:LEU:HD13	2:F:694:LEU:HD12	1.67	0.76
1:B:236:LYS:O	1:B:238:PRO:HD3	1.86	0.75
1:B:227:LYS:NZ	1:B:227:LYS:HB3	2.04	0.73
1:A:228:ILE:HD13	1:A:229:ASP:N	2.04	0.72
3:B:202:9CR:H25	3:B:202:9CR:O2	1.89	0.71
1:A:295:LYS:H	1:A:295:LYS:HE2	1.56	0.70
1:B:259:ARG:HH11	1:B:259:ARG:HG3	1.57	0.69
1:A:400:ARG:NH1	4:A:15:HOH:O	2.25	0.69
2:E:690:LEU:HD22	2:E:694:LEU:CD1	2.23	0.69
1:B:281:GLU:OE1	1:B:400:ARG:HD3	1.95	0.66
1:B:235:GLN:O	1:B:236:LYS:O	2.13	0.66
1:A:318:THR:HG23	4:A:36:HOH:O	1.98	0.63
1:A:318:THR:CG2	4:A:36:HOH:O	2.46	0.62
2:F:690:LEU:HD13	2:F:694:LEU:CD1	2.29	0.62
1:B:361:GLN:OE1	1:B:361:GLN:HA	2.00	0.61
1:B:281:GLU:OE1	1:B:400:ARG:HA	2.01	0.61
1:B:266:LEU:O	1:B:267:PRO:C	2.40	0.59
1:A:230:THR:O	1:A:231:TYR:HB2	2.02	0.59
1:B:218:LEU:HG	1:B:339:THR:OG1	2.02	0.59
1:A:283:LEU:HB3	3:A:201:9CR:H11	1.86	0.58
1:B:236:LYS:O	1:B:238:PRO:CD	2.52	0.58
1:A:230:THR:O	1:A:231:TYR:CB	2.52	0.58
1:B:226:PRO:HD2	4:B:37:HOH:O	2.04	0.57
1:A:319:ILE:HD11	1:A:402:ILE:HG23	1.85	0.57
2:E:690:LEU:HD22	2:E:694:LEU:HD12	1.87	0.56
1:A:231:TYR:HA	1:A:303:GLY:O	2.06	0.55
1:B:227:LYS:HB3	1:B:227:LYS:HZ1	1.71	0.55
1:B:378:THR:CG2	4:B:29:HOH:O	2.56	0.54
1:A:272:VAL:HB	2:E:690:LEU:HD13	1.90	0.53
1:A:228:ILE:HD13	1:A:228:ILE:C	2.27	0.53
1:B:312:HIS:HE1	1:B:321:ASP:OD1	1.91	0.52
1:A:421:ILE:HG23	1:A:425:LEU:HD23	1.91	0.52
1:A:280:ASN:O	1:A:284:ILE:HD12	2.11	0.51
1:A:289:HIS:O	1:A:292:ILE:HD12	2.11	0.50
1:A:295:LYS:HE2	1:A:295:LYS:N	2.25	0.50
1:B:312:HIS:CD2	1:B:317:GLY:HA3	2.47	0.50
1:A:215:GLU:CD	1:A:215:GLU:H	2.16	0.49
2:E:690:LEU:HD22	2:E:694:LEU:HD11	1.93	0.49
1:B:424:PHE:HZ	2:F:690:LEU:HD23	1.76	0.49
1:A:228:ILE:CD1	1:A:228:ILE:C	2.81	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:290:ARG:HH22	3:A:201:9CR:C15	2.27	0.48
1:A:378:THR:HG21	1:A:389:PHE:HB2	1.95	0.48
1:B:378:THR:HG22	1:B:379:LYS:N	2.28	0.48
1:A:219:GLU:OE1	1:A:219:GLU:HA	2.15	0.47
1:A:213:PRO:HB2	1:A:215:GLU:OE2	2.16	0.46
1:A:415:LEU:O	1:A:416:ILE:C	2.53	0.46
1:B:412:PHE:CE1	1:B:416:ILE:HD11	2.51	0.46
1:B:259:ARG:NH1	1:B:259:ARG:HG3	2.29	0.46
1:A:249:GLN:HA	1:A:252:THR:HG23	1.98	0.45
3:B:202:9CR:C8	3:B:202:9CR:C18	2.89	0.45
1:A:318:THR:HG22	4:A:36:HOH:O	2.14	0.45
1:B:389:PHE:CZ	1:B:393:LEU:HD11	2.52	0.45
1:A:230:THR:O	1:A:231:TYR:CD2	2.70	0.44
1:A:429:LEU:O	1:A:430:GLU:HB2	2.17	0.44
1:B:236:LYS:HD2	4:B:32:HOH:O	2.17	0.44
1:A:337:ASP:OD2	1:A:340:GLU:HG3	2.17	0.44
1:B:350:PHE:CE2	1:B:366:LEU:HD13	2.52	0.44
1:A:210:ASN:HB3	1:A:211:ASP:H	1.66	0.44
1:B:300:LEU:N	1:B:300:LEU:CD1	2.80	0.43
1:A:269:GLU:HA	1:A:269:GLU:OE1	2.19	0.43
1:A:210:ASN:O	1:A:211:ASP:CB	2.66	0.43
1:A:218:LEU:HG	1:A:339:THR:OG1	2.19	0.43
1:B:412:PHE:CE1	1:B:416:ILE:CD1	3.02	0.42
3:B:202:9CR:H8	3:B:202:9CR:H10	1.78	0.42
1:B:268:LEU:O	1:B:272:VAL:HG23	2.20	0.42
1:B:229:ASP:N	1:B:229:ASP:OD2	2.52	0.42
1:B:249:GLN:HG3	3:B:202:9CR:O1	2.20	0.42
1:A:394:LEU:HA	1:A:394:LEU:HD12	1.90	0.42
1:B:235:GLN:C	1:B:236:LYS:O	2.57	0.42
2:F:691:HIS:ND1	4:F:31:HOH:O	2.37	0.41
1:A:221:GLU:OE2	1:A:345:ARG:NH1	2.47	0.41
1:B:284:ILE:HA	1:B:287:PHE:CE2	2.55	0.41
1:B:237:ASP:HA	1:B:238:PRO:HD2	1.83	0.41
1:B:313:GLN:HE21	1:B:313:GLN:HB2	1.60	0.41
1:B:365:GLN:HB2	1:B:365:GLN:HE21	1.63	0.41
1:B:260:ILE:O	1:B:261:PRO:C	2.59	0.41
1:B:267:PRO:O	1:B:270:ASP:HB2	2.21	0.41
1:B:290:ARG:HH22	3:B:202:9CR:C15	2.33	0.41
1:A:415:LEU:O	1:A:418:ASP:HB2	2.22	0.40
1:B:400:ARG:HH11	1:B:400:ARG:HD3	1.51	0.40
1:B:246:ALA:HB2	3:B:202:9CR:C12	2.52	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:410:LEU:HA	1:B:410:LEU:HD23	1.80	0.40

All (1) 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:A:230:THR:O	1:B:231:TYR:O[6_655]	2.07	0.13

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	219/230 (95%)	205 (94%)	11 (5%)	3 (1%)	13	23
1	B	222/230 (96%)	206 (93%)	11 (5%)	5 (2%)	7	11
2	E	10/15 (67%)	9 (90%)	0	1 (10%)	1	0
2	F	8/15 (53%)	5 (62%)	2 (25%)	1 (12%)	0	0
All	All	459/490 (94%)	425 (93%)	24 (5%)	10 (2%)	8	12

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	229	ASP
1	B	236	LYS
1	B	420	PRO
2	F	689	ILE
1	A	231	TYR
2	E	697	GLY
1	B	431	ASN
1	A	418	ASP
1	B	296	ASP

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Mol	Chain	Res	Type
1	B	421	ILE

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	188/197 (95%)	161 (86%)	27 (14%)	4	7
1	B	188/197 (95%)	156 (83%)	32 (17%)	2	4
2	E	11/14 (79%)	7 (64%)	4 (36%)	0	0
2	F	9/14 (64%)	8 (89%)	1 (11%)	7	13
All	All	396/422 (94%)	332 (84%)	64 (16%)	3	5

All (64) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	210	ASN
1	A	218	LEU
1	A	219	GLU
1	A	228	ILE
1	A	232	ILE
1	A	236	LYS
1	A	248	LYS
1	A	252	THR
1	A	259	ARG
1	A	272	VAL
1	A	282	LEU
1	A	295	LYS
1	A	300	LEU
1	A	302	THR
1	A	318	THR
1	A	327	LEU
1	A	335	LYS
1	A	361	GLN
1	A	376	GLU
1	A	378	THR

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Mol	Chain	Res	Type
1	A	381	ARG
1	A	394	LEU
1	A	395	ARG
1	A	400	ARG
1	A	418	ASP
1	A	424	PHE
1	A	429	LEU
1	B	210	ASN
1	B	218	LEU
1	B	222	LEU
1	B	227	LYS
1	B	229	ASP
1	B	236	LYS
1	B	252	THR
1	B	255	GLU
1	B	259	ARG
1	B	265	GLU
1	B	282	LEU
1	B	293	MET
1	B	300	LEU
1	B	310	SER
1	B	313	GLN
1	B	327	LEU
1	B	357	LEU
1	B	371	TYR
1	B	376	GLU
1	B	378	THR
1	B	380	SER
1	B	395	ARG
1	B	400	ARG
1	B	401	SER
1	B	405	LYS
1	B	407	LEU
1	B	415	LEU
1	B	419	GLN
1	B	424	PHE
1	B	428	MET
1	B	430	GLU
1	B	431	ASN
2	E	688	LYS
2	E	690	LEU
2	E	693	LEU

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Mol	Chain	Res	Type
2	E	695	GLN
2	F	692	ARG

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

Mol	Chain	Res	Type
1	A	312	HIS
1	B	209	ASN
1	B	216	GLN
1	B	312	HIS
1	B	313	GLN
1	B	365	GLN
2	E	695	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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

2 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	9CR	A	201	-	19,22,22	2.44	5 (26%)	26,30,30	2.72	11 (42%)
3	9CR	B	202	-	19,22,22	2.50	6 (31%)	26,30,30	3.08	12 (46%)

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	9CR	A	201	-	-	0/13/32/32	0/1/1/1
3	9CR	B	202	-	-	0/13/32/32	0/1/1/1

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	202	9CR	C1-C6	-3.81	1.48	1.53
3	B	202	9CR	C5-C6	2.28	1.38	1.34
3	B	202	9CR	C14-C13	3.34	1.39	1.35
3	A	201	9CR	C14-C13	3.83	1.40	1.35
3	B	202	9CR	C7-C8	4.07	1.45	1.33
3	A	201	9CR	C7-C8	4.19	1.46	1.33
3	A	201	9CR	C11-C12	4.85	1.47	1.34
3	A	201	9CR	C10-C9	4.87	1.42	1.35
3	B	202	9CR	C11-C12	4.89	1.47	1.34
3	A	201	9CR	C5-C6	5.42	1.43	1.34
3	B	202	9CR	C10-C9	6.48	1.44	1.35

All (23) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	202	9CR	C11-C10-C9	-8.15	115.68	127.31
3	A	201	9CR	C11-C10-C9	-7.53	116.56	127.31
3	B	202	9CR	C7-C8-C9	-6.00	117.19	126.21
3	B	202	9CR	C18-C5-C6	-6.00	117.80	124.51
3	A	201	9CR	C7-C8-C9	-5.90	117.35	126.21
3	A	201	9CR	C19-C9-C10	-4.89	116.08	122.92
3	B	202	9CR	C17-C1-C6	-4.05	103.74	110.31
3	B	202	9CR	C19-C9-C10	-3.61	117.86	122.92
3	A	201	9CR	C17-C1-C6	-3.38	104.82	110.31
3	B	202	9CR	C10-C11-C12	-3.10	113.74	123.23
3	A	201	9CR	C12-C13-C14	-2.71	111.84	118.74
3	B	202	9CR	C16-C1-C6	-2.69	105.94	110.31

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	201	9CR	C10-C11-C12	-2.67	115.05	123.23
3	B	202	9CR	C3-C4-C5	-2.29	109.84	113.78
3	A	201	9CR	C8-C7-C6	-2.06	121.48	127.25
3	A	201	9CR	C11-C12-C13	-2.04	120.67	126.42
3	B	202	9CR	C8-C7-C6	-2.01	121.61	127.25
3	A	201	9CR	C2-C3-C4	2.12	116.40	111.34
3	B	202	9CR	C20-C13-C12	2.12	121.48	118.10
3	A	201	9CR	C20-C13-C12	2.17	121.56	118.10
3	B	202	9CR	C18-C5-C4	2.26	117.73	113.45
3	A	201	9CR	C19-C9-C8	4.21	124.80	118.10
3	B	202	9CR	C19-C9-C8	5.00	126.06	118.10

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	201	9CR	2	0
3	B	202	9CR	7	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	221/230 (96%)	-0.19	3 (1%) 75 76	30, 42, 59, 77	0
1	B	224/230 (97%)	-0.21	7 (3%) 49 52	32, 45, 63, 85	0
2	E	12/15 (80%)	1.42	3 (25%) 1 0	54, 67, 95, 99	0
2	F	10/15 (66%)	0.77	2 (20%) 1 1	66, 70, 91, 94	0
All	All	467/490 (95%)	-0.14	15 (3%) 48 51	30, 44, 68, 99	0

All (15) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	E	698	SER	9.5
2	E	697	GLY	5.0
2	F	697	GLY	4.5
2	F	696	GLU	3.6
1	A	227	LYS	3.5
1	B	432	PRO	3.3
1	B	209	ASN	3.1
1	B	282	LEU	2.6
2	E	696	GLU	2.6
1	B	229	ASP	2.4
1	B	283	LEU	2.4
1	B	210	ASN	2.2
1	B	284	ILE	2.1
1	A	282	LEU	2.0
1	A	236	LYS	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, 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	LLDF	B-factors(\AA^2)	Q<0.9
3	9CR	B	202	22/22	0.97	0.16	0.13	38,42,49,52	0
3	9CR	A	201	22/22	0.97	0.14	0.06	39,43,48,51	0

6.5 Other polymers [i](#)

There are no such residues in this entry.